

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:11 ; Search time 100.13 Seconds  
(without alignments)  
1022.800 Million cell updates/sec

Title: US-09-771-382-10  
Perfect score: 2988  
Sequence: 1 MNKIVRIIMNSALNMAWVVS.....TASGNSRGHFGASASVGYQW 592

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_plant:\*  
10: sp\_prodent:\*  
11: sp\_virus:\*  
12: sp\_vertebrate:\*  
13: sp\_unclassified:\*  
14: sp\_virus:\*  
15: sp\_bacteriap:\*  
16: sp\_archaeap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2988	100.0	592	16	09JQW4		09jpw4 neisseria m
2	2821	94.4	592	2	09JPS9		09jps9 neisseria m
3	2779	93.0	592	2	093QY2		093qy2 neisseria m
4	2725	91.2	600	2	09JPS5		09jps5 neisseria m
5	2721.5	91.1	595	2	09JPH0		09jph0 neisseria m
6	2720.5	91.0	599	2	09JPS8		09jps8 neisseria m
7	2719	91.0	598	2	09JPR7		09jpr7 neisseria m
8	2637.5	88.3	589	2	09JPI0		09jpi0 neisseria m
9	2626.5	87.9	589	2	093QY1		093qy1 neisseria m
10	2587.5	86.6	599	2	09JPR8		09jpr8 neisseria m
11	2553	85.4	594	2	09JPI3		09jpi3 neisseria m
12	2552	85.4	594	2	09JPR7		09jpr7 neisseria m
13	2549	85.3	594	2	09JPS2		09jps2 neisseria m
14	2541	85.0	598	2	09JPR9		09jpr9 neisseria m
15	2533	84.8	594	2	093QY4		093qy4 neisseria m
16	2530	84.7	590	2	09JPS3		09jps3 neisseria m

17	2530	84.7	598	2	09JPT0		09jpt0 neisseria m
18	2524	84.5	598	2	09JPS0		09jps0 neisseria m
19	2521	84.4	598	2	093QY5		093qy5 neisseria m
20	2502	83.7	600	2	09JPS6		09jps6 neisseria m
21	2464.5	82.5	591	16	09JRI8		09jri8 neisseria m
22	2460.5	82.3	591	2	09JPS7		09jps7 neisseria m
23	2445.5	81.8	591	2	093QY3		093qy3 neisseria m
24	2443	81.8	592	2	09JQF0		09jqf0 neisseria m
25	2250.5	75.3	526	2	09JPS4		09jps4 neisseria m
26	2248.5	75.0	530	2	09JPS1		09jps1 neisseria m
27	1135	38.0	1098	2	048152		048152 haemophilus
28	1132.5	37.9	2353	2	P71401		P71401 haemophilus
29	441.5	14.8	1299	16	09F3X6		09f3x6 pasteurella
30	410.5	13.7	2059	16	09PD50		09pd50 xylella fas
31	394.5	13.2	1190	16	09PC04		09pc04 xylella fas
32	375.5	12.6	1107	2	09F2D8		09f2d8 salmonella
33	365	12.2	2712	16	09F3X5		09f3x5 pasteurella
34	267.5	9.0	1291	16	092KQ7		092kq7 rhizobium m
35	261.5	8.8	1953	16	098HJ2		098hj2 rhizobium l
36	252	8.4	1004	16	09PD63		09pd63 xylella fas
37	233.5	7.8	1265	2	09FDA0		09fda0 xanthomonas
38	226.5	7.6	989	2	09XD84		09xd84 escherichia
39	224.5	7.5	1557	2	09RNI2		09rni2 haemophilus
40	220.5	7.4	3930	16	098E20		098e20 rhizobium l
41	219	7.3	1018	16	09HWU6		09hwu6 pseudomonas
42	214	7.2	873	2	091960		091960 moraxella c
43	214	7.2	2065	2	093DC7		093dc7 yersinia en
44	212	7.1	1417	16	09HVN6		09hvn6 pseudomonas
45	211.5	7.1	892	2	09KX38		09kx38 moraxella c

#### ALIGNMENTS

RESULT 1  
09JQW4 PRELIMINARY; PRT; 592 AA.  
AC 09JQW4:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PUTATIVE SURFACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).  
GN NMA1200 OR GNA992.  
OS Neisseria meningitidis (serogroup A), and  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699, 487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE-20222556; PubMed-10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491".  
RL Nature 404:502-506(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-205900, B2133, F6124, AND 22491;  
RX MEDLINE-20175756; PubMed-10710308;  
RA Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brocker M., Hundt E., Knapp B., Blatt E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing".

RL Science 287:1816-1820(2000).  
 DR EMBL: AL162755; CAB84461.1; -  
 DR EMBL: AF226357; AAF42506.1; -  
 DR EMBL: AF226365; AAF42514.1; -  
 DR EMBL: AF226373; AAF42522.1; -  
 DR EMBL: AF226386; AAF42535.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 100.0%; Score 2988; DB 16; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 5, 6e-120;  
 Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIRIRINMSALNAMAWESELTNRNHTKRASATVKTAVLTLLFATVQANATDEDEEEL 60  
 DB 1 MNKIRIRINMSALNAMAWESELTNRNHTKRASATVKTAVLTLLFATVQANATDEDEEEL 60  
 QY 61 ESVQSVVSGSIQASMEGSELEFISLMTNDSKEFVDPYIVVTLKADNLIKONTNENT 120  
 DB 61 ESVQSVVSGSIQASMEGSELEFISLMTNDSKEFVDPYIVVTLKADNLIKONTNENT 120  
 QY 121 NASFTYSLKDDLTGLINVTETKLSFGANGKKNVITSDTGKLNFAKFTAGNGDTVHLN 180  
 DB 121 NASFTYSLKDDLTGLINVTETKLSFGANGKKNVITSDTGKLNFAKFTAGNGDTVHLN 180  
 QY 181 GIGSTLFDTLGASASHVDAGNOSTHYTRAASIKDVLNAGNINIKGVGTGGSENVDF 240  
 DB 181 GIGSTLFDTLGASASHVDAGNOSTHYTRAASIKDVLNAGNINIKGVGTGGSENVDF 240  
 QY 241 VRIYDVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVKEKDGKLVYGGKGEENGSS 300  
 DB 241 VRIYDVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVKEKDGKLVYGGKGEENGSS 300  
 QY 301 TDBEEGLVTAKEVIDANVAKGWRMKTITANGOGADKFEIVTSGTNVTFASGKTATV 360  
 DB 301 TDBEEGLVTAKEVIDANVAKGWRMKTITANGOGADKFEIVTSGTNVTFASGKTATV 360  
 QY 361 SKDOGNITVAVDVNVDALNVNOLNSGMNLDKRAVAGSSGKVISGNVSPSKKMDTV 420  
 DB 361 SKDOGNITVAVDVNVDALNVNOLNSGMNLDKRAVAGSSGKVISGNVSPSKKMDTV 420  
 QY 421 NINAGNNIEISRKNKIDDIATSMAPOFSSVSLGAGADPTLSVDEGALNVGSKDANKPV 480  
 DB 421 NINAGNNIEISRKNKIDDIATSMAPOFSSVSLGAGADPTLSVDEGALNVGSKDANKPV 480  
 QY 481 RITVNAVPGVKGEDVTNVAOLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKS 540  
 DB 481 RITVNAVPGVKGEDVTNVAOLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKS 540  
 QY 541 MMAIGGGTGRGEAGYAIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 592  
 DB 541 MMAIGGGTGRGEAGYAIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 592

RESULT 2  
 Q9JPS9 PRELIMINARY; PRT; 592 AA.  
 AC Q9JPS9;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA92.  
 GN GNA92.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=860800;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masigiani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Grais D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226361; AAF42510.1; -  
 SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 94.4%; Score 2821; DB 2; Length 592;  
 Best Local Similarity 94.9%; Pred. No. 7, 2e-113;  
 Matches 564; Conservative 9; Mismatches 17; Indels 4; Gaps 2;

QY 1 MNKIRIRINMSALNAMAWESELTNRNHTKRASATVKTAVLTLLFATVQANATDEDEEEL 60  
 DB 1 MNKIRIRINMSALNAMAWESELTNRNHTKRASATVKTAVLTLLFATVQANATDEDEEEL 60  
 QY 61 ESVQSVVSGSIQASMEGSELEFISLMTNDSKEFVDPYIVVTLKADNLIKONTNENT 120  
 DB 61 ESVQSVVSGSIQASMEGSELEFISLMTNDSKEFVDPYIVVTLKADNLIKONTNENT 120  
 QY 121 NASFTYSLKDDLTGLINVTETKLSFGANGKKNVITSDTGKLNFAKFTAGNGDTVHLN 180  
 DB 121 NASFTYSLKDDLTGLINVTETKLSFGANGKKNVITSDTGKLNFAKFTAGNGDTVHLN 180  
 QY 181 GIGSTLFDTLGASASHVDAGNOST--HYTRAASIKDVLNAGNINIKGVGTGGSENV 238  
 DB 181 GIGSTLFDTLGASASHVDAGNOST--HYTRAASIKDVLNAGNINIKGVGTGGSENV 238  
 QY 239 DVEYTDVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVKEKDGKLVYGGKGEENG 298  
 DB 239 DVEYTDVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVKEKDGKLVYGGKGEENG 298  
 QY 299 SFTBEGGLVTAKEVIDANVAKGWRMKTITANGOGADKFEIVTSGTNVTFASGKTATV 358  
 DB 299 SFTBEGGLVTAKEVIDANVAKGWRMKTITANGOGADKFEIVTSGTNVTFASGKTATV 358  
 QY 359 TVSKDDGNITVAVDVNVDALNVNOLNSGMNLDKRAVAGSSGKVISGNVSPSKKMDTV 418  
 DB 359 TVSKDDGNITVAVDVNVDALNVNOLNSGMNLDKRAVAGSSGKVISGNVSPSKKMDTV 418  
 QY 419 TVNINAGNNIEISRKNKIDDIATSMAPOFSSVSLGAGADPTLSVDEGALNVGSKDANK 478  
 DB 419 TVNINAGNNIEISRKNKIDDIATSMAPOFSSVSLGAGADPTLSVDEGALNVGSKDANK 478  
 QY 479 PVRTTNAVPGVKGEDVTNVAOLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPK 538  
 DB 479 PVRTTNAVPGVKGEDVTNVAOLKGVANLNRRIDNVGNARAGIAQAIAATAGLVQAYLPK 538  
 QY 539 KSMMAIGGGTGRGEAGYAIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 592  
 DB 539 KSMMAIGGGTGRGEAGYAIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 592

RESULT 3  
 Q930Y2 PRELIMINARY; PRT; 592 AA.  
 AC Q930Y2;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H41;  
 RA Peak I.R., Srikantha V., Dieckelman M., Moxon R., Jennings M.P.;



"Identification and characterization of a gene encoding a novel outer membrane protein of *Neisseria meningitidis*.";  
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157609; AAK68870.1; -  
 SQ SEQUENCE 592 AA; 61869 MW; F9403A0B4A1BEEA7 CRC64;

Query Match 93.0%; Score 2779; DB 2; Length 592;  
 Best Local Similarity 93.9%; Pred. No. 4.4e-111;  
 Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

QY 1 MNKIYRIIWSALNANWAVSELTNRNHTKASATVTAVALATLLFAVQANATDEDEEEL 60  
 DB 1 MNKIYRIIWSALNANWAVSELTNRNHTKASATVTAVALATLLFAVQANATDEDEEEL 60  
 QY 61 ESVORSVVGSIQASMEGSELETSLSMTNDSEKFEVPIYVTLKAGDNLIKONTNENT 120  
 DB 61 ESVORSVVGSIQASMEGSELETSLSMTNDSEKFEVPIYVTLKAGDNLIKONTNENT 120  
 QY 121 NASFTYSLKLDGLINVEETKLSFGANGKKVNTISDTKGLNFAKETAGTNGDTVHLN 180  
 DB 121 NASFTYSLKLDGLINVEETKLSFGANGKKVNTISDTKGLNFAKETAGTNGDTVHLN 180  
 QY 181 GIGSTLDTLAGSSASHVDAGNOST--HYTRAASIKDYLNAGWNKGVKGTGTTGQSENV 238  
 DB 181 GIGSTLDTLAGSSASHVDAGNOST--HYTRAASIKDYLNAGWNKGVKGTGTTGQSENV 238  
 QY 239 DEVTYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSYIKKDGKLTGKKGENG 298  
 DB 239 DEVTYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSYIKKDGKLTGKKGENG 298  
 QY 299 SSTBEGELVYAKVEYIDAVNKAEMKTTTANGOTGOADKFEVTSGTNVFPASGKTGA 358  
 DB 299 SSTBEGELVYAKVEYIDAVNKAEMKTTTANGOTGOADKFEVTSGTNVFPASGKTGA 358  
 QY 359 TSVKDDQGNITVMTDVNVDALNVQNLQNSGMNLSKAVASSGKVIISGNVSPSKGKDE 418  
 DB 359 TSVKDDQGNITVMTDVNVDALNVQNLQNSGMNLSKAVASSGKVIISGNVSPSKGKDE 418  
 QY 419 TVNINAGNINIELSRNGKIDIDATSMAPOFSSVSLGAGADAPLTVSDDEGALNVGSKDANK 478  
 DB 419 TVNINAGNINIELSRNGKIDIDATSMAPOFSSVSLGAGADAPLTVSDDEGALNVGSKDANK 478  
 QY 479 PVRTINVAPEGEGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIATAGLVAAYLP 538  
 DB 479 PVRTINVAPEGEGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIATAGLVAAYLP 538  
 QY 539 KSMALIGGTYRGEAGYALGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 592  
 DB 539 KSMALIGGTYRGEAGYALGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 592

## RESULT 4

Q9JPS5 PRELIMINARY; PRT; 600 AA.  
 AC Q9JPS5;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS *Neisseria meningitidis*.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scariato V., Mastignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT *Meningococcus* by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226372; AAF42521.1; -  
 SQ SEQUENCE 600 AA; 62606 MW; 13C35F1C46392524 CRC64;

Query Match 91.2%; Score 2725; DB 2; Length 600;  
 Best Local Similarity 91.3%; Pred. No. 8.8e-109;  
 Matches 549; Conservative 13; Mismatches 29; Indels 10; Gaps 4;

QY 1 MNKIYRIIWSALNANWAVSELTNRNHTKASATVTAVALATLLFAVQANATDEDEEEL 60  
 DB 1 MNKIYRIIWSALNANWAVSELTNRNHTKASATVTAVALATLLFAVQANATDEDEEEL 60  
 QY 61 ESVORSV-VGSIQASMEGSELETSLSMTNDSEKFEVPIYVTLKAGDNLIKON 114  
 DB 61 ESVORSV-VGSIQASMEGSELETSLSMTNDSEKFEVPIYVTLKAGDNLIKON 114  
 QY 115 ---NTNENTNASSFTYSLKLDLTGLINVEETKLSFGANGKKVNTISDTKGLNFAKETAGT 179  
 DB 120 NTNENTNENTNASSFTYSLKLDLTGLINVEETKLSFGANGKKVNTISDTKGLNFAKETAGT 179  
 QY 172 NGDPTVHLNGIGSTLDTLAGSSASHVDAGNOSTHYTRAASIKDYLNAGWNKGVKGTST 231  
 DB 180 NGDPTVHLNGIGSTLDTLAGSSASHVDAGNOSTHYTRAASIKDYLNAGWNKGVKGTST 239  
 QY 232 TGQSENVDVFRITDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSYIKKDGKLTG 291  
 DB 240 TGQSENVDVFRITDYVEFLSADTKTTTVNVEKDKGKTEVKGAKTSYIKKDGKLTG 299  
 QY 292 KKGENGSTDEGELVYAKVEYIDAVNKAEMKTTTANGOTGOADKFEVTSGTNVTPA 351  
 DB 300 KKGENGSTDEGELVYAKVEYIDAVNKAEMKTTTANGOTGOADKFEVTSGTNVTPA 359  
 QY 352 SKGTTATVPSKDDQGNITVMTDVNVDALNVQNLQNSGMNLSKAVASSGKVIISGNVSP 411  
 DB 360 SKGTTATVPSKDDQGNITVMTDVNVDALNVQNLQNSGMNLSKAVASSGKVIISGNVSP 419  
 QY 412 SKGKDETVNINAGNINIELSRNGKIDIDATSMAPOFSSVSLGAGADAPLTVSDDEGALNV 471  
 DB 420 SKGKDETVNINAGNINIELSRNGKIDIDATSMAPOFSSVSLGAGADAPLTVSDDEGALNV 479  
 QY 472 GSKDANKPVRTINVAPEGEGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIATAGL 531  
 DB 480 GSKDANKPVRTINVAPEGEGDVTVNAOLKGYAONLNRRIDVNDGNARAGIAQAIATAGL 539  
 QY 532 VQAYLPKSMALIGGTYRGEAGYALGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 591  
 DB 540 VQAYLPKSMALIGGTYRGEAGYALGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 599

## RESULT 5

Q9JPH0 PRELIMINARY; PRT; 595 AA.  
 AC Q9JPH0;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS *Neisseria meningitidis*.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=528, AND 1000;

RX MEDLINE=20175756; Pubmed=10710308;  
 RA Pizzia M., Scariatto V., Masiangiro V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolotti E., Capocchi B.,  
 RA Galeotti C.L., Luzzi E., Mamelli R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Scorn E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettehn H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.D., Granoft D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226360; AAF42509.1; -;  
 DR EMBL: AF226365; AAF42505.1; -;  
 SO SEQUENCE 395 AA; 62120 MW; 8212096380142BFC CRC64;

Query Match	91.1%;	Score 2721.5;	DB 2;	Length 595;
Best Local Similarity	91.6%;	Pred. No. 1.2e-108;		
Matches 546;	Conservative 14;	Mismatches 31;	Indels 5;	Gaps 3

Db	1	MNKIRIIMNSALNAWYVSELTRNHTKRASAFETAVLATLLEFATQANATDDEDEL	60
Qy	61	ESVQRS-VGSIQASMGSGLEF---ISLSMTDSKEFPDYIVTLKAGDNLIKONT	116
Db	61	BPVNSALVLOFMDIKDEGNGEIESTGIGMSIYYDHNHTLHG-ATYLLKAGDNLIKONT	119
Qy	117	NENTMASSFTYSLKKDLTGLINLETKEKLSFGANKKNITISDPKGLNFAKETAGTNDTT	176
Db	120	DENTMASSFTYSLKKDLTDLTSVTEELSTEGANCKKNITISDPKGLNFAKTACTIONDTT	179
Qy	177	VHLNGISGTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDYLNAGWNIKGVKGTSGTGOSE	236
Db	180	VHLNGISGTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDYLNAGWNIKGVKGTSGTGOSE	239
Qy	237	NVDFPRITDYEFESADPKTTTAVVESDNCKRFEVIGKATSVIKRDKKILVTKRKE	286
Db	240	NVDFPRITDYEFESADPKTTTAVVESDNCKRFEVIGKATSVIKRDKKILVTKRKE	299
Qy	297	NGSSTDEGEGLVTAKEVIDA VNKAGWRKTTTANGQTQADKFEPTVSGTNVTFASGKT	356
Db	300	NGSSTDEGEGLVTAKEVIDA VNKAGWRKTTTANGQTQADKFEPTVSGTNVTFASGKT	359
Qy	357	TATVSKDDOQGITWYKYDVNVGDALANVOLONSGNNLDSKAVAGSSGKVISGNSPSRSGKM	416
Db	360	TATVSKDDOQGITWYKYDVNVGDALANVOLONSGNNLDSKAAVAGSSGKVISGNSPSRSGKM	419
Qy	417	DETVINAGNNIEISRNGKNIDITASMAPORSSVSLGADADAPLTSLVDDDEGALVWSKDA	476
Db	420	DETVINAGNNIEITRNCKNIDITASMPORSSVSLGADADAPLTSLVDDDEGALVWSKDA	479
Qy	477	NKPVKITWAVAGVKEGDTYNVLAOLKGVAAQLNINRVIDNVGNARAGIAQAATAAGLYOAYL	536
Db	480	NKPVKITWAVAGVKEGDTYNVLAOLKGVAAQLNINRVIDNVGNARAGIAQAATAAGLYOAYL	539
Qy	537	PKCSMMAIGGGTGTGEGALYATGYSISIDSGMWIIKKTGASGNSRCHFPASASVYGOW	592
Db	540	PKCSMMAIGGGTGTGEGALYATGYSISIDSGMWIIKKTGASGNSRCHFPASASVYGOW	595

RESULT	6		
Q9JPS8			
ID	Q9JPS8	PRELIMINARY;	PTI; 599 AA.
AC	Q9JPS8;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GMA992.		
GN	GMA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria		
OX	NCBI_TaxID=487;		

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A22;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecehi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226364; AAF42513.1; -  
 SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF778E9 CRC64;

Query Match	91.0%;	Score 2720.5;	DB 2;	Length 599;
Best Local Similarity	90.9%;	Pred. No. 1.4e-108;		
Matches 549;	Conservative 15;	Mismatches 23;	Indels 17;	Gaps 4;

QY	1	MNKYIRIIMNLANWAAVSELTENHNRKRAAVKTVLTLTLLFAVQANADDEEEL	60
Db	1	MNKYIRIIMNLANWAAVSELTENHNRKRAAVKTVLTLTLLFAVQANADDEEEL	60
QY	61	ESVOR-SVVGSIQASMEGSELETTISLMTNDS-----KEFVDPYIVYTLKAGNLIK	112
Db	61	EPVKTAVLVISFRDKEGTEGEKE-----VTEDSIMGVEYDEKCEVLKAGITTLKAGNLIK	115
QY	113	KQ-----NNENTNASSPEYTSILKKDLTGIIIVETREKXISFGANGKKVNIISPTKGLNFAKET	168
Db	116	KQNTDENTENTNASSPEYTSILKKDLTLTVEYEEKISFGANGKKVNIISPTKGLNFAKET	175
QY	169	AGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDYVLAGNNIKGYT	228
Db	176	AGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDYVLAGNNIKGYT	235
QY	229	GSTTGOSENNDFVRYTYTVEFLSADPTKTTYTVNYESKDNKRETEYKIGARTSVYKENDGL	288
Db	236	GSTTGOSENNDFVRYTYTVEFLSADPTKTTYTVNYESKDNKRETEYKIGARTSVYKENDGL	295
QY	289	VTGKKGKGENSGSTDEGEGLYTAKFVDAVNAKKAGRMKTTTANQOTQADKFEFVTSGETV	348
Db	296	VTGKKGKGENSGSTDEGEGLYTAKFVDAVNAKKAGRMKTTTANQOTQADKFEFVTSGETV	355
QY	349	TFASGKGTATVASKDDGNTTVMYDVNVGDLNVNQLQNSGMNLDKSAVAGSSGKVIISGN	408
Db	356	TFASGKGTATVASKDDGNTTVMYDVNVGDLNVNQLQNSGMNLDKSAVAGSSGKVIISGN	415
QY	409	VSPSKGKADDEVYVNIAGNNIEISNGKNIDIASMAPOFSSVSLGAGADAPTLTSLVDDGA	468
Db	416	VSPSKGKADDEVYVNIAGNNIEITNGKNIDIASMTQOFSSVSLGAGADAPTLTSLVDDGA	475
QY	469	LNVGSKDKANKPVRTITNVAPGVKEEDVYVNAOLKGVAAONLNRRIDNDVGNARAGIAOLAAT	528
Db	476	LNVGSKDKANKPVRTITNVAPGVKEEDVYVNAOLKGVAAONLNRRIDNDVGNARAGIAOLAAT	535
QY	529	AGLVQATYLPKGSMAIIGGGTYRGEAGYAIGYSSISDGGNNIINKGTASGNSRGHFPGASAV	588
Db	536	AGLVQATYLPKGSMAIIGGGTYRGEAGYAIGYSSISDGGNNIINKGTASGNSRGHFPGASAV	595
QY	589	GYQW 592	
Db	596	GYQW 599	

RESULT	7	
Q9JPR7		
ID	Q9JPR7	PRELIMINARY;
AC	Q9JPR7;	PRT; 598 AA.
DT	01-OCT-2000	(TREMblurel, 15, Created)
DT	01-OCT-2000	(TREMblurel, 15, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SW2107;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226385; AAF42534.1; -  
SO SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 91.0%; Score 2719; DB 2; Length 598;  
Best Local Similarity 91.7%; Pred. No. 1.6e-108;  
Matches 550; Conservative 13; Mismatches 27; Indels 10; Gaps 5;

OY 1 MNKYRIIWSNALNMAVAVSELTNRNHRASATVATVATLTLFATVQANATDEDEEEL 60  
DB 1 MNKYRIIWSNALNMAVAVSELTNRNHRASATVATVATLTLFATVQANATDEDEEEL 59  
OY 61 ESVORS-VGSIOASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLIKIKO-- 114  
DB 60 ESVORS-VGSIOASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLIKIKO-- 118  
OY 115 -NTNENMTNASSFTYSLKDLTGLINVEFEKLSFGANGKKNIIISDTKGLNFAKETAGTN 172  
DB 119 DENTDEMTNASSFTYSLKDLTGLINVEFEKLSFGANGKKNIIISDTKGLNFAKETAGTN 178  
OY 173 GDTTVHLNGISLTLDLTLGSSASHVDAGNOSTHYTRAASIKDVLNAGWNIKGVKGTSTT 232  
DB 179 GDTTVHLNGISLTLDLTLGSSASHVDAGNOSTHYTRAASIKDVLNAGWNIKGVKGTSTT 238  
OY 233 GOSNVNPFVRYDYVEELSDTKTTTVNVEKDKGKREVKIGAKTSYIKEDKGLVYTK 292  
DB 239 GOSNVNPFVRYDYVEELSDTKTTTVNVEKDKGKREVKIGAKTSYIKEDKGLVYTK 298  
OY 293 GKGNGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEFTVSGTNVTFAS 352  
DB 299 GKGNGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEFTVSGTNVTFAS 358  
OY 353 GKGTTATVSKDQGNITVMDVNVGDALNVNQLONGMNLDSKAVAGSSGKVIISGNVSPS 412  
DB 359 GKGTTATVSKDQGNITVMDVNVGDALNVNQLONGMNLDSKAVAGSSGKVIISGNVSPS 418  
OY 413 KKKDEVTNINAGNNIEITRRGNKIDATSMAPOFSSVSLGAGADAPTLSDDDGALNVG 472  
DB 419 KKKDEVTNINAGNNIEITRRGNKIDATSMAPOFSSVSLGAGADAPTLSDDDGALNVG 478  
OY 473 SKDANKFVRITNVAPGVEGDTVNAQLKGAQNLNRRIDVNDGNARAGIAQAIATAGLV 532  
DB 479 SKDANKFVRITNVAPGVEGDTVNAQLKGAQNLNRRIDVNDGNARAGIAQAIATAGLV 538  
OY 533 QAVLPKSSMAAIGGGTYRGEAGVAGVSSISDGNMIITKGTASGNSRGHFGASASVGYOM 592  
DB 539 QAVLPKSSMAAIGGGTYRGEAGVAGVSSISDGNMIITKGTASGNSRGHFGASASVGYOM 598

DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGP165, 90/18311, AND 93/4286;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226384; AAF42533.1; -  
DR EMBL: AF226362; AAF42511.1; -  
DR EMBL: AF226363; AAF42512.1; -  
SO SEQUENCE 589 AA; 61520 MW; 2B2A95DA4868566A6 CRC64;

Query Match 88.3%; Score 2637.5; DB 2; Length 589;  
Best Local Similarity 89.4%; Pred. No. 4.6e-105;  
Matches 533; Conservative 12; Mismatches 40; Indels 11; Gaps 4;

OY 1 MNKYRIIWSNALNMAVAVSELTNRNHRASATVATVATLTLFATVQANATDEDEEEL 60  
DB 1 MNKYRIIWSNALNMAVAVSELTNRNHRASATVATVATLTLFATVQANATDEDEEEL 60  
OY 61 ESVORS-VGSIOASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLIKIKO-- 116  
DB 60 ESVORS-VGSIOASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLIKIKO-- 117  
OY 117 NENTNASSFTYSLKDLTGLINVEFEKLSFGANGKKNIIISDTKGLNFAKETAGTN 176  
DB 118 NENTNASSFTYSLKDLTGLINVEFEKLSFGANGKKNIIISDTKGLNFAKETAGTN 173  
OY 177 VHLNGISLTLDLTLGSSASHVDAGNOSTHYTRAASIKDVLNAGWNIKGVKGTSTT 236  
DB 174 VHLNGISLTLDLTLGSSASHVDAGNOSTHYTRAASIKDVLNAGWNIKGVKGTSTT 233  
OY 237 NVDFRTYDYVEELSDTKTTTVNVEKDKGKREVKIGAKTSYIKEDKGLVYTK 296  
DB 234 NVDFRTYDYVEELSDTKTTTVNVEKDKGKREVKIGAKTSYIKEDKGLVYTK 293  
OY 297 NGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEFTVSGTNVTFAS 356  
DB 294 NGSSTDEGEGLVTAKEVIDAVNKAQRMKTTTANGOTGOADKFEFTVSGTNVTFAS 353  
OY 357 TATVSKDQGNITVMDVNVGDALNVNQLONGMNLDSKAVAGSSGKVIISGNVSPS 416  
DB 354 TATVSKDQGNITVMDVNVGDALNVNQLONGMNLDSKAVAGSSGKVIISGNVSPS 413  
OY 417 DETVINAGNNIEITRRGNKIDATSMAPOFSSVSLGAGADAPTLSDDDGALNVG 476  
DB 414 DETVINAGNNIEITRRGNKIDATSMAPOFSSVSLGAGADAPTLSDDDGALNVG 473  
OY 477 NKPVRTNVAPGVEGDTVNAQLKGAQNLNRRIDVNDGNARAGIAQAIATAGLV 536  
DB 474 NKPVRTNVAPGVEGDTVNAQLKGAQNLNRRIDVNDGNARAGIAQAIATAGLV 533  
OY 537 PKSSMAAIGGGTYRGEAGVAGVSSISDGNMIITKGTASGNSRGHFGASASVGYOM 592  
DB 534 PKSSMAAIGGGTYRGEAGVAGVSSISDGNMIITKGTASGNSRGHFGASASVGYOM 589

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RESULT 9
Q030Y1 ID 0930Y1 PRELIMINARY: PRT: 589 AA.
AC 0930Y1:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
OS NHHA.
GN Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157610; AAK68871.1; -
SQ SEQUENCE 589 AA: 61448 MW: 1F1A80CD610CB230 CRC64;

Query Match 87.9%; Score 2626.5; DB 2; Length 589;
Best Local Similarity 89.1%; Pred. No. 1.3e-104;
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

QY 1 MNKTYRIINMSALNAMAAYVSELTRNHTKRASATYKTVAVLTFLFATYQVQANATDEDEEEL 60
DB 1 MNKTYRIINMSALNAMAAYVSELTRNHTKRASATYKTVAVLTFLFATYQVQANATDEDEEEL 60
QY 61 ESVORS-VVGSIOASMGESELET---ISLMTNDSKEFVDPYVTVLKAGDNLIKIKONT 116
DB 61 ESVARSALVLOFMIDKNGEIEISTGDIQMSIYDDHNTLHG-ATVTLKAGDNLIKIKO-- 117
QY 117 NEPTMASFFYSLKDKLTGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPT 176
DB 118 ---SGKDFYSLKELKDLTSLVETKLSFGANGKNVNIISDTKGLNFAKETAGTNGDPT 173
QY 177 VHLNGIGSTLDTPLAGSSASHVDAGNOSTHYTRASTIKDVLNAGWNIKKYVSGSTGQSE 236
DB 174 VHLNGIGSTLDTPLAGSSASHVDAGNOSTHYTRASTIKDVLNAGWNIKKYVSGSTGQSE 233
QY 237 NVDFVRTDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVYKKEKDKLVYGGKGE 296
DB 234 NVDFVRTDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVYKKEKDKLVYGGKGE 293
QY 297 NGSTDEGEGLYTAKEVIDAVNKRAGMRKTTTANGQTGOADKFEFTVTSCTVTFASGNGT 353
DB 294 NGSTDEGEGLYTAKEVIDAVNKRAGMRKTTTANGQTGOADKFEFTVTSCTVTFASGNGT 353
QY 357 TATVSKDQGNITVYVYVNGDALNVNQLONGNLDKSKAVAGSSGVIISGNVSPSGKM 416
DB 354 TATVSKDQGNITVYVYVNGDALNVNQLONGNLDKSKAVAGSSGVIISGNVSPSGKM 413
QY 417 DETVYNAGNNEISRNKGNIDATSMAPOFSSVSLGAGADAPTLSDVDEGALVVGSKDA 476
DB 414 DETVYNAGNNEISRNKGNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALVVGSKDA 473
QY 477 NKPVRTINVAPEKGEVDYTNVAOLKGYAONLNINRDNVDGNARAGIAQAIATAGLYOAYL 536
DB 474 NKPVRTINVAPEKGEVDYTNVAOLKGYAONLNINRDNVDGNARAGIAQAIATAGLYOAYL 533
QY 537 PGKSMAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGTASGNSRKHFEASASVGYQM 592
DB 534 PGKSMAIGGGTYRGEAGYAIIGYSSISDGTGNWIKGTASGNSRKHFEASASVGYQM 589

RESULT 10
Q03PR8 ID 093PR8 PRELIMINARY: PRT: 599 AA.
AC 093PR8:
DT 01-OCT-2000 (Tremblrel. 15, Created)
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DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
OS GNA992 OR NHHA.
GN Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piazza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
  RA Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
  RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
  RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,
  RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  RA Moxon E.R., Grandi G., Rappuoli R.;
  RT "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF24252.1; -
DR EMBL: AF157608; AAK68869.1; -
SQ SEQUENCE 599 AA: 62844 MW: BBA16EBF53C1970C CRC64;
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Query Match 86.6%; Score 2587.5; DB 2; Length 599;
Best Local Similarity 88.0%; Pred. No. 6.3e-103;
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

QY 1 MNKTYRIINMSALNAMAAYVSELTRNHTKRASATYKTVAVLTFLFATYQVQANATDEDEEEL 60
DB 1 MNKTYRIINMSALNAMAAYVSELTRNHTKRASATYKTVAVLTFLFATYQVQANATDEDEEEL 60
QY 61 ESVORS-VVGSIOASMGESELET---ISLMTNDSKEFVDPYVTVLKAGDNLIKIKONT 114
DB 61 ESVARSALVLOFMIDKNGEIEISTGDIQMSIYDDHNTLHG-ATVTLKAGDNLIKIKO-- 119
QY 115 --NPTNENMASFFYSLKDKLTGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTN 172
DB 120 NKTNENMTNDSFFYSLKDKLTGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTN 179
QY 173 GDTVHLNGIGSTLDTPLAGSSASHVDAGNOST--HYTRASIKDVLNAGWNIKKYVSGTGS 230
DB 180 GDTVHLNGIGSTLDTPLAGSSASHVDAGNOSTHYTRASIKDVLNAGWNIKKYVSGTGS 239
QY 231 TTGQSENVDFVRTDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVYKKEKDKLVY 290
DB 240 TA--SDNVDFVRTDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVYKKEKDKLVY 297
QY 291 GKKGGENSSSTDEEGEGLYTAKEVIDAVNKRAGMRKTTTANGQTGOADKFEFTVTSCTVTF 350
DB 298 GKKGGENSSSTDEEGEGLYTAKEVIDAVNKRAGMRKTTTANGQTGOADKFEFTVTSCTVTF 357
QY 351 ASGKGTATVSKDQGNITVYVYVNGDALNVNQLONGNLDKSKAVAGSSGVIISGNVSPSGKM 410
DB 358 ASGKGTATVSKDQGNITVYVYVNGDALNVNQLONGNLDKSKAVAGSSGVIISGNVSPSGKM 417
QY 411 PSKGMDETVINAGNNEISRNKGNIDATSMAPOFSSVSLGAGADAPTLSDVDEGALN 470
DB 418 PSKGMDETVINAGNNEISRNKGNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALN 477
QY 471 VGSKDANKPVRTINVAPEKGEVDYTNVAOLKGYAONLNINRDNVDGNARAGIAQAIATAG 530
DB 478 VGSKDANKPVRTINVAPEKGEVDYTNVAOLKGYAONLNINRDNVDGNARAGIAQAIATAG 537
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QY 531 LVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGMNIIKKTASGNSRHFASASVGY 590
DB 538 LVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGMNIIKKTASGNSRHFASASVGY 597
QY 591 QW 592
DB 598 QW 599

RESULT 11
Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND B2232;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42518.1; -
DR EMBL; AF226369; AAF42518.1; -
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 85.4%; Score 2553; DB 2; Length 594;
Best Local Similarity 86.9%; Pred. No. 1.8e-101;
Matches 523; Conservative 18; Mismatches 43; Indels 18; Gaps 6;

QY 1 MNKIYRIIWNALNMAVAVSELRNHTKRASATVKTAVLATLFAVQANATDEDEEEL 60
DB 1 MNKIYRIIWNALNMAVAVSELRNHTKRASATVKTAVLATLFAVQASTD-DDDLYL 59
QY 61 ESVQRSV-VGSIQASMEGSELETISLSMTNDS-----KEFVDPYIVYTLKAGDNKI 112
DB 60 EPVQRTAVLSFHAHDSGTGEKE-----VTEDSNMGVYFDDKGVTLTACITTLKAGDNKI 114
QY 113 KONTEMENTNASSFTYSLKKDLTGLINVEETKISFGANGKRYNIISDTYKGLNFAKETAGN 172
DB 115 KONTEMENTNASSFTYSLKKDLTGLTSLVETKELFSGANGKRYNITSDTKGLNFAKETAGN 174
QY 173 GDTYVHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRASIKRYLVANGMKIKVKGCS 230
DB 175 GDTYVHLNGIGSTLTDLTLLNCGATNTVNDVTDDEKKRAASVRYLVANGMKIKVKGCP 234
QY 231 TTGQSENVDFATYDVEFLSADTKTTTVNVEESKDNKRTEVIGAKTSVIEKDGKLYT 290
DB 235 TA--SDNVDFTYDVEFLSADTKTTTVNVEESKDNKRTEVIGAKTSVIEKDGKLYT 292
QY 291 GKKGKNGSSSTDEGEGLYTAKEVIDAVNKKAGRMKTTTANGOTGOADKFEYVTSCTNVT 350
DB 293 GKDGKNGSSSTDEGEGLYTAKEVIDAVNKKAGRMKTTTANGOTGOADKFEYVTSCTKVF 352
QY 351 ASGKGTATVSGKDDGNTITVMDVAVDALNVLNOLONGSWMNDSKAVVSGSSKGVISGNS 410
DB 353 ASGNTTATVSGDDGNTITVMDVAVDALNVLNOLONGSWMNDSKAVVSGSSKGVISGNS 412
QY 411 PSKGMDETVINAGNNIEISHRGNKIDIAITSMAPQSSSVSLGAGADAPTLISVDEGALN 470
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DB 413 PSKGMDETVINAGNNIEISHRGNKIDIAITSMAPQSSSVSLGAGADAPTLISVDEGALN 472
QY 471 VGSKANRPVRTTNVAPRGKEDYTNVADLKGYAQLNLRINDVQDNAGIAQALATAG 530
DB 473 VGSKANRPVRTTNVAPRGKEDYTNVADLKGYAQLNLRINDVQDNAGIAQALATAG 532
QY 531 LVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGMNIIKKTASGNSRHFASASVGY 590
DB 533 LVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGMNIIKKTASGNSRHFASASVGY 592
QY 591 QW 592
DB 593 QW 594

RESULT 12
Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GMA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GMA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198, AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizarro M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226368; AAF42517.1; -
DR EMBL; AF226358; AAF42507.1; -
DR EMBL; AF157604; AAK68865.1; -
SQ SEQUENCE 594 AA; 62361 MW; 436BDD68263C5C CRC64;

Query Match 85.4%; Score 2552; DB 2; Length 594;
Best Local Similarity 86.8%; Pred. No. 2e-101;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

QY 1 MNKIYRIIWNALNMAVAVSELRNHTKRASATVKTAVLATLFAVQANATDEDEEEL 60
DB 1 MNKIYRIIWNALNMAVAVSELRNHTKRASATVKTAVLATLFAVQANATD-DDDLYL 59
QY 61 ESVQRSV-SVGSIQASMEGSELETISLSMTNDSKEFVDPYI-----VYTLKAGDNKI 110
DB 60 EPVQRTAVLSFHAHDSGTGEKE-----TEDSNMGVYFDDKGVTLTACITTLKAGDNKI 112
QY 111 KIKONTMENTNASSFTYSLKKDLTGLINVEETKELFSGANGKRYNISDPKGLNFAKETAG 170
DB 113 KIKONTMENTNASSFTYSLKKDLTGLTSLVETKELFSGANGKRYNITSDTKGLNFAKETAG 172
QY 171 TNGDFTVHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRASIKRYLVANGMKIKVKG 228
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Db 173 TNGDPVHLNGISLTLDLTLNTGATTNTNDVYDDEKRRASVVDYLNAGNINIGVVP 232  
QY 229 GSTTGOSENVDFRYDYVEFLSADPFTKTTTVNESKDNKGRTEVKIGAKTSVIEKEDKL 288  
Db 233 GTTA--SDNVDFRTYDTEVEFLSADPFTKTTTVNESKDNKGRTEVKIGAKTSVIEKEDKL 290  
QY 289 VTGKKGKNGSSSTDEEGELVTAKVEIDAVNKAGWRMKTATTANGOTGOADKFEVTSCTNV 348  
Db 291 VTGKKGKNGSSSTDEEGELVTAKVEIDAVNKAGWRMKTATTANGOTGOADKFEVTSCTNV 350  
QY 349 TFGSGKRTTATVSKDOGNITVAVDVGALVNOLONSGWNLDKRAVAGSSGKVIISGN 408  
Db 351 TFGSGKRTTATVSKDOGNITVAVDVGALVNOLONSGWNLDKRAVAGSSGKVIISGN 410  
QY 409 VSPKGMDEFTVINAGNNIEISRNKNIDIASMAPOFSSVSLGAGADAPTLSDVEDEGA 468  
Db 411 VSPKGMDEFTVINAGNNIEISRNKNIDIASMAPOFSSVSLGAGADAPTLSDVEDEGA 470  
QY 469 LNVGSKDANKPVRITNVAPGVKEGDTVNVQOLKGVQNLNRRIDNDVGNARAGIAQAIAT 528  
Db 471 LNVGSKDANKPVRITNVAPGVKEGDTVNVQOLKGVQNLNRRIDNDVGNARAGIAQAIAT 530  
QY 529 AGLVQATLPKSMMAIGGGYRGEAGYAGYSSISDGNMIIKGTASGNSRGHFGASASV 588  
Db 531 AGLVQATLPKSMMAIGGGYRGEAGYAGYSSISDGNMIIKGTASGNSRGHFGASASV 590  
QY 589 GYQW 592  
Db 591 GYQW 594

RESULT 13  
Q9JPS2 ID Q9JPS2 PRELIMINARY; PRT; 594 AA.  
AC Q9JPS2:  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -  
SO SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 85.3%; Score 2549; DB 2; Length 594;  
Best Local Similarity 86.7%; Pred. No. 2.7e-101;  
Matches 522; Conservative 18; Mismatches 44; Indels 18; Gaps 6;

QY 1 MNKYRIITMNSALNAWAVSELTRNHTKRASATYKTAVALATLLPATVOANNTDEDEEEL 60  
Db 1 MNKYRIITMNSALNAWAVSELTRNHTKRASATYKTAVALATLLPATVOASTTD- DDD-LYL 59  
QY 61 ESYQRSV-VGSIQSMESGSELETLISMTNDS-----KEFDPYIVVLTKAGDNLKI 112  
Db 60 EPOVTAIVLSFHDSSBSTGEK-----VTEDSNMGVYFDKGVLTACTITLKAGDNLKI 114

QY 113 KONTNENTNASFTYSLKRLTLGILINVEKLSFGANGKAVNIISDPTKGINFAKTAAGTN 172  
Db 115 KONTNENTNASFTYSLKRLTLGILINVEKLSFGANGKAVNIISDPTKGINFAKTAAGTN 174  
QY 173 GDTTVHLNGISLTLDLTLNTGATTNTNDVYDDEKRRASVVDYLNAGNINIGVVP 230  
Db 175 GDTTVHLNGISLTLDLTLNTGATTNTNDVYDDEKRRASVVDYLNAGNINIGVVP 234  
QY 231 TFGOSENVDFRYDYVEFLSADPFTKTTTVNESKDNKGRTEVKIGAKTSVIEKEDKLVT 290  
Db 235 TA--SDNVDFRTYDTEVEFLSADPFTKTTTVNESKDNKGRTEVKIGAKTSVIEKEDKLVT 292  
QY 291 GKGKNGSSSTDEEGELVTAKVEIDAVNKAGWRMKTATTANGOTGOADKFEVTSCTNV 350  
Db 293 GKGKNGSSSTDEEGELVTAKVEIDAVNKAGWRMKTATTANGOTGOADKFEVTSCTNV 352  
QY 351 ASGKGTATVSKDOGNITVAVDVGALVNOLONSGWNLDKRAVAGSSGKVIISGNV 410  
Db 353 ASGKGTATVSKDOGNITVAVDVGALVNOLONSGWNLDKRAVAGSSGKVIISGNV 412  
QY 411 PSKGMDEFTVINAGNNIEISRNKNIDIASMAPOFSSVSLGAGADAPTLSDVEDEGALN 470  
Db 413 PSKGMDEFTVINAGNNIEISRNKNIDIASMAPOFSSVSLGAGADAPTLSDVEDEGALN 472  
QY 471 VGSKDANKPVRITNVAPGVKEGDTVNVQOLKGVQNLNRRIDNDVGNARAGIAQAIATAG 530  
Db 473 VGSKDANKPVRITNVAPGVKEGDTVNVQOLKGVQNLNRRIDNDVGNARAGIAQAIATAG 532  
QY 531 LVQAVLPKSMMAIGGGYRGEAGYAGYSSISDGNMIIKGTASGNSRGHFGASASV 590  
Db 533 LVQAVLPKSMMAIGGGYRGEAGYAGYSSISDGNMIIKGTASGNSRGHFGASASV 592  
QY 591 QW 592  
Db 593 QW 594

RESULT 14  
Q9JPR9 ID Q9JPR9 PRELIMINARY; PRT; 598 AA.  
AC Q9JPR9:  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH36;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226382; AAF42531.1; -  
SO SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 85.0%; Score 2541; DB 2; Length 598;  
Best Local Similarity 86.2%; Pred. No. 5.9e-101;  
Matches 524; Conservative 16; Mismatches 42; Indels 26; Gaps 8;

QY 1 MNKYRIITMNSALNAWAVSELTRNHTKRASATYKTAVALATLLPATVOANNTDEDEEEL 60  
Db 1 MNKYRIITMNSALNAWAVSELTRNHTKRASATYKTAVALATLLPATVOANNTDEDEEEL 60

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Db      1  MNKIRIIMNSALNANMNVVSVSLTNNHNRKRAATATATVATLNLFAFYQANANTD--DDLTYL  59
QY      61  ESVOR-SVYSGISQASMEGSGLELTISLSMTDSKEEVDPI-----VTLKAGDNL  110
Db      60  EPVQVATVLFSPRSDEKTEGKEG-----TEDSWMVA--YDEKERVAKAGITLAKADNL  112
QY      111  KIKONTNNTNTA----SEFTYSLKKDLTLGLINVEETKLSPCANKKNIIISDPKGLNFAK  166
Db      113  KIKONTNNTNMENTNDSFTYSLKKDLTLGLSVTEKLSFGANKKNIIISDPKGLNFAK  173
QY      167  ETAGNNGDTYVHLNGISGTLTDTLAGSASHVDAGNOST--HYRAASIKDVLNAGNIK  224
Db      173  ETAGNNGDPYVHLNGISGTLTDLTLNGATNTNTNDVNTDDEKKRAASVADYVLNAGNIK  233
QY      225  GVKRTGTTGQSENVDFVRTYDVEFLSADRTKTTTVNYESKDNKRTVEKIGAKTSVIREK  284
Db      233  GVKPGTTP--SDNDVFRYDVEFLSADRTKTTTVNYESKDNKRTVEKIGAKTSVIREK  290
QY      285  DGKLTVTKGKREKNSSTDEGGGLYTAKEVIDAVNKAQRKAKTTTANQTOGADKFEITYS  344
Db      291  DGKLTVTKGKREKNSSTDEGGGLYTAKEVIDAVNKAQRKAKTTTANQTOGADKFEITYS  350
QY      345  GTNNTFASGCKFTPTVSKDDQGNITVAVDVVGSALVNVNOLNSGMULDASKAVGSSGV  404
Db      351  GTNNTFASGCKTTTATVSKDDQGNITVAKDVVGSALVNVNOLNSGMULDASKAVGSSGV  410
QY      405  ISGNVSPSKGMDEVTVINAGNNINIEISNKNKIDIIATSMAPQFSSVSLGAGADPTLSYD  464
Db      411  ISGNVSPSKGMDEVTVINAGNNINIEIRNKNKIDIIATSMAPQFSSVSLGAGADPTLSYD  470
QY      465  DEGALNVGSKANKRPVRTTNVAPCVKBCDVTNVNQLKGVAONLNRIIDVNGNARAGIAQ  524
Db      471  DEGALNVGSKDPTNRPVRTTNVAPCVKEBDVTNVNQLKGVAONLNRIIDVNGNARAGIAQ  530
QY      525  AIAFAGLVQATLPCKSMAICGGYTRGAGAGATGYSSTSDSGNNIITGTSAGNSRGHFGA  584
Db      531  AIAFAGLVQATLPCKSMAICGGYTRGAGAGATGYSSTSDSGNNIITGTSAGNSRGHFGA  590
QY      585  SASVGYQW  592
Db      591  SASVGYQW  598

RESULT  15
Q930Y4  PRELIMINARY;          PRT;          594 AA.
AC      0930Y4:
DT      01-DEC-2001 (TRMBLrel. 19, Created)
DT      01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE      NHHA OUTER MEMBRANE PROTEIN.
GN      NHHA.
OS      Neisseria meningitidis.
OC      Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX      NCBI_taxid=487;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=EG327.
RA      Peak I.R., Stikhanata Y., Dieckelman M., Moxon R., Jennings M.P.;
RT      "Identification and characterization of a gene encoding a novel outer
RL      membrane protein of Neisseria meningitidis.";
DR      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF157605; AAK68866.1; -
SQ      SEQUENCE 594 AA: 62297 MW: 9DD048B043BA8EA2 CRC64;

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Query Match	84.8%;	Score 2533;	DB 2;	Length 594;
Best Local Similarity	86.4%;	Pred. NO. 1.3e-100;		
Matches 520;	Conservative 20;	Mismatches 44;	Indels 18;	Gaps 6

OY 1 MNKYIRIINNSALNANVAVSELTNRNHTKASATYKTAVLATLLEFATVOANATDEDEEEEL 600  
| | | | | | | | | | | | | | | | : | : : |  
Db 1 MNKYIRIINNSALNANVAVSELTRNHTKRASATYKTAVLATLLEFATVOASTTD-DDDLYL 59

[illegible]

Search completed: July 3, 2002, 08:48:13  
Job time: 704 sec





QY 301 TDEGGLTAKEVIDAVNKAGWRMKTYYANGQTGC

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Db 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360  
QY 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420  
Db 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420  
QY 421 NINAGNNIEITRNCKNIDDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
Db 421 NINAGNNIEITRNCKNIDDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
QY 481 ITNAPGVKEDDYTNVQOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQATLPKSKM 540  
Db 481 ITNAPGVKEDDYTNVQOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQATLPKSKM 540  
QY 541 MAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASGYQW 591  
Db 541 MAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASGYQW 591

## RESULT 2

US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 100.0%; Score 3003; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2,7e-225;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKTYRIIMNSALNAMYVSELTRNHRKRASATYKTAVALTLFATVQOASANNEOEEDL 60  
Db 1 MNKTYRIIMNSALNAMYVSELTRNHRKRASATYKTAVALTLFATVQOASANNEOEEDL 60  
QY 61 YLDPVORTVAVLIVNSDEKGEKEVEENSDMAVYFENEKCVLTAREITTLKAGDNLIKQ 120  
Db 61 YLDPVORTVAVLIVNSDEKGEKEVEENSDMAVYFENEKCVLTAREITTLKAGDNLIKQ 120  
QY 121 NGTNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKLNAFAKETAGNGDTYHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKLNAFAKETAGNGDTYHLN 180  
QY 181 GIGSTLDTLLNTGATNTVNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTASDNVDF 240  
Db 181 GIGSTLDTLLNTGATNTVNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDKLVYKDKGNGSS 300  
Db 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDKLVYKDKGNGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360

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Db 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360  
QY 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420  
Db 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420  
QY 421 NINAGNNIEITRNCKNIDDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
Db 421 NINAGNNIEITRNCKNIDDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKDNKPV 480  
QY 481 ITNAPGVKEDDYTNVQOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQATLPKSKM 540  
Db 481 ITNAPGVKEDDYTNVQOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQATLPKSKM 540  
QY 541 MAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASGYQW 591  
Db 541 MAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASGYQW 591

## RESULT 3

US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 99.4%; Score 2984; DB 4; Length 591;  
Best Local Similarity 99.5%; Pred. No. 8.1e-224;  
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKTYRIIMNSALNAMYVSELTRNHRKRASATYKTAVALTLFATVQOASANNEOEEDL 60  
Db 1 MNKTYRIIMNSALNAMYVSELTRNHRKRASATYKTAVALTLFATVQOASANNEOEEDL 60  
QY 61 YLDPVORTVAVLIVNSDEKGEKEVEENSDMAVYFENEKCVLTAREITTLKAGDNLIKQ 120  
Db 61 YLDPVORTVAVLIVNSDEKGEKEVEENSDMAVYFENEKCVLTAREITTLKAGDNLIKQ 120  
QY 121 NGTNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKLNAFAKETAGNGDTYHLN 180  
Db 121 NGTNFTYSLKKDLTDLTSVGEKLSFSANGKNVITSDTKLNAFAKETAGNGDTYHLN 180  
QY 181 GIGSTLDTLLNTGATNTVNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTASDNVDF 240  
Db 181 GIGSTLDTLLNTGATNTVNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDKLVYKDKGNGSS 300  
Db 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDKLVYKDKGNGSS 300  
QY 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360  
Db 301 TDEGGLVTAKEVIDAVNKKAGWRKTTTANGOTQADKFEFVTSCTNVTFASGGTTATV 360  
QY 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420  
Db 361 SKDOGNITVYDVNVGDALNVNOLNSGMNLDKRAVAGSSGKYISGNVSPSKKMDTV 420

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|||||
Db 361 SKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 420
Qy 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPV 480
Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPV 480
Qy 481 ITNVAPGVEGDVTNVAOLKGVAQNLRIDVGNARAGIAQAITAGLVQAYLPKGS 540
Db 481 ITNVAPGVEGDVTNVAOLKGVAQNLRIDVGNARAGIAQAITAGLVQAYLPKGS 540
Qy 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 591
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RESULT 4
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11
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Query Match 99.4%; Score 2984; DB 4; Length 591;
Best Local Similarity 99.5%; Pred. No. 8.1e-224;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MNKIYRIINNSALNMAVWVSELTNRHTKRASATVKTAVLATLLEFATVOASANNEQEDL 60
Db 1 MNELIRIINNSALNMAVWVSELTNRHTKRASATVKTAVLATLLEFATVOASANNEQEDL 60
Qy 61 YLDPVQRTVAVLIVNSDKGTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 120
Db 61 YLDPVQRTVAVLIVNSDKGTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 120
Qy 121 NGTNFTYSLKQDLTDLTSGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNDTTHLN 180
Db 121 NGTNFTYSLKQDLTDLTSGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNDTTHLN 180
Qy 181 GIGSTLTDLTLNTGATTNTNDNVTDDEKKRAASVQDVNLNAGNINIGVPGTTASDNV 240
Db 181 GIGSTLTDLTLNTGATTNTNDNVTDDEKKRAASVQDVNLNAGNINIGVPGTTASDNV 240
Qy 241 VRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIEKDGKLVYTGDKGENSS 300
Db 241 VRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIEKDGKLVYTGDKGENSS 300
Qy 301 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVTSQNTVTFASGKGTATV 360
Db 301 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVTSQNTVTFASGKGTATV 360
Qy 361 SKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 420
Db 361 SKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 420
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Db 361 SKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 420
Qy 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPV 480
Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPV 480
Qy 481 ITNVAPGVEGDVTNVAOLKGVAQNLRIDVGNARAGIAQAITAGLVQAYLPKGS 540
Db 481 ITNVAPGVEGDVTNVAOLKGVAQNLRIDVGNARAGIAQAITAGLVQAYLPKGS 540
Qy 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 591
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RESULT 5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2
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Query Match 99.0%; Score 2971.5; DB 4; Length 592;
Best Local Similarity 99.0%; Pred. No. 7.6e-223;
Matches 586; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MNKIYRIINNSALNMAVWVSELTNRHTKRASATVKTAVLATLLEFATVOASANNEQED 59
Db 1 MNKIYRIINNSALNMAVWVSELTNRHTKRASATVKTAVLATLLEFATVOASANNEQED 60
Qy 60 YLDPVQRTVAVLIVNSDKGTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 119
Db 61 YLDPVQRTVAVLIVNSDKGTEGKEKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 120
Qy 120 QNGTNFTYSLKQDLTDLTSGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNDTTHL 179
Db 121 QNGTNFTYSLKQDLTDLTSGTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNDTTHL 180
Qy 180 NGIGSTLTDLTLNTGATTNTNDNVTDDEKKRAASVQDVNLNAGNINIGVPGTTASDNV 239
Db 181 NGIGSTLTDLTLNTGATTNTNDNVTDDEKKRAASVQDVNLNAGNINIGVPGTTASDNV 240
Qy 240 FVRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIEKDGKLVYTGDKGENS 299
Db 241 FVRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIEKDGKLVYTGDKGENS 300
Qy 300 STDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVTSQNTVTFASGKGTATV 359
Db 301 STDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVTSQNTVTFASGKGTATV 360
Qy 360 VSKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 419
Db 361 VSKDDGDNITVMYDVNVGDLNVNOLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETV 420
Qy 420 VNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPV 479
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Db 421 VNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKDNKPV 480  
QY 480 RITVAVGKRGKGDVTNVAQLKGVAQNLNRRIDNDVGNARAGIAAIAATAGLVQATLPKKS 539  
Db 481 RITVAVGKRGKGDVTNVAQLKGVAQNLNRRIDNDVGNARAGIAAIAATAGLVQATLPKKS 540  
QY 540 MMAIGGGTGTREAGYAGTSSISDGMNIIKGTASGNSRGHFGASASVGYOM 591  
Db 541 MMAIGGGTGTREAGYAGTSSISDGMNIIKGTASGNSRGHFGASASVGYOM 592

RESULT 6  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 99.0%: Score 2971.5; DB 4: Length 592;

Best Local Similarity 99.0%: Pred. No. 7.6e-223; Matches 586; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSNALNAAVWVSELTNRHTRKASATYKATAVATLTLFATVQASANNNEQED 59  
Db 1 MNKIYRIIWSNALNAAVWVSELTNRHTRKASATYKATAVATLTLFATVQASANNNEPRKD 60  
QY 60 LYDPVORTAVAVLIYNSDEKGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLIK 119  
Db 61 LYDPVORTAVAVLIYNSDEKGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLIK 120  
QY 120 ONGNFTYSLKDLTDLTSVTEKLSFSANGKNVITSDTGLNPAKTAETAGNGDTVHL 179  
Db 121 ONGNFTYSLKDLTDLTSVTEKLSFSANGKNVITSDTGLNPAKTAETAGNGDTVHL 180  
QY 180 NGISTLTDLTLNLTGATNTVNDVYDDEKRAASVYKDVLAAGNIIKGVKPTASDND 239  
Db 181 NGISTLTDLTLNLTGATNTVNDVYDDEKRAASVYKDVLAAGNIIKGVKPTASDND 240  
QY 240 FVRTYDVEFLSADTKTTTAVESKDNKKTVEKIGATSVYIKERDGLVYTGKDGNGS 299  
Db 241 FVRTYDVEFLSADTKTTTAVESKDNKKTVEKIGATSVYIKERDGLVYTGKDGNGS 300  
QY 300 STDGEGLYTAKKEYIDAVNKGWRMKTATTANGOTGQADKFEVYSGTNTVTFASGKTAT 359  
Db 301 STDGEGLYTAKKEYIDAVNKGWRMKTATTANGOTGQADKFEVYSGTNTVTFASGKTAT 360  
QY 360 VSKDQGNITVAVYVNDVAGDALNVNOLONGSNLDSKAVAGSSGKVISGNVPSKGMDET 419  
Db 361 VSKDQGNITVAVYVNDVAGDALNVNOLONGSNLDSKAVAGSSGKVISGNVPSKGMDET 420  
QY 420 VNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKDNKPV 479

Db 421 VNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKDNKPV 480  
QY 480 RITVAVGKRGKGDVTNVAQLKGVAQNLNRRIDNDVGNARAGIAAIAATAGLVQATLPKKS 539  
Db 481 RITVAVGKRGKGDVTNVAQLKGVAQNLNRRIDNDVGNARAGIAAIAATAGLVQATLPKKS 540  
QY 540 MMAIGGGTGTREAGYAGTSSISDGMNIIKGTASGNSRGHFGASASVGYOM 591  
Db 541 MMAIGGGTGTREAGYAGTSSISDGMNIIKGTASGNSRGHFGASASVGYOM 592

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRF  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 91.9%: Score 2758.5; DB 4: Length 594;  
Best Local Similarity 92.3%: Pred. No. 2.7e-206; Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSNALNAAVWVSELTNRHTRKASATYKATAVATLTLFATVQASANNNEQED 60  
Db 1 MNKIYRIIWSNALNAAVWVSELTNRHTRKASATYKATAVATLTLFATVQASANNNEPRKD 57  
QY 61 LYDPVORTAVAVLIYNSDEKGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLIK 120  
Db 58 LYDPVORTAVAVLIYNSDEKGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLIK 116  
QY 121 -----NGNFTYSLKDLTDLTSVTEKLSFSANGKNVITSDTGLNPAKTAETAGNGD 174  
Db 117 NTNENTNASSFTYSLKDLTDLTSVTEKLSFSANGKNVITSDTGLNPAKTAETAGNGD 176  
QY 175 TTVHLNGISTLTDLTLNLTGATNTVNDVYDDEKRAASVYKDVLAAGNIIKGVKPTGA 234  
Db 177 TTVHLNGISTLTDLTLNLTGATNTVNDVYDDEKRAASVYKDVLAAGNIIKGVKPTGA 236  
QY 235 SDNVFVRTYDVEFLSADTKTTTAVESKDNKKTVEKIGATSVYIKERDGLVYTGKDG 294  
Db 237 SDNVFVRTYDVEFLSADTKTTTAVESKDNKKTVEKIGATSVYIKERDGLVYTGKDG 296  
QY 295 GENGSTDEGEGLYTAKKEYIDAVNKGWRMKTATTANGOTGQADKFEVYSGTNTVTFASG 354  
Db 297 GENGSTDEGEGLYTAKKEYIDAVNKGWRMKTATTANGOTGQADKFEVYSGTNTVTFASG 356  
QY 355 GTTATVSKDQGNITVAVYVNDVAGDALNVNOLONGSNLDSKAVAGSSGKVISGNVPSKGM 414  
Db 357 GTTATVSKDQGNITVAVYVNDVAGDALNVNOLONGSNLDSKAVAGSSGKVISGNVPSKGM 416  
QY 415 KMDETVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSK 473  
Db 417 KMDETVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSK 476  
QY 474 KDNKPVRTITNVAAGVKEGDVTNVAQLKGVAQNLNRRIDNDVGNARAGIAAIAATAGLVQ 533

Db 477 DANKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 536  
QY 534 YLPGKSMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591  
Db 537 YLPGKSMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 594

## RESULT 8

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 91.9%; Score 2758.5; DB 4; Length 594;  
Best Local Similarity 92.3%; Pred. No. 2.7e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

QY 1 MNKIRIINSLNMAVYVSELTNRNHTKRASATVATLTLFATVQASANNEQEDL 60  
Db 1 MNKIRIINSLNMAVYVSELTNRNHTKRASATVATLTLFATVQASATD---DDL 57  
QY 61 YLDPVORTAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKGDNLIKQ 120  
Db 58 YLEPQORTAVLVSFRSDKEGTEKE-VTEDSNMGVYFDKRGVLTAGTTLKAGDNLIKQ 116  
QY 121 -----NGINFTYSLAKDLTDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTND 174  
Db 117 NTNEMTNMNSFFYSLSKDLTDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTND 176  
QY 175 TTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKKRAASVADVLNAGNNIKGVRPGTTA 234  
Db 177 TTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKKRAASVADVLNAGNNIKGVRPGTTA 236  
QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVEESKDKTEVKIGAKTSYIKKDKLVTGKDK 294  
Db 237 SDNVDFVRTYDVEFLSADTKTTTVNVEESKDKTEVKIGAKTSYIKKDKLVTGKDK 296  
QY 295 GENGSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKEFTVYSGTNVTFASGK 354  
Db 297 GENGSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKEFTVYSGTNVTFASGK 356  
QY 355 GTTATVSKDDOGNITVYVNVGDALNVQNLONGNLDLSKAVAGSSGKVIISGNVSPSKG 414  
Db 357 GTTATVSKDDOGNITVYVNVGDALNVQNLONGNLDLSKAVAGSSGKVIISGNVSPSKG 416  
QY 415 KMDETVINAGNNIETTRGNKIDATSMTPQFSSVSLGAGADAPLTVSDGD-ALNVGSK 473  
Db 417 KMDETVINAGNNIETTRGNKIDATSMTPQFSSVSLGAGADAPLTVSDGDALNVGSK 476  
QY 474 KDKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 533  
Db 477 KDKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 536

Db 477 DANKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 536  
QY 534 YLPGKSMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591  
Db 537 YLPGKSMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 594

## RESULT 9

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 91.3%; Score 2740.5; DB 4; Length 594;  
Best Local Similarity 92.1%; Pred. No. 6.7e-205;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

QY 1 MNKIRIINSLNMAVYVSELTNRNHTKRASATVATLTLFATVQASANNEQEDL 60  
Db 1 MNKIRIINSLNMAVYVSELTNRNHTKRASATVATLTLFATVQASATD---DDL 57  
QY 61 YLDPVORTAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKGDNLIKQ 120  
Db 58 YLEPQORTAVLVSFRSDKEGTEKEED-SNMAVYFDEKRVLKAGATTLKAGDNLIKQ 116  
QY 121 -----NGINFTYSLAKDLTDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTND 174  
Db 117 NTNEMTNMNSFFYSLSKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAGTND 176  
QY 175 TTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKKRAASVADVLNAGNNIKGVRPGTTA 234  
Db 177 TTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKKRAASVADVLNAGNNIKGVRPGTTA 236  
QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVEESKDKTEVKIGAKTSYIKKDKLVTGKDK 294  
Db 237 SDNVDFVRTYDVEFLSADTKTTTVNVEESKDKTEVKIGAKTSYIKKDKLVTGKDK 296  
QY 295 GENGSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKEFTVYSGTNVTFASGK 354  
Db 297 GENGSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKEFTVYSGTNVTFASGK 356  
QY 355 GTTATVSKDDOGNITVYVNVGDALNVQNLONGNLDLSKAVAGSSGKVIISGNVSPSKG 414  
Db 357 GTTATVSKDDOGNITVYVNVGDALNVQNLONGNLDLSKAVAGSSGKVIISGNVSPSKG 416  
QY 415 KMDETVINAGNNIETTRGNKIDATSMTPQFSSVSLGAGADAPLTVSDGD-ALNVGSK 473  
Db 417 KMDETVINAGNNIETTRGNKIDATSMTPQFSSVSLGAGADAPLTVSDGDALNVGSK 476  
QY 474 KDKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 533  
Db 477 DTKPVRITNVA PGYEGDVTVNAQLKGVAQNLMNHIDVNDGNARAGIAQAIATAGLVQA 536  
QY 534 YLPGKSMAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

Db 537 YLPKSMMAIGDPTGREGAGYAIGYSSISDGMWIKGTASGNSRGHFGASASVGYOM 594

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RESULT 10
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 594
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
US-09-669-974-7
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Query Match 91.3%; Score 2740.5; DB 4; Length 594;

Best Local Similarity 92.1%; Pred. No. 6,7e-205; Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

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QY 1 MNKIRITMNSALNAMYVSELTRNHTKRASATYKATVATLTLFATVQASANNEOEEDL 60
Db 1 MNKIRITMNSALNAMYVSELTRNHTKRASATYKATVATLTLFATVQANATD---DDDL 57
QY 61 YLDPVORTAVLYNSDEKGEKEKEEENSMAVYFENEKGVLTAREITLKAGDNLIKQ 120
Db 58 YLEPVORTAVLYNSDEKGEKEKEEED-SMAVYFENEKGVLTAREITLKAGDNLIKQ 116
QY 121 -----NGNFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTGLNFAKTAGTGD 174
Db 117 NTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTGLNFAKTAGTGD 176
QY 175 TTVHLNGIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKDYLANAGWNIKGVPCTTA 234
Db 177 PTVHLNGIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKDYLANAGWNIKGVPCTTA 236
QY 235 SDNDVFRVTVTEFELSADTKTTTVNYESKDNKGKTEVKGAKTSVYKEKDGKLVYTGDK 294
Db 237 SDNDVFRVTVTEFELSADTKTTTVNYESKDNKGKTEVKGAKTSVYKEKDGKLVYTGDK 296
QY 295 GENGSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKEFYVTSCTNTYFASGK 354
Db 297 DENSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKEFYVTSCTNTYFASGK 356
QY 355 GTTATVSKDDGNTTVMYDVNVDALNVNQLONGSMWLDKRAVAGSSGKVISGNVSPSKG 414
Db 357 GTTATVSKDDGNTTVMYDVNVDALNVNQLONGSMWLDKRAVAGSSGKVISGNVSPSKG 416
QY 415 KMDTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDG-ALNVSGK 473
Db 417 KMDTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDG-ALNVSGK 476
QY 474 KDNKPVRTTNVAPGVKEDGVNVAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQA 533
Db 477 DTNKPVRTTNVAPGVKEDGVNVAOLKGVANLNRRIDNVGNARAGIAQAIATAGLVQA 536
QY 534 YLPKSMMAIGDPTGREGAGYAIGYSSISDGMWIKGTASGNSRGHFGASASVGYOM 591
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Db 537 YLPKSMMAIGDPTGREGAGYAIGYSSISDGMWIKGTASGNSRGHFGASASVGYOM 594

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RESULT 11
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 598
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
US-09-377-155-13
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Query Match 90.8%; Score 2725.5; DB 4; Length 598;

Best Local Similarity 91.0%; Pred. No. 1e-203; Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

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QY 1 MNKIRITMNSALNAMYVSELTRNHTKRASATYKATVATLTLFATVQASANNEOEEDL 60
Db 1 MNKIRITMNSALNAMYVSELTRNHTKRASATYKATVATLTLFATVQANATD---DDDL 57
QY 61 YLDPVORTAVLYNSDEKGEKEKEEENSMAVYFENEKGVLTAREITLKAGDNLIKQ 120
Db 58 YLEPVORTAVLYNSDEKGEKEKEEED-SMAVYFENEKGVLTAREITLKAGDNLIKQ 116
QY 121 -----NGNFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTGLNFAKTAGTGD 170
Db 117 NTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTGLNFAKTAGTGD 176
QY 171 TNGDTVHLNGIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKDYLANAGWNIKGVP 230
Db 177 TNGDTVHLNGIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKDYLANAGWNIKGVP 236
QY 231 GTTASDNDVFRVTVTEFELSADTKTTTVNYESKDNKGKTEVKGAKTSVYKEKDGKLVY 290
Db 237 GTTASDNDVFRVTVTEFELSADTKTTTVNYESKDNKGKTEVKGAKTSVYKEKDGKLVY 296
QY 291 GKDGENGSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKEFYVTSCTNTY 350
Db 297 GKDGENGSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGOADKEFYVTSCTNTY 356
QY 351 ASGKTATVSKDDGNTTVMYDVNVDALNVNQLONGSMWLDKRAVAGSSGKVISGNV 410
Db 357 ASGKTATVSKDDGNTTVMYDVNVDALNVNQLONGSMWLDKRAVAGSSGKVISGNV 416
QY 411 PSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDG-ALN 469
Db 417 PSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDG-ALN 476
QY 470 VGSKKDNKPVRTTNVAPGVKEDGVNVAOLKGVANLNRRIDNVGNARAGIAQAIATAG 529
Db 477 VGSKKDNKPVRTTNVAPGVKEDGVNVAOLKGVANLNRRIDNVGNARAGIAQAIATAG 536
QY 530 LVOAYLPKSMMAIGDPTGREGAGYAIGYSSISDGMWIKGTASGNSRGHFGASASVGY 589
Db 537 LAOAYLPKSMMAIGDPTGREGAGYAIGYSSISDGMWIKGTASGNSRGHFGASASVGY 596
QY 590 QW 591
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QY	1	MNKYIRIIMNSALNAMYVVS	SELTNRHTRKASATVTAVALATLLFTVVASANNEEDL	60
Db	1	MNKYIRIIMNSALNAMYVVS	SELTNRHTRKASATVTAVALATLLFTVVASANNEEDL	57
QY	61	YLDPOQRIYAVLIYNSDEKGE	GKKEKVVENSWMAYFENKGYLIRREITLAKGDUKIKQ	120
Db	58	YLEPQRIYAVLIYNSDEKGE	GKKEKVVENSWMAYFENKGYLIRREITLAKGDUKIKQ	116
QY	121	-----	NGTNETYSILKRDJLPLTSVGEFKLSFSANGNKNVTJTSPTKGINFAKETAG	170
Db	117	NTNENTNENTNDSPTYS	ELKRDJLPLTSVGEFKLSFSANGNKNVTJTSPTKGINFAKETAG	176
QY	171	TNGDTTVHLNGIGSTL	DTJLTLNTGATTNVJNDNVTDDEKKRAASVKDVLNAGMNIKGVP	230
Db	177	TNGDTTVHLNGIGSTL	DTJLTLNTGATTNVJNDNVTDDEKKRAASVKDVLNAGMNIKGVP	236
QY	231	GTTASDNDVFRPTDY	TVEFLSADPRTTVJNVESSKNGKKEVYKIAKTSVTEKEKGKLYT	290
Db	237	GTTASDNDVFRPTDY	TVEFLSADPRTTVJNVESSKNGKKEVYKIAKTSVTEKEKGKLYT	296
QY	291	GKDKGENSSSTDEGGL	YTAKEVIDAVNKAAGRMKTTTANGOTGQADRFEVYTSCTNYF	350
Db	297	GKDKGENSSSTDEGGL	YTAKEVIDAVNKAAGRMKTTTANGOTGQADRFEVYTSCTNYF	356
QY	351	ASGKGTATVSKDDOG	NTVMADVNGDALNVNOLNSGWNIDSKRAVAGSSKGVISGNVS	410
Db	357	ASGKGTATVSKDDOG	NTVMADVNGDALNVNOLNSGWNIDSKRAVAGSSKGVISGNVS	416
QY	411	PSKGMDETVINAGNN	IEITRNGKNIDIASMTPOFSSVLSGAADAPTLTSLVDDGALN	469
Db	417	PSKGMDETVINAGNN	IEITRNGKNIDIASMTPOFSSVLSGAADAPTLTSLVDDGALN	476
QY	470	VGSKKDNKPVRTIT	NVAPGVKEGDVTNVNQAOLKGAONLNNRIDNVGDMARAGIAQAATAG	529
Db	477	VGSKKDNKPVRTIT	NVAPGVKEGDVTNVNQAOLKGAONLNNRIDNVGDMARAGIAQAATAG	536
QY	530	LVQATLPKSSMMAIGG	YTRGBAGATGYSSTSDGGMNIKTASGNSRGHGASASVGY	589

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0Y 1 MNKIVRIIMNSALNAMVYVSELTRNHTKASATVKTAVLATLTLFATVQASANNEOEEDL 60
Db 1 MNKISRIITMNSALNAMVYVSELTRNHTKASATVKTAVLATLTLFATVQANATD---DDL 57
0Y 61 YLDPQVRVAVLIVNSDKEGTGEKKEVENSQWAVYFNPKGVLTJAREITLTKAGDNLTKQ 120
Db 58 YLEPQRTAVVLSFRSDKEGTGEKGTED-SMWAVYFDEKRYLKKGATLLKAGDNLTKQ 116
0Y 121 -----NCTNFTTSLKXDLTDLTDSYGETKSEFSANGKNVNTSPDKGLNFAKETAG 170
Db 117 NTNEMTNENTNDSSTTYSLKXDLTDLTDSYETPKLSFGANGKNVNTSPDKGLNFAKETAG 176
0Y 171 TNGDTPVHLNGISGFLTDLTLNTGATTVYNDNVJTDDDEKKRAASYKDVYLNAGMNTIGVXP 230
Db 177 TNGDTPVHLNGISGFLTDLTLNTGATTVYNDNVJTDDDEKKRAASYKDVYLNAGMNTIGVXP 236
0Y 231 GTTASDNDVFWYPTVVEFLSADFTTYYNVESKONGKTEVKISAKTSVIEKXGKLT 290
Db 237 GTTASDNDVFWYPTVVEFLSADFTTYYNVESKONGKTEVKISAKTSVIEKXGKLT 296
0Y 291 GKDKENGSSSTDEGBGLYAKVEIDAVNKAQGRMKTTTANGOTGOADKEFYTSGTNYVF 350
Db 297 GKDKENGSSSTDEGBGLYAKVEIDAVNKAQGRMKTTTANGOTGOADKEFYTSGTNYVF 356
0Y 351 ASGKGTATVSKDQDGNITTVYNDVNVGDLANVQNLQNSGWNLSKRAVAGSSGKVISGNYV 410
Db 357 ASGKGTATVSKDQDGNITTVYNDVNVGDLANVQNLQNSGWNLSKRAVAGSSGKVISGNYV 416
0Y 411 PSKGMDETVINNAANNIEITPNGKNIDIASMTPOFSSVSLGACADAPTLTSDDD-ALN 469
Db 417 PSKGMDETVINNAANNIEITPNGKNIDIASMTPOFSSVSLGACADAPTLTSDDEGALN 476
0Y 470 VGSKDKNCPVRTITNAPGVKEGDVYNVALQKVAONLNNRIDNVGNNRAGITQAQIATAG 529
Db 477 VGSKANNCPPVRTITNAPGVKEGDVYNVALQKVAONLNNRIDNVGNNRAGITQAQIATAG 536
0Y 530 LVQAVLPGKSMATGGTGYRGEAGYALGYSISDQGNWIIKGTASGNSRGHFGASASVGY 589

```



Db 537 LAQAYLPKSKMAIGGCTYRGAGYAIGYSSISDGTGNMWIKGTASNSRQHGTSAVGI 596  
QY 590 QW 591  
Db 597 QW 598

## RESULT 14

US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 90.5%; Score 2716.5; DB 4; Length 598;  
Best Local Similarity 90.7%; Pred. No. 5e-203; Indels 15; Gaps 4;  
Matches 546; Conservative 13; Mismatches 28;

QY 1 MNKYYRIIWSALNAAWVSELTFRNHTRKASATVKTAVLATLTFATVQASANNEOEEDL 60  
Db 1 MNKYSRIIWSALNAAWVSELTFRNHTRKASATVKTAVLATLTFATVQANATD---DDDL 57  
QY 61 YLDFQRTAVLAVLIVSDKEGTEKEKEEENSMAVYNEKEGCVLTAREITLAKGDNLIKQ 120  
Db 58 YLEFVQRTAVLAVLIVSDKEGTEKEKEEED-SMAVYFDEKRVLAKAGITLLKAGDNLIKQ 116  
QY 121 -----NGTFFYSLLKDLTDLTSVGTKEKLSFGANGKKNVITSDTKGLNPAKETAG 170  
Db 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKKNVITSDTKGLNPAKETAG 176  
QY 171 TNGDTYHLNIGISTLIDTLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKP 230  
Db 177 TNGDTYHLNIGISTLIDTLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKP 236  
QY 231 GTTASDNDVDFVRYDYEFISADTKTTTVNESKDNKKEVEKIGAKTSVKEKDGKLYT 290  
Db 237 GTTASDNDVDFVRYDYEFISADTKTTTVNESKDNKKEVEKIGAKTSVKEKDGKLYT 296  
QY 291 GKDGGENSSSTDEEGELVTAKVIDAVNKAAGRMTTTTANGOTGOADFEFVTSGTNTF 350  
Db 297 GKDGGENSSSTDEEGELVTAKVIDAVNKAAGRMTTTTANGOTGOADFEFVTSGTNTF 356  
QY 351 ASGKGTATVATSKDOGNITVAVDVGDLVNVOLNONGMNLDSKAVAGSSGKVIISGNVS 410  
Db 357 ASGKGTATVATSKDOGNITVAVDVGDLVNVOLNONGMNLDSKAVAGSSGKVIISGNVS 416  
QY 411 PSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDG-ALN 469  
Db 417 PSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALN 476  
QY 470 VGSKKDNKPVRTITNVAPGVKEGDTNVNQAOLKGVAQNLNRRIDNDVGNARAGIAQAIATAG 529

Db 477 VGSKDANKPVRTITNVAPGVKEGDTNVNQAOLKGVAQNLNRRIDNDVGNARAGIAQAIATAG 536  
QY 530 LVQAYLPKSKMAIGGCTYRGAGYAIGYSSISDGTGNMWIKGTASNSRQHGTSAVGI 589  
Db 537 LAQAYLPKSKMAIGGCTYRGAGYAIGYSSISDGTGNMWIKGTASNSRQHGTSAVGI 596  
QY 590 QW 591  
Db 597 QW 598

## RESULT 15

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 89.4%; Score 2685; DB 4; Length 599;  
Best Local Similarity 89.4%; Pred. No. 1.4e-200; Indels 14; Gaps 4;  
Matches 538; Conservative 16; Mismatches 34;

QY 1 MNKYYRIIWSALNAAWVSELTFRNHTRKASATVKTAVLATLTFATVQASANNEOEEDL 60  
Db 1 MNKYSRIIWSALNAAWVSELTFRNHTRKASATVKTAVLATLTFATVQANATDDEDEE- 59  
QY 61 YLDFQRTAVLAVLIVSDKEGTEKEKEEENSMAVYNEKEGCVLTAREITLAKGDNLIKQ 120  
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QY 121 -----NGTFFYSLLKDLTDLTSVGTKEKLSFGANGKKNVITSDTKGLNPAKETAG 170  
Db 118 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKKNVITSDTKGLNPAKETAG 177  
QY 171 TNGDTYHLNIGISTLIDTLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKP 230  
Db 178 TNGDTYHLNIGISTLIDTLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKP 237  
QY 231 GTTASDNDVDFVRYDYEFISADTKTTTVNESKDNKKEVEKIGAKTSVKEKDGKLYT 290  
Db 238 GTTASDNDVDFVRYDYEFISADTKTTTVNESKDNKKEVEKIGAKTSVKEKDGKLYT 297  
QY 291 GKDGGENSSSTDEEGELVTAKVIDAVNKAAGRMTTTTANGOTGOADFEFVTSGTNTF 350  
Db 298 GKDGGENSSSTDEEGELVTAKVIDAVNKAAGRMTTTTANGOTGOADFEFVTSGTNTF 357  
QY 351 ASGKGTATVATSKDOGNITVAVDVGDLVNVOLNONGMNLDSKAVAGSSGKVIISGNVS 410  
Db 358 ASGKGTATVATSKDOGNITVAVDVGDLVNVOLNONGMNLDSKAVAGSSGKVIISGNVS 417  
QY 411 PSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDG-DALN 469  
Db 418 PSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGKALN 477  
QY 470 VGSKKDNKPVRTITNVAPGVKEGDTNVNQAOLKGVAQNLNRRIDNDVGNARAGIAQAIATAG 529



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Db 478 VSSKDANKPVRIITNVAPGVKESGDYTNVAQLKGVAAQLNNRIDNDGNARAGIAQAATAG 537
QY 530 LVQATLPGKSMMAIGGTYRGAGTAIGYSSISDGGNWTIKGTASGNSRGHFGASASVGY 589
Db 538 LVQATLPGKSMMAIGGTYRGAGTAIGYSSISDGGNWTIKGTASGNSRGHFGASASVGY 597
QY 590 QW 591
Db 598 QW 599
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Search completed: July 3, 2002, 08:10:12  
Job time: 524 sec

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PT meningitidis infections  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
CC The invention provides proteins (AA22201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AA22201-245) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g., a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to *Neisseria* bacteria, especially *Neisseria meningitidis*.  
CC  
XX  
SQ Sequence 591 AA:  
  
Query Match 100.0%; Score 3003; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2,1e-171;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNKIRIIMNSALNAMYVSELTRNHTKRASATVKTAVLATLLPFAVQASANNEQEDL 60  
DB 1 mkiylilmsalnawvvselttrnhkkrasatvktavlatllfatvgasannegeedl 60  
  
QY 61 YLDPVQRTAVAVLIVNSDKETGKEKEVEENSDMAVFNKGVLTAREITLKAGDNLIKQ 120  
DB 61 yldpvrtrvavllvnsdkegkgekeveensdwayfnkgyvltareitlkagdnlikq 120  
  
QY 121 NGTNTYSLKRDLDLTSVGTETKLSFANGKVNISDPKGLNFAKETAGTNDTTHLN 180  
DB 121 ngntfyslkkdlldltsvgteklsfsangknvnltsdtkglnfaketagtndtthln 180  
  
QY 181 GIGSLTDLTLTGATNTVNDVTDDEKRAASVKKVILNAGNIGKVRPGTTASDNVDF 240  
DB 181 gigsldtldtlngatntvndvtddekkraasvkkvilmnagwikvrgpttasdnvdf 240  
  
QY 241 VRTYDVEFLSADTKTTTAVNESKDKGKTEVKIGAKTSVIRKDDKLYTGDKGNGSS 300  
DB 241 vrtydveflsadtktttavnveskdngkktevkiqatsvirkddklytgdkngngss 300  
  
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DB 301 tdegglvtakevidavnkgarmktttanqgtgqadkfetvsgtnvtfasgkgtatv 360  
  
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DB 361 skddgntlvwvdyvndvdlvnvnlqnsqwnldskavagssgkvisgavspskmdetv 420  
  
QY 421 NINAGNNIETTRNGKNIDTSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKMPVR 480  
DB 421 ninagnniettrngknidtsmtpfssvslgagadaptlisvldgaldnvsgkdkmpvr 480  
  
QY 481 ITNVAPEGKEDVTNVAOLKGVANLNNRIDNVGNAAGIAQAIATAGLVQAYLPKGS 540  
DB 481 itnvapegkedvtvnvaolkgvannlnnrldnvgnagiaqaiataglvaylpkgs 540  
  
QY 541 MAIGGTYRGEAGYAIYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 591  
DB 541 maiggtyrgeagayaiyssisdgmniikgtasgnsrghfgasasvgyqw 591  
  
RESULT 2  
AA223746  
ID AA223746 standard; Protein; 591 AA.  
XX  
AC AA223746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of *Neisseria meningitidis*.  
XX  
KM Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX

OS *Neisseria meningitidis*.  
XX  
XX WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
XX 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
XX (UYOU) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI: 1999-418754/35.  
XX  
XX N-PSDB; AA85798.  
XX  
PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA:  
  
Query Match 100.0%; Score 3003; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2,1e-171;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNKIRIIMNSALNAMYVSELTRNHTKRASATVKTAVLATLLPFAVQASANNEQEDL 60  
DB 1 mkiylilmsalnawvvselttrnhkkrasatvktavlatllfatvgasannegeedl 60  
  
QY 61 YLDPVQRTAVAVLIVNSDKETGKEKEVEENSDMAVFNKGVLTAREITLKAGDNLIKQ 120  
DB 61 yldpvrtrvavllvnsdkegkgekeveensdwayfnkgyvltareitlkagdnlikq 120  
  
QY 121 NGTNTYSLKRDLDLTSVGTETKLSFANGKVNISDPKGLNFAKETAGTNDTTHLN 180  
DB 121 ngntfyslkkdlldltsvgteklsfsangknvnltsdtkglnfaketagtndtthln 180  
  
QY 181 GIGSLTDLTLTGATNTVNDVTDDEKRAASVKKVILNAGNIGKVRPGTTASDNVDF 240  
DB 181 gigsldtldtlngatntvndvtddekkraasvkkvilmnagwikvrgpttasdnvdf 240  
  
QY 241 VRTYDVEFLSADTKTTTAVNESKDKGKTEVKIGAKTSVIRKDDKLYTGDKGNGSS 300  
DB 241 vrtydveflsadtktttavnveskdngkktevkiqatsvirkddklytgdkngngss 300  
  
QY 301 TDEGGLVTAKETIDAVNKGAMKTTTANGOTGADKFEVTSGTNVTFASGKGTATV 360  
DB 301 tdegglvtakevidavnkgarmktttanqgtgqadkfetvsgtnvtfasgkgtatv 360  
  
QY 361 SKDDGNTVWYDVNVDALNVNOLQNSGWNIDSKAVAGSSGKVISGAVSPSKMDETV 420  
DB 361 skddgntlvwvdyvndvdlvnvnlqnsqwnldskavagssgkvisgavspskmdetv 420  
  
QY 421 NINAGNNIETTRNGKNIDTSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKMPVR 480  
DB 421 ninagnniettrngknidtsmtpfssvslgagadaptlisvldgaldnvsgkdkmpvr 480  
  
QY 481 ITNVAPEGKEDVTNVAOLKGVANLNNRIDNVGNAAGIAQAIATAGLVQAYLPKGS 540  
DB 481 itnvapegkedvtvnvaolkgvannlnnrldnvgnagiaqaiataglvaylpkgs 540

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DB 481 itnvapvkegdvtvnvaqlkgyvaqlnmridnvgnaraglaqataglvqaylpgkxm 540
OY 541 MAIGGTYRGEGAGYAIGYSSISDGGNMIKGTASGNSRGRHFGASASVGYQW 591
DB 541 malggtlyrgeagyalgyssisdggnmlkgtasgnsrghfgasasvgyqw 591

RESULT 3
AAU06171
ID AAU06171 standard; Protein; 591 AA.
XX
AC AAU06171;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain PMC21.
XX
FH Key
FT Peptide
FT Location/Qualifiers
FT 1..51
FT /label= Signal_peptide
FT 1..50
FT /label= C1
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FT 51..108
FT /label= V1
FT /note= "Variable region 1"
FT 52..591
FT /label= Mature_Nhha
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
FT 109..120
FT /label= C2
FT /note= "Conserved region 2"
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FT /label= V2
FT /note= "Variable region 2"
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FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT /label= V3
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FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..591
FT /label= C5
FT /note= "Conserved region 5"

XX WO20015182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09161.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from

```

```

PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
PS
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX Sequence 591 AA:

Query Match 100.0%; Score 3003; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No.2.1e-171;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKIYRIINMSALNANWVVSSELTNRNHTKRASATVATLTLFATVQASANNEQEDL 60
DB 1 mkiyriinmsalnanwvvseltlrnhtkrasatvlatllfavgasaneqeedl 60
OY 61 YIDPQRTAVAVLIVNSDKBGTGKEKEVEENSDMAVVENEGVLTAREITLKADNLKIQ 120
DB 61 yidpqrtaavlivnsdkbgtgkekeveensdvaayfnegyvltarelitkagdnlkikg 120
OY 121 NGTNFTYSLKKDLTDLTSVGTETKLSFSANGKNVNIISDTFGKLFARFETAGTNDTTVHLN 180
DB 121 ngtnftyslkkdldtldtsvgtetklsfsangknvnisdtfgklfarfetagtndttvhl 180
OY 181 GIGSTLTDTLLNGATTNVTNDNVTDDEKKRAASVKVDVLNAGNNIKGVKPGTTASNDVF 240
DB 181 gigtstltdtllngattnvtndnvtddekkraasvkvdlvnagnnikgvkpgttasndv 240
OY 241 VRTYDVEFELSNPTKTTTVNVEKDKGKTEVRIKATSYIRKKDKLVTGKRGKNGSS 300
DB 241 vrttydvefelssnptktttvnvekdkgktevrikatsyirkkdklvtgkrgkngss 300
OY 301 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANNGOTGOADKFETVSGTNVTFASGKTATV 360
DB 301 tdegeglvtakevidavnkragmrktttannngotgoadkfetvsgtnvtfasgkttatv 360
OY 361 SKDDGNTITVMVDVNGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSPSKKNDDEV 420
DB 361 skddgntitvmvdvngdallvnvqlnsgnldskaavagssgkviisgnvspkknndev 420
OY 421 NINAGNNIETLRGNKIDTATSMTPOPSVSLGAGDAPLPLSLDGLANVSKKDKPVR 480
DB 421 ninagnnietlrgnkidtatsmtpposvslgagdaplplslldglanvskkdkpvr 480
OY 481 ITNVAPVKEGDVTNVAOLKGVAQNINNRIDNDVGNARAGIAOIAITAGLVQAYLPKSKM 540
DB 481 itnvapvkegdvtvnvaqlkgyvaqlnmridnvgnaraglaqataglvqaylpgkxm 540
OY 541 MAIGGTYRGEGAGYAIGYSSISDGGNMIKGTASGNSRGRHFGASASVGYQW 591
DB 541 malggtlyrgeagyalgyssisdggnmlkgtasgnsrghfgasasvgyqw 591

RESULT 4
AAI23741
ID AAI23741 standard; Protein; 591 AA.
XX
XX AAI23741;

```

```

XX 08-SEP-1999 (first entry)
DE A surface protein of Neisseria meningitidis.
XX Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX Neisseria meningitidis.
OS Neisseria meningitidis.
XX MO9931132-A1.
XX 24-JUN-1999.
XX 14-DEC-1998; 98WC-AU01031.
XX 12-DEC-1997; 97GB-0026398.
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYOU) UNIV QUEENSLAND.
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85793.
XX Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX Claim 1; Page 104-106; 132pp; English.
XX The present sequence represents a surface protein of Neisseria
XX meningitidis which is approximately 62 kDa. The N. meningitidis
XX surface glycoproteins, nucleic acids, the primers and optionally
XX a thermostable polymerase, or antibodies are useful in a kit for
XX the detection or diagnosis of N. meningitidis infection in humans.
XX The N. meningitidis surface glycoproteins can also be used to
XX prevent or treat N. meningitidis infection in humans, especially
XX in the form of vaccines. The proteins and antibodies can also
XX be used to identify immunoreactive peptides.
XX
SQ Sequence 591 AA:

Query Match          99.4%; Score 2984; DB 20; Length 591;
Best Local Similarity 99.5%; Pred. No. 2,9e-170;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKIRIIMNSALNAMYVSELTFRNHTRKASATVATVATLTFATVQASANEQEDL 60
   ||:|||||
   1 mne||r||l||m||ns||al||na||m||v||se||lt||fr||nh||tr||k||a||s||a||t||v||a||t||v||a||t||l||f||a||t||v||q||a||s||a||n||e||q||e||d||
Db 1 me||l||r||l||m||ns||al||na||m||v||se||lt||fr||nh||tr||k||a||s||a||t||v||a||t||l||f||a||t||v||q||a||s||a||n||e||q||e||d|| 60

QY 61 YLDVQVQTVAVLIYNSDKEGEGEKEKEEENSDMAVFNREKGVFLARETTLKAGDNLIKQ 120
   |||||
   61 yldvq|v|q|t|v|a|v|l|i|y|n|s|d|k|e|g|e|g|e|k|e|k|e|e|e|n|s|d|m|a|v|f|n|e|k|g|v|f|l|a|r|e|t|t|l|k|a|g|d|n|i|k|q|
Db 61 yldvq|v|t|v|a|v|l|i|y|n|s|d|k|e|g|e|k|e|k|e|e|e|n|s|d|w|a|v|i|n|e|k|g|v|l|a|r|e|t|l|k|a|g|d|i|k|q| 120

QY 121 NGTFSTSLKEDLDLFSVTEKLSFSANGKNVITSDTKGLNFPAKETAGTNGDTTVHLN 180
   |||||
   121 ng|t|f|s|t|s|l|k|e|d|l|d|l|f|s|v|t|e|k|l|s|f|s|a|n|g|k|n|v|i|t|s|d|t|k|g|l|n|f|a|k|e|t|a|g|t|n|g|d|t|v|h|l|n|
Db 121 ng|t|f|y|s|i|k|k|d|i|c|l|s|v|g|e|k|l|s|f|s|a|n|g|k|n|v|i|t|s|d|t|k|g|l|n|f|a|k|e|t|a|g|t|n|g|d|t|v|h|l|n| 180

QY 181 GIGSTLDTLTANTGATTNVTNDNTTDEKKRAASVKDVLNAGWNIKGVPPTASDNVDF 240
   |||||
   181 gi|g|s|t|l|d|t|l|t|n|g|a|t|t|n|v|t|n|d|n|t|t|d|e|k|k|r|a|a|s|v|k|d|v|l|n|a|g|w|n|i|k|g|v|p|p|t|a|s|d|n|v|d|f|
Db 181 gi|g|s|t|l|d|t|l|n|g|a|t|t|n|v|t|n|d|n|t|d|e|k|k|r|a|a|s|v|k|d|v|l|n|a|g|w|i|k|g|v|k|p|p|t|a|s|d|n|v|d|f| 240

QY 241 VRTYDVEFLSADTKRTTVNVEKDKNGKTEVKIGAKISYIKKDKGLVTGDKGENSS 300
   |||||
   241 v|r|t|y|d|v|e|f|l|s|a|d|t|k|r|t|t|v|n|v|e|k|d|k|n|g|k|t|e|v|i|g|a|k|i|s|y|i|k|k|d|k|g|l|v|t|g|d|k|e|n|s|s|
Db 241 v|r|t|y|d|v|e|f|l|s|a|d|t|k|t|t|v|n|v|e|k|d|k|n|g|k|t|e|v|i|g|a|k|i|s|y|i|k|e|k|g|k|l|v|t|g|k|d|k|e|n|s|s| 300

QY 301 TDEEGGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEFTVTSCTNTYFASGKGTATV 360
   |||||
   301 t|d|e|e|g|g|l|v|t|a|k|e|v|i|d|a|v|n|k|a|q|m|r|k|t|t|t|a|n|g|o|t|g|o|a|d|k|f|e|f|t|v|t|s|c|t|n|t|y|f|a|s|g|k|g|t|a|t|v|
Db 301 t|d|e|g|e|g|l|v|t|a|k|e|v|i|d|a|v|n|k|a|q|m|r|k|t|t|a|n|g|t|c|g|a|d|k|f|e|l|v|t|s|c|t|n|t|f|a|s|g|k|t|a|t|v| 360

QY 361 SKDQGNITVYDVNVGDLNVLNOLNSGMNLDKRAVAGSSGKVIISGNVSPSKGMDET 420
   |||||
   361 s|k|d|q|g|n|i|t|v|y|d|v|n|v|g|d|l|n|v|l|n|o|l|n|s|g|m|n|l|d|k|r|a|v|a|g|s|s|g|k|v|i|i|s|g|n|v|s|p|s|k|g|m|d|e|t|v|

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Db 361 skddqgnltvmydvnvgdalnvnqdlqnsqwnldskavagsgkviisgnvpskqkmdetv 420
   |||||
QY 421 NINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVYGDALNVGSKKDKKPYR 480
   |||||
Db 421 nina|g|n|n|i|e|i|t|r|n|g|k|n|i|d|a|t|s|m|t|p|q|f|s|s|v|s|l|g|a|g|a|d|a|p|t|l|v|y|g|d|a|l|n|v|g|s|k|k|d|k|k|p|y|r| 480

QY 481 ITNVAPKVEGDVTNVAQLKVAQNANNRIDNVDAARAGIAQATATAGIYQAYLPGKSM 540
   |||||
Db 481 i|t|n|v|a|p|k|v|e|g|d|v|t|n|v|a|q|l|k|v|a|q|n|a|n|n|r|i|d|n|v|d|a|r|a|g|i|a|q|a|t|a|t|a|g|i|y|q|a|y|l|p|g|k|s|m| 540

QY 541 MATGGTYGEGAGYATGYSTSDGNNMIIKGTASGNSRCHFGASASVGYQM 591
   |||||
Db 541 ma|t|g|g|t|y|g|e|g|a|g|y|a|t|g|y|s|t|s|d|g|n|n|m|i|i|k|g|t|a|s|g|n|s|r|c|h|f|g|a|s|a|s|v|g|y|q|m| 591

RESULT 5
AAU06175
ID AAU06175 standard; Protein; 591 AA.
XX AC
XX AAU06175;
XX 24-OCT-2001 (first entry)
XX N. meningitidis EG329 surface antigen Nhma polypeptide sequence.
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain EG329.
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..108
FT /label= V1
FT /note= "Variable region 1"
FT Region 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT Region 121..124
FT /label= V2
FT /note= "Variable region 2"
FT Region 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT Region 189..210
FT /label= V3
FT /note= "Variable region 3"
FT Region 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT Region 230..236
FT /label= V4
FT /note= "Variable region 4"
FT Region 237..591
FT /label= C5
FT /note= "Conserved region 5"
PN W0200155182-A1.
XX 02-AUG-2001.
PD 25-JAN-2001; 2001WO-AU00069.
PF 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYOU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
PI WPI; 2001-488774/53.
XX N-PSDB; AAS09165.
DR

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XX New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain EG329 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 591 AA:
Query Match 99.4%; Score 2984; DB 22; Length 591;
Best Local Similarity 99.5%; Pred. No. 2.9e-170;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNKTYRIINSLNMAWVSELTNRHTRKASATVTAVALATLTFATVOASANEQEEDL 60
Db 1 mnelirllmalnaawvsvseltrhrtrkasaatvtavlatllftvtgasanneqe 60
QY 61 YLDVQRTVAALIVNSDEKGEKEKEVEBNSDVAVYENKGVLTAREITLAKGNLIKQ 120
Db 61 yldpvlrtvavllivnsdkegkgekevnsdwayfnekgyltareitlkagdnlikq 120
QY 121 NGTNTYSLKKDLDNLTSGVTEKISFSANGNKVNITSDPTKGNFKETAGTQDTVHN 180
Db 121 ngnttlyslkkdldltsgvtekisfsanagnvnitlstdtkgnlftaketaagtqdtvhn 180
QY 181 GIGSLTDTLLNTGATVNTNDNVTDDEKRRASVADVLNAGMNTKGVPGTTASDNVDF 240
Db 181 gigslltldtllntgatvntndnvtddekrraasvadvlnagwnlkgykpgttaadnvd 240
QY 241 GIGSLTDTLLNTGATVNTNDNVTDDEKRRASVADVLNAGMNTKGVPGTTASDNVDF 240
Db 241 gigslltldtllntgatvntndnvtddekrraasvadvlnagwnlkgykpgttaadnvd 240
QY 241 VRTYDTVEFLSADRTKTTVNVESKNGKRTVEYKIGAKTSVIEKDKLVTKGKGENGSS 300
Db 241 vrtydteflsadtktttvnnveskngkrtveykigaktsviekdkglvtgkdgengss 300
QY 301 TDEGGLTAKVETIDAVNKAQRMTTANOTGADKFEYVTSCTNVTFAAGKGTATV 360
Db 301 tdeggltakevidavnkagrmtttanotgadkfevytsctnvtfagsgkgtatv 360
QY 361 SKDDGNTTVMVDVNGDALVYNQLONSGMNDSKAVAGSSGKTVISGNVSPKGMDET 420
Db 361 skddgnttvmvdvngdalvynqlosgmndskavagssgkvtvisgnvspkgymdetv 420
QY 421 NINAGNIEITFRGNKNIDIASMTPOFSSVSIGAGADAPTLISVDGALNVGSKKNK 480
Db 421 ninagnieitfrgnknidiasmtpoessvsigagadaptilsvdgdalnvsgkknk 480
QY 481 ITNVAPEGVGTNVAQLKGAOVLNLRIDVNCNARAGTQATATAGTQVAYLPKSM 540
Db 481 itnvapegvgtntvaqlkgaovlnlrldvncnaratgtaqatagtlvaylpkxsm 540
QY 541 MAIGGTYRGEAGYAIAGSSISDGNMIIKGTASGNSRGHFAGASAVGQW 591
Db 541 maiggtyrgeagyaigssisdggnwllkgtasgnsrghfagaassvgqw 591

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XX AAY57045;
AC 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029: Nisseria meningitidis: surface fibril protein; HSF; diagnosis;
XX infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90
FT /note= "Encoded by AAT"
FT Misc-difference 92
FT /note= "Encoded by GAT"
FT Misc-difference 98
FT /note= "Encoded by AAC"
FT Misc-difference 108
FT /note= "Encoded by AATC"
FT Misc-difference 123
FT /note= "Encoded by ACA"
FT Misc-difference 269
FT /note= "Encoded by AAA"
FT Misc-difference 389
FT /note= "Encoded by CGT"
XX
PN W0958683-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-053103/04.
XX
DR N-PSDB: AA239865.
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.
XX
PS This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes.
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
SQ Sequence 591 AA:
Query Match 99.1%; Score 2977; DB 21; Length 591;

```

Best Local Similarity 99.0%; Pred. No. 7.6e-170;  
Matches 585; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNKIRIIMNSALNAMYVSELTRNHTKRASATYKTAVALTLFLPATVQASANNEOEEDL 60
DB 1 mnkiriimnsalnawavseltrnhkkrasatvktavlatllifavqasanneegeeidl 60
OY 61 YLDPVORTVAVLIVNSDKETGKEKEVEENSDMAVFNENGVLTAREITLKAGDNLIKQ 120
DB 61 yldpvgortvaavllvnsdkegtgekeveesdmavfydenkvltarelitlkagdnlikq 120
OY 121 NGNFTYSLKKDLTDLTSVTEKISFSANGKNVITSDTGLNPAKTAGTNGTTHLN 180
DB 121 ngnftyslkkdltdltsvtekisfsangknvitsdtglnpaktagtngtthln 180
OY 181 GIGSTLTDLTLLNGATNNVNDVTDDEKKRAASVKKVLAAGNMIKVKKGTGTSDDVDF 240
DB 181 gisgstdltdllngatnnvndvtddekkraasvkvlaagnmikvkkgtgtsddvdf 240
OY 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSVIEKEDGKLVYGDKNGSS 300
DB 241 vrydveflsadtktttvnveskdkngktevkgaktsviekedgklvygdngss 300
OY 301 TDBEGGLVTAKEVIDAVNKAAGMRKTTTANGQTQADKEFTVTSNTVTPASGKTATV 360
DB 301 tdegglvtakevidavnkagmrktttangqtqadkeftvtsntvtpasgkttatv 360
OY 361 SKDDQGNITVMYDVNVGDALNVNQLONSGMNIDSKAVAGSSGKVISGNVSPSKKMDETV 420
DB 361 skddqgnitvmylvdvnvgdalnvnqlngsgwnldskavagssgkvisgnvpskkgmdelv 420
OY 421 NINAGNNIETTRNGKNIDTATSMTPQSSVSLGAGADAPTLVSDGALNVGSKKDNKPV 480
DB 421 ninagnniettrngknidatatsmtppqssvslgagadaptlvsgdalnvsgskkdnkpv 480
OY 481 ITTNVAPVKEGSDVTNVAOLKGVQONLNNRIDNDVGNARAGIAQAIATAGLYQAYLPKSKM 540
DB 481 ittnvapvkegsdvtvnvaolkgvqonlnnriddndvgnaragiagaiaataglyqaylpkksm 540
OY 541 MAIGGCTYRGEAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYQW 591
DB 541 maiggtcyrgeagyaigyssisdgnmiiikgtasgnsrghfgasasvgyqw 591

RESULT 7
AAY23737
ID AAY23737 standard; Protein; 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
  immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98MO-A01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PA (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
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DR N-PSDB; AAX85788.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections

PS Claim 1; Page 86-87; 132pp; English.

XX  
The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX  
SQ Sequence 592 AA;

Query Match 99.0%; Score 2971.5; DB 20; Length 592;

Best Local Similarity 99.0%; Pred. No. 1.6e-169;  
Matches 586; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

```
OY 1 MNKIRIIMNSALNAMYVSELTRNHTKRASATYKTAVALTLFLPATVQASANNEE-OEED 59
DB 1 mnkiriimnsalnawavseltrnhkkrasatvktavlatllifavqasanneerpkkd 60
OY 60 LYDPVORTVAVLIVNSDKETGKEKEVEENSDMAVFNENGVLTAREITLKAGDNLIK 119
DB 61 lydpvgortvaavllvnsdkegtgekeveesdmavfydenkvltarelitlkagdnlik 120
OY 120 QNGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTGLNPAKTAGTNGTTHVL 179
DB 121 qngtnftyslkkdltdltsvteklsfsangknvitsdtglnpaktagtngtthvl 180
OY 180 NGIGSTLTDLTLLNGATNNVNDVTDDEKKRAASVKKVLAAGNMIKGVKPGTTASDND 239
DB 181 ngigstdltdltdllngatnnvndvtddekkraasvkvlaagnmikgvkpgttasdhvd 240
OY 240 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSVIEKEDGKLVYGDKNGSS 299
DB 241 fvrydveflsadtktttvnveskdkngktevkgaktsviekedgklvygdkgngss 300
OY 300 STDEGGLVTAKEVIDAVNKAAGMRKTTTANGQTQADKEFTVTSNTVTPASGKTATV 359
DB 301 stdegglvtakevidavnkagmrktttangqtqadkeftvtsntvtpasgkttat 360
OY 360 VSKDDQGNITVMYDVNVGDALNVNQLONSGMNIDSKAVAGSSGKVISGNVSPSKKMDET 419
DB 361 vskddqgnitvmylvdvnvgdalnvnqlngsgwnldskavagssgkvisgnvpskkgmdet 420
OY 420 VNINAGNNIETTRNGKNIDTATSMTPQSSVSLGAGADAPTLVSDGALNVGSKKDNKPV 479
DB 421 vninagnniettrngknidatatsmtppqssvslgagadaptlvsgdalnvsgskkdnkpv 480
OY 480 RITNVAPVKEGSDVTNVAOLKGVQONLNNRIDNDVGNARAGIAQAIATAGLYQAYLPKSK 539
DB 481 ritnvapvkegsdvtvnvaolkgvqonlnnriddndvgnaragiagaiaataglyqaylpkks 540
OY 540 MMAIGGCTYRGEAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYQW 591
DB 541 mmaiggtcyrgeagyaigyssisdgnmiiikgtasgnsrghfgasasvgyqw 592

RESULT 8
AAY23740
ID AAY23740 standard; Protein; 594 AA.
XX
AC AAY23740;
XX
DT 08-SEP-1999 (first entry)
XX
```



DE A surface protein of Neisseria meningitidis.  
 XX Surface protein; surface glycoprotein; infection; vaccine;  
 KM immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.  
 PN MO9931132-A1.  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX (OYUO ) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA.  
 XX  
 DR WPI: 1999-418754/35.  
 DR N-PSDB: AAX85792.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 100-101; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX  
 SO Sequence 594 AA:

Query Match 91.9%; Score 2758.5; DB 20; Length 594;  
 Best Local Similarity 92.3%; Pred. No. 8.4e-157;  
 Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

OY 1 MNKIYRIIWNLSALNAWVSELTNRNHTKRASATVKTAVLATLLEFATVOASANNEOEEDL 60  
 DB 1 mkkiYRIIwnsAlnAwvseLtrnhkRasAtvAtLaTlLfAtVgStld--dddl 57  
 OY 61 YLDPVQRTAVAVLIIVNSDEGEGERKEVEENSDWAYFENKGVLTARETTIKAGDNLKTKQ 120  
 DB 58 YLdpvqRtAvAvLIivNsDeGeGeRkEvEeNsDwAyFenKgvLtArEtTiKAgDnLkTkQ 116  
 OY 121 -----NGTNFTYSLKKDLTDLTSVTEKLSFSAKNGKNVITSPTKGLINFAKETAGTNGD 174  
 DB 117 ntntentnassfyslKkdltldtsvgtelksfsansknvitsdckglnfakktetngd 176  
 OY 175 TTVHLNAGSGSTITDPLLTGATNTVNDVYDDEKKRAASVKDVINAGNNIKGVPGTTA 234  
 DB 177 TtvhLnAgSgStITdPlLTgATnTvNdVYdDeKkRAASvKdVINAGnNIKGVpGtTa 236  
 OY 235 SDNVQFVRYDVEFLSADTKTTTNNVESKONGKTEYKIGKTSVIRKEDOKLVTGKMK 294  
 DB 237 sDnvQfVrYdVeFlsAdTKtTTnNvEsKongKtEyKIGkTsVIRkEdOkLvtGkMk 296  
 OY 295 GENSGSTDEGEGLVTAKEVIDAVNKRAGRMKTTTANGOTGQADKEETVYSTNTVFASGK 354  
 DB 297 gEnSgStDeGeGLvTAkEViDAVNKRAGRMkTTtANGoTGQADkEEtVysTnTvfASgK 356  
 OY 335 GTTATVSKDDGCGNTVTVDVNGALNNQLONSGMNLDKSAVAGSGKVISGNVSPSKG 414  
 DB 357 gTtAtVskDdGcgNtVtVdVNgAlNnQlOnSGMnLDkSAvAGsGkViSGnVspSkG 416

OY 415 KMDFTVINAGNNIETTRNGKNIDIATSWTPOFSSSVSLGADAPLTSDGD-ALNVGSK 473  
 DB 417 kmDftvInAGnnIEtTRngKniDiATsWtPofSSsvSlGAdApLTsDgD-ALnvGsk 476  
 OY 474 KDNKPYRITNNVAPGVKEGDVTNVAQLKGVAQNLLNNRIDVNDGNARAGIAQAIATAGLYQA 533  
 DB 477 dKnKpYrItNnVApGvKEgDvTnVaqLkGvAQnLLnnRIdVnDgnARaGiAQAIATaGLyQa 536  
 OY 534 YLPGKSMMAIGGCTTRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFCASASVGYQW 591  
 DB 537 yLpGksMmaIGgCtTrGeAGyAIIGySSisDgnWIIkGtASgNsRGhFcASaSVgyQw 594

RESULT 9  
 ID AAY57044 standard; Protein; 594 AA.  
 AC AAY57044;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
 XX  
 KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
 XX infection; treatment; prevent; antibacterial drug.  
 OS Neisseria meningitidis.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 104  
 FT /note= "Encoded by AATC"  
 PN WO9958683-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99WO-EP03255.  
 XX  
 PR 13-MAY-1998; 98GB-0010276.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Ruelle J;  
 XX  
 DR WPI: 2000-053103/04.  
 DR N-PSDB: AAZ39864.  
 PT  
 PT New polypeptide from neisseria meningitidis useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal -  
 XX  
 PS Claim 4; Fig 2; 74pp; English.  
 XX

This is the Nisseria meningitidis BASB029 amino acid sequence from  
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
 CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
 CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
 CC meningitidis infection in a mammal. Compositions containing BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with Neisseria  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.



```

OY 175 TVVHLNGISGTLTDLTLNTGATTNTNDVTDDEKKRAASVVDVNLAGNNIKGVKPGTTA 234
    |||
Db 177 tvvhlingisgltldtlntgattntvndvtddekkraasvkdvlagnmllgvykpgtta 236
OY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESSKDNKGKTEVRIGAKTSYIKERDKLYTGKDK 294
    |||
Db 237 sdnvdfvrtcydveflsadtktttvnevskdngkrlevkigaktsvikekdglvygkdk 296
OY 295 GENGSTDEGELVTAKEVIDAVNKGWMMKTTTANGQGOADKFTVTYSGTNVTPASRG 354
    |||
Db 297 gendstdegeglvtakevldavnkagwmmktttangqgqadkftvtsgtnvtpasrg 356
OY 355 GTTATVSKDDQGNITVMYDVNVDALNVNQLONGNNLDSKAVAGSSGKVISGNVSPSKG 414
    |||
Db 357 gttatvskddqgnitvmvdyvndvdaalnvnqlongnynlaskavagssgkvysgnvpskrg 416
OY 415 KMDETVINAGNNIETTRNGKNIDITATSMTPQFSSVSLGAGADPRTLSDVGD-ALNVGSK 473
    |||
Db 417 kmdevlnagnnielttrngknidiatmtcpqfssvslgagadaprtlsvddagalnvgsk 476
OY 474 KDNKPVRTTNVAPGYKEGDTVNAQLKGYAQNUNNRIDVNDGNARAGIAQAIATAGLVQA 533
    |||
Db 477 dnkpvrtlnvapgykegdtvnaqlkgyaqnlnnrldvndgnaraglaqalaglvqa 536
OY 534 YLPGKSMAIIGGCTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYQW 591
    |||
Db 537 ylpgksmaiggyctyrgeagyaigyssisdggnmllkgtasgnsrghfgasasvgyqw 594

```

RESULT 11  
AAV23739  
ID AAV23739 standard; Protein; 594 AA.

XX AAV23739;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;  
KM Immunoreactive peptide.

OS Neisseria meningitidis.

PN W0931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98MO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85791.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX Claim 1; Page 95-97; 132pp; English.

CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 594 AA;

Query Match 91.3%; Score 2740.5; DB 20; Length 594;  
Best Local Similarity 92.1%; Pred. No. 1e-155;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

```

OY 1 MNKIRIINNSALINAVVSELRNHTKRASATVKTAVLATFLPATVQASANNEQEDL 60
    |||
Db 1 mnlkryilwnsalnavvselrnlhtkrasatvatlatllfavegnact---dddl 57
OY 61 YDVPQRTAVAVLVNSDKETGEKEKEVENSQWAVFNEKGVLTARELTAKADNKKIQ 120
    |||
Db 58 ylepvqrtaavlvsfrsdegekegeked-smnavyfderyvkaagaitlkagdnllkrg 116
OY 121 -----NGTNFTYSLKKDFTDLTSVTEKLSFSANKNVNTSDTKGLNFAKETAGTNGD 174
    |||
Db 117 nhtentndesfgyalskkdltdltsveteklsfnganknitsdctglnfaketagtngd 176
OY 175 TVVHLNGISGTLTDLTLNTGATTNTNDVTDDEKKRAASVVDVNLAGNNIKGVKPGTTA 234
    |||
Db 177 tvvhlingisgltldtlntgattntvndvtddekkraasvkdvlagnmllgvykpgtta 236
OY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESSKDNKGKTEVRIGAKTSYIKERDKLYTGKDK 294
    |||
Db 237 sdnvdfvrtcydveflsadtktttvnevskdngkrlevkigaktsvikekdglvygkdk 296
OY 295 GENGSTDEGELVTAKEVIDAVNKGWMMKTTTANGQGOADKFTVTYSGTNVTPASRG 354
    |||
Db 297 dengstdegeglvtakevldavnkagwmmktttangqgqadkftvtsgtnvtpasrg 356
OY 355 GTTATVSKDDQGNITVMYDVNVDALNVNQLONGNNLDSKAVAGSSGKVISGNVSPSKG 414
    |||
Db 357 gttatvskddqgnitvmvdyvndvdaalnvnqlongnynlaskavagssgkvysgnvpskrg 416
OY 415 KMDETVINAGNNIETTRNGKNIDITATSMTPQFSSVSLGAGADPRTLSDVGD-ALNVGSK 473
    |||
Db 417 kmdevlnagnnielttrngknidiatmtcpqfssvslgagadaprtlsvddagalnvgsk 476
OY 474 KDNKPVRTTNVAPGYKEGDTVNAQLKGYAQNUNNRIDVNDGNARAGIAQAIATAGLVQA 533
    |||
Db 477 dnkpvrtlnvapgykegdtvnaqlkgyaqnlnnrldvndgnaraglaqalaglvqa 536
OY 534 YLPGKSMAIIGGCTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYQW 591
    |||
Db 537 ylpgksmaiggyctyrgeagyaigyssisdggnmllkgtasgnsrghfgasasvgyqw 594

```

RESULT 12  
AAU06179  
ID AAU06179 standard; Protein; 594 AA.  
XX AAU06179;  
AC AAU06179;  
XX 24-OCT-2001 (first entry)  
DT N. meningitidis B2198 surface antigen Nhma polypeptide sequence.  
XX N. meningitidis B2198 surface antigen Nhma polypeptide sequence.  
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
XX Neisseria meningitidis strain B2198.  
OS  
XX  
FH Key Location/Qualifiers  
FH 1..50 /label= C1  
FH Region /note= "Conserved region 1"  
FH 51..104 /label= V1  
FH /note= "Variable region 1"  
FH 105..116 /label= C2  
FH Region



CC prevent or treat *N. meningitidis* infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX Sequence 598 AA:

Query Match 90.8%; Score 2725.5; DB 20; Length 598;  
 Best Local Similarity 91.0%; Pred. No. 7.9e-155;  
 Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

```

QY 1 MNKIRIINNSALNMAWVSELTNRNHTKRASATVKTAVLATLLEFATVQASANNEOEEDL 60
DB 1 mkiyriiwnsalnawvsseltrnhtrkasatvatatlilfatvganard---dddl 57
QY 61 YLDPQRYVAVLIVNSDKGEKGEKEEENSMWAVYENKGVLAAREITLAKADNLKIKQ 120
DB 58 ylepvgrlavvlisfrsdekgekteged-snwavyfdekrylkagatlkkagdnlkikq 116
QY 121 -----NCTNPFYSLKDLTDLTSVCTEKLSFASAGNKNVNTSDTKINFAKETAG 170
DB 117 ntentnentndssftyslkkdltdltsvereklsifganqknvnltsdtklnfaketaq 176
QY 171 TNGDTTTLNGLIGISTLTDTLTNTGATTNTNTNDNTDDEKRRASVQDVNAGMNIGKVP 230
DB 177 tngdptvlhnglsglstdltdlntgatlntvndnvddekkrasvkvdvlnagwnlkgyvp 236
QY 231 GTTASDNDVFRVYDVEFLSADIKTTTVNVEKDKGKTEVKIGAKTSVIREKDGKLVY 290
DB 237 gtltaadndvfrlygtvelflsadlktltvnveskngkktevkigaktsvirekdgklyt 296
QY 291 GKDKGENSSPTDEGGIYTAKEVIDAVNKAQRMTTNTANGQTGADKREYTSIGNVTF 350
DB 297 gkqkdeangsstdegeylvakevidavnkagwrmtltanagqlgqadklevtsglkyvlf 356
QY 351 ASGKGTATVSKDQGNITVMTDVNWGDALNVNOLONGSMNLSKAVAGSSGKVISGANS 410
DB 357 asgngtatavsddgnglvtkydvngvdalnvnqngnswndskavagssgkvisgans 416
QY 411 PSKGMDEFTVINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADPTLSVDCD-ALN 469
DB 417 pskymdeftvinnagnniettrngknidiatmtpfssvslgagadpctlsvddegaln 476
QY 470 VSKKDNKPVRTTNAPGKEGDVNVNQLKGVANLNRRINNVGNMAAGIQAQIATFG 529
DB 477 vskkdnkpvrttnapgkegdvnnvnlkqvannlnrrinnvgnmaagiqaqiatag 536
QY 530 LVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGMNIIKGTASNSRCHFGASASVGY 589
DB 537 laqaylppksmmaiggtyrgeagyaigyssisdgmniiikgtasnsrghfgaasvgy 596
QY 590 QW 591
DB 597 qw 598

```

RESULT 14

AAU06177 ID AAU06177 standard; Protein: 598 AA.

AC AAU06177;

DT 24-OCT-2001 (first entry)

DE *N. meningitidis* H15 surface antigen Nhma polypeptide sequence.

KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.

OS *Neisseria meningitidis* strain H15.

XX Key Location/Qualifiers

FT Region 1..50 /Label= C1

```

FT /note= "Conserved region 1"
FT Region 51..104
FT /Label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /Label= C2
FT /note= "Conserved region 2"
FT Region 117..130
FT /Label= V2
FT /note= "Variable region 2"
FT Region 131..194
FT /Label= C3
FT /note= "Conserved region 3"
FT Region 195..216
FT /Label= V3
FT /note= "Variable region 3"
FT Region 217..235
FT /Label= C4
FT /note= "Conserved region 4"
FT Region 236..242
FT /Label= V4
FT /note= "Variable region 4"
FT Region 243..598
FT /Label= C5
FT /note= "Conserved region 5"

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PM WO20015182-A1.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-AU00069.

PR 25-JAN-2000; 2000US-0177917.

PA (UYOU ) UNITV QUEENSLAND.

PI Peak IRA, Jennings MP;

DR WPI: 2001-488774/53.

DR N-PSDB: AAS09167.

PT New Nhma surface antigen polypeptides and polynucleotides from  
 PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
 PT preventing broad spectrum of *Neisseria meningitidis* -

PS Claim 9; Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel *Neisseria*  
 CC *meningitidis* mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of *N. meningitidis*, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of *N. meningitidis* strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhma  
 CC from *N. meningitidis* strain H15 is 1 of 10 Nhma polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
 CC the present invention.

XX Sequence 598 AA:

Query Match 90.8%; Score 2725.5; DB 22; Length 598;  
 Best Local Similarity 91.0%; Pred. No. 7.9e-155;  
 Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

```

QY 1 MNKIRIINNSALNMAWVSELTNRNHTKRASATVKTAVLATLLEFATVQASANNEOEEDL 60
DB 1 mkiyriiwnsalnawvsseltrnhtrkasatvatatlilfatvganard---dddl 57

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XX The invention provides proteins (AAV27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AAV99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX  
SQ Sequence 591 AA:

Query Match 9.8%; Score 59; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVINAGNNIEI 442  
DB 372 ydvnvgdalnvvnqlqngswnlidskavagssgkvisgnvpskgykndetvlnagnniel 430

RESULT 11

AAV23741 ID AAV23741 standard; Protein; 591 AA.

AC AAV23741;

DT 08-SEP-1999 (first entry)

DE A surface protein of *Neisseria meningitidis*.

KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.

OS *Neisseria meningitidis*.

PN W09931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.  
(UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.  
N-PSDB; AAX85793.

PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
meningitidis infections

PS Claim 1; Page 104-106; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

SQ Sequence 591 AA:

Query Match 9.8%; Score 59; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVINAGNNIEI 442  
DB 372 ydvnvgdalnvvnqlqngswnlidskavagssgkvisgnvpskgykndetvlnagnniel 430

RESULT 12

AAV23746 ID AAV23746 standard; Protein; 591 AA.

AC AAV23746;

DT 08-SEP-1999 (first entry)

DE A surface protein of *Neisseria meningitidis*.

KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.

OS *Neisseria meningitidis*.

PN W09931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.  
(UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.  
N-PSDB; AAX85798.

PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
meningitidis infections

PS Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

SQ Sequence 591 AA:

Query Match 9.8%; Score 59; DB 20; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVINAGNNIEI 442  
DB 372 ydvnvgdalnvvnqlqngswnlidskavagssgkvisgnvpskgykndetvlnagnniel 430

RESULT 13

AAV57045 ID AAV57045 standard; Protein; 591 AA.

AC AAV57045;

DT 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from *N. meningitidis* strain H44/76.

XX BASB029: Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
 KW infection; treatment; prevent; antibacterial drug.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 FH Key Location/Qualifiers  
 FH Misc-difference 90  
 FT /note= "Encoded by AAT"  
 FT Misc-difference 92  
 FT /note= "Encoded by GAT"  
 FT Misc-difference 98  
 FT /note= "Encoded by AAC"  
 FT Misc-difference 108  
 FT /note= "Encoded by AATC"  
 FT Misc-difference 123  
 FT /note= "Encoded by ACA"  
 FT Misc-difference 269  
 FT /note= "Encoded by AAA"  
 FT Misc-difference 389  
 FT /note= "Encoded by CGT"  
 FT  
 XX WO9558683-A2.  
 XX  
 XX 18-NOV-1999.  
 PD  
 XX 07-MAY-1999; 99WO-EP03255.  
 PF  
 XX 13-MAY-1998; 98GB-0010276.  
 PR  
 XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX Ruelle J;  
 PI  
 XX WPI: 2000-053103/04.  
 DR N-PSDB; AAZ39865.  
 DR  
 XX New polypeptide from neisseria meningitidis useful for diagnosis,  
 PT treatment or prevention of bacterial infections in mammal -  
 PT  
 Claim 4; Fig 2; 74pp; English.  
 PS  
 XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
 CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
 CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
 CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
 CC polypeptide sequences (AAV57044-V57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
 CC meningitidis infection in a mammal. Compositions containing BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with Neisseria  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes.  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.  
 CC  
 CC Sequence 591 AA;  
 SQ  
 Query Match 9.8%; Score 59; DB 21; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

XX	AAU06171	standard; Protein: 591 AA.
XX	AAU06171;	
DT	24-OCT-2001	(first entry)
XX	N. meningitidis PMC21	surface antigen Nhma polypeptide sequence.
XX	Surface antigen Nhma;	meningococcal disease; meningitis vaccine.
XX	Neisseria meningitidis strain PMC21.	
OS	Neisseria meningitidis	strain PMC21.
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..51
FT		/label= Signal_peptide
FT	Region	1..50
FT		/label= C1
FT		/note= "Conserved region 1"
FT	Region	51..108
FT		/label= V1
FT		/note= "Variable region 1"
FT		52..591
FT	Protein	/label= Mature_Nhma
FT		/note= "Predicted mature protein, specifically
FT		claimed in claim 12."
FT	Region	109..120
FT		/label= C2
FT		/note= "Conserved region 2"
FT	Region	121..124
FT		/label= V2
FT		/note= "Variable region 2"
FT	Region	125..188
FT		/label= C3
FT		/note= "Conserved region 3"
FT	Region	189..210
FT		/label= V3
FT		/note= "Variable region 3"
FT	Region	211..229
FT		/label= C4
FT		/note= "Conserved region 4"
FT	Region	230..236
FT		/label= V4
FT		/note= "Variable region 4"
FT	Region	237..591
FT		/label= C5
FT		/note= "Conserved region 5"
XX		
PN	WO20015182-A1.	
XX	02-AUG-2001.	
PD	25-JAN-2001;	2001WO-AU00069.
XX		
PF	25-JAN-2001;	2000US-0177917.
XX		
PR	25-JAN-2000;	2000US-0177917.
XX		
PA	(UYOU ) UNIV QUEENSLAND.	
XX		
PI	Peak IRA, Jennings MP;	
XX		
DR	WPI: 2001-488774/53.	
DR	N-PSDB; AAS09161.	
XX		
PT	New Nhma surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	preventing broad spectrum of Neisseria meningitidis -	
XX		
PS	Claim 9; Fig 1; 91pp; English.	
XX		
CC	The present invention relates to the isolation of novel Neisseria	

The present invention relates to the isolation of novel *Neisseria*

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:21 ; Search time 64.11 Seconds  
(without alignments)  
230.121 Million cell updates/sec

Title: US-09-771-382-11  
Perfect score: 2499  
Sequence: 1 MNXIXRIIWNLSALNMAWVYS.....TASGNSRGHGXSASVGYOW 604

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA: \*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCYUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/Backfilltest.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2235	89.4	598	4	US-09-377-155-5
2	2235	89.4	598	4	US-09-669-974-5
3	2234	89.4	598	4	US-09-377-155-13
4	2234	89.4	598	4	US-09-669-974-13
5	2231.5	89.3	589	4	US-09-377-155-19
6	2231.5	89.3	589	4	US-09-669-974-19
7	2231.5	89.3	599	4	US-09-377-155-15
8	2231.5	89.3	599	4	US-09-669-974-15
9	2230.5	89.3	591	4	US-09-377-155-11
10	2230.5	89.3	591	4	US-09-669-974-11
11	2230.5	89.3	591	4	US-09-377-155-21
12	2230.5	89.3	591	4	US-09-669-974-21
13	2230	89.2	594	4	US-09-377-155-9
14	2230	89.2	594	4	US-09-669-974-9
15	2223	89.0	594	4	US-09-377-155-7
16	2223	89.0	594	4	US-09-669-974-7
17	2216	88.7	592	4	US-09-377-155-2
18	2216	88.7	592	4	US-09-669-974-2
19	2216	88.7	592	4	US-09-377-155-17
20	2216	88.7	592	4	US-09-669-974-17
21	918.5	36.8	2411	4	US-09-268-347-36
22	917.5	36.7	2353	4	US-09-377-155-33
23	917.5	36.7	2353	4	US-08-913-942-4
24	917.5	36.7	2353	4	US-09-669-974-33
25	916.5	36.7	2354	4	US-09-268-347-47
26	880	35.2	1098	1	US-08-409-995-2
27	880	35.2	1098	3	US-08-685-467-2

28	880	35.2	1098	4	US-09-377-155-32	Sequence 32, Appl
29	880	35.2	1098	4	US-08-913-942-2	Sequence 2, Appl
30	880	35.2	1098	4	US-09-669-974-32	Sequence 32, Appl
31	880	35.2	1098	4	US-09-268-347-44	Sequence 44, Appl
32	876	35.1	658	1	US-08-409-995-5	Sequence 5, Appl
33	876	35.1	658	1	US-08-685-467-5	Sequence 5, Appl
34	876	35.1	658	4	US-08-913-942-5	Sequence 5, Appl
35	857	34.3	607	1	US-08-409-995-6	Sequence 6, Appl
36	857	34.3	607	3	US-08-685-467-6	Sequence 6, Appl
37	857	34.3	607	4	US-08-913-942-6	Sequence 6, Appl
38	857	34.3	1912	1	US-08-409-995-4	Sequence 4, Appl
39	857	34.3	1912	3	US-08-685-467-4	Sequence 4, Appl
40	825	33.0	1094	4	US-09-268-347-32	Sequence 32, Appl
41	754.5	30.2	679	4	US-08-913-942-15	Sequence 15, Appl
42	754.5	30.2	679	4	US-09-268-347-26	Sequence 26, Appl
43	583	23.3	1004	4	US-09-268-347-30	Sequence 30, Appl
44	558	22.3	1002	4	US-09-268-347-24	Sequence 24, Appl
45	513	20.5	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1	US-09-377-155-5	Sequence 5, Application US/09377155
Patent No. 6197312		
GENERAL INFORMATION:		
APPLICANT: PEAK, Ian Richard Anselm		
APPLICANT: JENNINGS, Michael Paul		
APPLICANT: MOXON, E. Richard		
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN		
FILE REFERENCE: 065064/0128		
CURRENT APPLICATION NUMBER: US/09/377,155		
CURRENT FILING DATE: 1999-08-19		
PRIOR APPLICATION NUMBER: PCT/AU98/01031		
PRIOR FILING DATE: 1998-12-14		
PRIOR APPLICATION NUMBER: GB 9726398.2		
PRIOR FILING DATE: 1997-12-12		
NUMBER OF SEQ ID NOS: 33		
SOFTWARE: PatentIn Ver. 2.0		
SEQ ID NO 5		
LENGTH: 598		
TYPE: PRT		
ORGANISM: Neisseria meningitidis		
US-09-377-155-5		
Query Match	89.4% Score 2235; DB 4; Length 598;	
Best Local Similarity	77.6% Pred. No. 2.2e-214;	
Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;		
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1 MKRISIIWNLSALNMAWVYSELTRNHTKRASATVAVATLTLFAVQA---NATDDDL 57		
61 XLXXVXXVXXXXXXGXXEXXXXXXXGXXXXXXGXXXXXXLTKAGDNKIKQ 120		
58 YLEPVQRTAVVLSFRSDKGEKE--GTEDSNVAVYFDEKRVLKAGATLTKADNKKIKQ 116		
121 XXXXXXXXXXXXXFYSLKKLXLLXVYXTEKLSFXANXXKXNIXSDPKGLNFAKXTAX 180		
117 NINENINENTNDSFFYSILKDLTDLTSVTEKLSFGANGKNYNTISDRKGLNFAKETAG 176		
181 TNGDXTVHLNIGISTLTDXLXXXXXXGXXXXXXRAASXKQVNLNAGNINIGVXX 240		
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241 GXTXXXXXVNDVXYTYDYEFSLADTKTTVNVESDNKNGKTEVKATGYAKENDGL 300		
237 GTT--ASDVADEVRYTDFEFLSADTKTTVNVESKDNKNGKTEVKATGYAKENDGL 294		
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Db      295 VTGKGGENGSSSTDEGEGLTAKVIDAVNKAQMRKTTTANQOTQADKFEVTSGTKV 354
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Db      355 TFASGXTTATVSKDOGNITTVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKATSGN 414
OY      421 VSPSKGMDETVNIAGNNIEIRNKNIDDIATSMXPOFSSVSLGAGADAPTLSDVXXXX 480
Db      415 VSPSKGMDETVNIAGNNIEIRNKNIDDIATSMXPOFSSVSLGAGADAPTLSDVDEGA 474
OY      481 LVNGSKXKXNRPVITTVAPVKEGDDVTNVAQLKGVAQNLNKNIDNXYGNARAGIAQAIAT 540
Db      475 LVNGSKXKXNRPVITTVAPVKEGDDVTNVAQLKGVAQNLNKNIDNXYGNARAGIAQAIAT 534
OY      541 AGLXQATLPKSKMMAIGGTYXGEGAGYAGYSISXGXNMXIKGTASGNSRGHFGXSASY 600
Db      535 AGLXQATLPKSKMMAIGGTYXGEGAGYAGYSISXGXNMXIKGTASGNSRGHFGXSASY 594
OY      601 GYOW 604
Db      595 GYOW 598

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## RESULT 2

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US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

```

Query Match 89.4%; Score 2235; DB 4; Length 598;

Best Local Similarity 77.6%; Pred. No. 2.2e-214; Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

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OY      1 MNXIXRIITNSALNAAWVYSELTRNHTKRASATYXTAVLATLTAATVOAAXXXXXXXXXXX 60
Db      1 MNXISRIITNSALNAAWVYSELTRNHTKRASATYXTAVLATLTAATVOAAXXXXXXXXXXX 57
OY      61 XLXVYXRXRXVXXXXXXXXXEGXEXXXXXXXXXXXXXXXXXXXXXXTTAKAGDLKTKQ 120
Db      58 YLEPQRTAAVLSFRSDKEGTEKE-GTEDSNMAVYFDEKRVLAAGATTLAAGDLKTKQ 116
OY      121 XXXXXXXXXXXXXFTYSLKRXLLXXVXTEKLSFXANXXKVNIXSDPTKGLNFAKXTAX 180
Db      117 NTNENTNENTNDSSFTYSLKRDLDLDTLSVETEKLSFGANGKVNITSDTKGLNFAKETAG 176
OY      181 TNGDXTVHLNIGISTLDLXKXAXXXXXXXXXXXXXXRAASKDYLVNAGMNIKGVXX 240
Db      177 TNGDPTVHLNIGISTLDLTLNTGATVNTDNTVDDEKRAASVYKDYLVNAGMNIKGVKP 236
OY      241 GXTXXXXXNVDFVXYTIVVEFLSADTKTTTVNVESKDKGKTEVYIGAKTSVIERKDGKL 300

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Db      237 GTT -ASDNVDFVRIYDVEFLSADTKTTTVNVESKDKGKTEVYIGAKTSVIERKDGKL 294
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Db      295 VTGKGGENGSSSTDEGEGLTAKVIDAVNKAQMRKTTTANQOTQADKFEVTSGTKV 354
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Db      355 TFASGXTTATVSKDOGNITTVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKATSGN 414
OY      421 VSPSKGMDETVNIAGNNIEIRNKNIDDIATSMXPOFSSVSLGAGADAPTLSDVXXXX 480
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OY      481 LVNGSKXKXNRPVITTVAPVKEGDDVTNVAQLKGVAQNLNKNIDNXYGNARAGIAQAIAT 540
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OY      541 AGLXQATLPKSKMMAIGGTYXGEGAGYAGYSISXGXNMXIKGTASGNSRGHFGXSASY 600
Db      535 AGLXQATLPKSKMMAIGGTYXGEGAGYAGYSISXGXNMXIKGTASGNSRGHFGXSASY 594
OY      601 GYOW 604
Db      595 GYOW 598

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## RESULT 3

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US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

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Query Match 89.4%; Score 2234; DB 4; Length 598;

Best Local Similarity 77.6%; Pred. No. 2.8e-214; Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

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Db      1 MNXISRIITNSALNAAWVYSELTRNHTKRASATYXTAVLATLTAATVOAAXXXXXXXXXXX 57
OY      61 XLXVYXRXRXVXXXXXXXXXEGXEXXXXXXXXXXXXXXXXXXXXXXTTAKAGDLKTKQ 120
Db      58 YLEPQRTAAVLSFRSDKEGTEKE-GTEDSNMAVYFDEKRVLAAGATTLAAGDLKTKQ 116
OY      121 XXXXXXXXXXXXXFTYSLKRXLLXXVXTEKLSFXANXXKVNIXSDPTKGLNFAKXTAX 180
Db      117 NTNENTNENTNDSSFTYSLKRDLDLDTLSVETEKLSFGANGKVNITSDTKGLNFAKETAG 176
OY      181 TNGDXTVHLNIGISTLDLXKXAXXXXXXXXXXXXXXRAASKDYLVNAGMNIKGVXX 240
Db      177 TNGDPTVHLNIGISTLDLTLNTGATVNTDNTVDDEKRAASVYKDYLVNAGMNIKGVKP 236
OY      241 GXTXXXXXNVDFVXYTIVVEFLSADTKTTTVNVESKDKGKTEVYIGAKTSVIERKDGKL 300

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Db 177 TNGDPTVHLNGIGSTLTDLTDLNTGATTVTNDVNDTEDEKRAASVKDVINAGNINIKVPR 236
QY 241 GXTXXXXXNVDFVXTVDVEFLSADTKTTTVNVEKDNCKXTEVKIGAKTSVYKEKDGKL 300
Db 237 GTT--ASDNVDFVRYTDVFEFLSADTKTTTVNVEKDNCKXTEVKIGAKTSVYKEKDGKL 294
QY 301 VYGGKXKXENXSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 360
Db 295 VTGKGDEGSSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 354
QY 361 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 420
Db 295 VTGKGDEGSSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 354
QY 361 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 420
Db 355 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 414
QY 421 VSPSGKMDETVINAGNNIETIRNGKNIDIAATSMKPOFSSVSLGAGADAPTLSDVDEGA 480
Db 415 VSPSGKMDETVINAGNNIETIRNGKNIDIAATSMKPOFSSVSLGAGADAPTLSDVDEGA 474
QY 481 LNVGSKXKXKPVRTVNAVGVKEGDVTNVAOLKGVANLNINXIDNVXGNARAGIAQAIAT 540
Db 475 LNVGSKDARKPVRTVNAVGVKEGDVTNVAOLKGVANLNINXIDNVXGNARAGIAQAIAT 534
QY 541 AGLXQAYLPKGSMAIIGXTYXGEGYAGYAGYSISXKXNMXXIKGTASGNSRGHFGASASY 600
Db 535 AGLQAYLPKGSMAIIGXTYXGEGYAGYAGYSISIDTGMWVLIKGTASGNSRGHFGASASY 594
QY 601 GYQW 604
Db 595 GYQW 598
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RESULT 4  
US-09-669-974-13  
Sequence 13, Application US/09669974  
Patent No. 6333173

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GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 13
LENGTH: 598
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-669-974-13.
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Query Match 89.4%; Score 2234; DB 4; Length 598;  
Best Local Similarity 77.6%; Pred. No. 2.8e-214;  
Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

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Db 1 MKIYRIIINNSALNMAVYSELTRNHTKRASATVTVAVLATLTLAFATVQ--NATDDDL 57
QY 61 XLXVYRXVXXXXXXGXXEXEXXXXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 120
Db 58 YLEPQVOTAVVLSFRSDKEGTEKE--GTEDSNWAVYFDEKRVLKAGATILKAGDNKIKQ 116
QY 121 XXXXXXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 180
Db 117 NMEENTNENTNDSFTYSLKDLTLTJVSYTEKLSFGANGKNVNTSDTKGLNFAKETAG 176
QY 181 TNGDXTVHLNGIGSTLTDLKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 240
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Db 177 TNGDPTVHLNGIGSTLTDLTDLNTGATTVTNDVNDTEDEKRAASVKDVINAGNINIKVPR 236
QY 241 GXTXXXXXNVDFVXTVDVEFLSADTKTTTVNVEKDNCKXTEVKIGAKTSVYKEKDGKL 300
Db 237 GTT--ASDNVDFVRYTDVFEFLSADTKTTTVNVEKDNCKXTEVKIGAKTSVYKEKDGKL 294
QY 301 VYGGKXKXENXSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 360
Db 295 VTGKGDEGSSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 354
QY 361 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 420
Db 295 VTGKGDEGSSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTOAQKFEVTSCTYV 354
QY 361 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 420
Db 355 TRASGXGTTATVYSKDOGNITVYXDVNVDALNVNOLNSGNMLDSKAAVAGSSGKVISGN 414
QY 421 VSPSGKMDETVINAGNNIETIRNGKNIDIAATSMKPOFSSVSLGAGADAPTLSDVDEGA 480
Db 415 VSPSGKMDETVINAGNNIETIRNGKNIDIAATSMKPOFSSVSLGAGADAPTLSDVDEGA 474
QY 481 LNVGSKXKXKPVRTVNAVGVKEGDVTNVAOLKGVANLNINXIDNVXGNARAGIAQAIAT 540
Db 475 LNVGSKDARKPVRTVNAVGVKEGDVTNVAOLKGVANLNINXIDNVXGNARAGIAQAIAT 534
QY 541 AGLXQAYLPKGSMAIIGXTYXGEGYAGYAGYSISXKXNMXXIKGTASGNSRGHFGASASY 600
Db 535 AGLQAYLPKGSMAIIGXTYXGEGYAGYAGYSISIDTGMWVLIKGTASGNSRGHFGASASY 594
QY 601 GYQW 604
Db 595 GYQW 598
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RESULT 5  
US-09-377-155-19  
Sequence 19, Application US/09377155  
Patent No. 6197312

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GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 19
LENGTH: 589
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-377-155-19
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Query Match 89.3%; Score 2231.5; DB 4; Length 589;  
Best Local Similarity 77.6%; Pred. No. 4.9e-214;  
Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;

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QY 1 MNXIXRIIINNSALNMAVYSELTRNHTKRASATVTVAVLATLTLAKATVQAXXXXXXXX 60
Db 1 MKIYRIIINNSALNMAVYSELTRNHTKRASATVTVAVLATLTLATVQ--NATDDEDE 58
QY 61 XLXVYRXVXXXXXXGXXEXEXXXXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 120
Db 59 ELESVARSAVLVQFMIDKNGEIE--STGDIGMSIYDDHNTLHGAVTLKAGDNKIKQ 117
QY 121 XXXXXXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 180
Db 118 -----SGKDFYSLKKELEKDLTJVSYTEKLSFGANGKNVNTSDTKGLNFAKETAG 167
QY 181 TNGDXTVHLNGIGSTLTDLKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 240
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Db 168 TNDPVTHLNGIGSTLDTLGLSSASHVDAGNOST--HYTAAASIKDVLNAGMNIKGVKT 225
OY 241 GXXYXXXXXNDVFXATYDVEFLSADTKTTTVNVEKNGKXTEVKTIGAKTSVIEKDGKL 300
Db 226 GSTTGOSENDVFXATYDVEFLSADTKTTTVNVEKNGKTEVKTIGAKTSVIEKDGKL 285
OY 301 VTGKXXKXNSSTDGEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKFEVTSCTXV 360
Db 286 VTGKXKGENSSDTEGEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKFEVTSCTXV 345
OY 361 TFAAGXTTATVSKDDGNTTVYDVNVGDALNVNOLONGSMNIDSKRAVAGSSGKVTISGN 420
Db 346 TFAAGXTTATVSKDDGNTTVYDVNVGDALNVNOLONGSMNIDSKRAVAGSSGKVTISGN 405
OY 421 VSPKSKMDETVNINAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLTSDVXXA 480
Db 406 VSPKSKMDETVNINAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLTSDVXXA 465
OY 481 LNVGSKXXNKPRITNVAAPGVEGDTNVAOLKGVNOLNXXIDNVXGNARAGIAQAIAT 540
Db 466 LNVGSKDANKPRITNVAAPGVEGDTNVAOLKGVNOLNXXIDNVXGNARAGIAQAIAT 525
OY 541 AGLXQATLPGKSMMAIGGTYLGEAGYALIGYSSISXXGNMXIKGTASGNSRGHGXSASV 600
Db 526 AGLXQATLPGKSMMAIGGTYLGEAGYALIGYSSISDGTGNMVIKGTASGNSRGHGTSASV 585
OY 601 GYQW 604
Db 586 GYQW 589

RESULT 6
US-09-669-974-19
; Sequence 19, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-19
```

```
Query Match 89.3%; Score 2231.5; DB 4; Length 589;
Best Local Similarity 77.6%; Pred. No. 4.9e-214;
Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;
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OY 1 MNXIXRIIWSALNAAWVSELTNRHTKRASATYXTAVLATLLKATVOAAXXXXXXXX 60
Db 1 MNKTYRIIWSALNAAWVSELTNRHTKRASATYXTAVLATLLKATVOA--NADDTDEDE 58
OY 61 XLXVYXRXVYXXXXXEGXEXXXXXXNXXXXXXXXXXXXXNXXXXXXXXXXXXTLAAGNLIKQ 120
Db 59 ELEVSASALVLOFMIDKEGNGEIE-STGIDGWSIYYDHNHTLHGATVTLKAGDNLKIKQ 117
OY 121 XXXXXXXXXXXXXFTTSLKXLLXVXTEKLSFXANXXKXVNI XSOTKGLNPAKXITAX 180
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Db 118 -----SGKDFYTSLLKELDLTSVETEKISFGANGKNVITSDTKGLNPAKTAG 167
OY 181 TNGDXTVHLNGIGSTLDPDLXXXXXAXXXXXXNXXXXXRAASKDVNLAGMNIKGVX 240
Db 168 TNDPVTHLNGIGSTLDTLGLSSASHVDAGNOST--HYTAAASIKDVLNAGMNIKGVKT 225
OY 241 GXXYXXXXXNDVFXATYDVEFLSADTKTTTVNVEKNGKXTEVKTIGAKTSVIEKDGKL 300
Db 226 GSTTGOSENDVFXATYDVEFLSADTKTTTVNVEKNGKRTVKTIGAKTSVIEKDGKL 285
OY 301 VTGKXXKXNSSTDGEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKFEVTSCTXV 360
Db 286 VTGKXKGENSSDTEGEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKFEVTSCTXV 345
OY 361 TFAAGXTTATVSKDDGNTTVYDVNVGDALNVNOLONGSMNIDSKRAVAGSSGKVTISGN 420
Db 346 TFAAGXTTATVSKDDGNTTVYDVNVGDALNVNOLONGSMNIDSKRAVAGSSGKVTISGN 405
OY 421 VSPKSKMDETVNINAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLTSDVXXA 480
Db 406 VSPKSKMDETVNINAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLTSDVXXA 465
OY 481 LNVGSKXXNKPRITNVAAPGVEGDTNVAOLKGVNOLNXXIDNVXGNARAGIAQAIAT 540
Db 466 LNVGSKDANKPRITNVAAPGVEGDTNVAOLKGVNOLNXXIDNVXGNARAGIAQAIAT 525
OY 541 AGLXQATLPGKSMMAIGGTYLGEAGYALIGYSSISXXGNMXIKGTASGNSRGHGXSASV 600
Db 526 AGLXQATLPGKSMMAIGGTYLGEAGYALIGYSSISDGTGNMVIKGTASGNSRGHGTSASV 585
OY 601 GYQW 604
Db 586 GYQW 589

RESULT 7
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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Query Match 89.3%; Score 2231.5; DB 4; Length 599;
Best Local Similarity 77.6%; Pred. No. 5e-214;
Matches 469; Conservative 0; Mismatches 130; Indels 5; Gaps 3;
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OY 1 MNXIXRIIWSALNAAWVSELTNRHTKRASATYXTAVLATLLKATVOAAXXXXXXXX 60
Db 1 MNKTYRIIWSALNAAWVSELTNRHTKRASATYXTAVLATLLKATVOA--NADDEDEE 58
OY 61 XLXVYXRXVYXXXXXEGXEXXXXXXNXXXXXXXXXXXXXNXXXXXXXXXXXXTLAAGNLIKQ 120
Db 59 ELEPVRSALVLOFMIDKEGNGENE-STGIDGWSIYYDHNHTLHGATVTLKAGDNLKIKQ 117
OY 121 XXXXXXXXXXXXXFTTSLKXLLXVXTEKLSFXANXXKXVNI XSOTKGLNPAKXITAX 180
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[illegible]

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RESULT# 9
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377, 155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

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	Query Match	Similarity	Score	DB	Length
Best Local	469	Conservative	89.3%	2230.5	591
Matches	469	Conservative	0	Pred. No. 6.1e-214	122
				Mismatches	13
				Indels	3
				Gaps	3

Db	61	YLDPLRTVAVLIVNSDKEGTEKEKEVEENSMDAMVAFENEKGVLFARETITLAKGDNLEIKQ	1 200
Qy	121	XXXXXXXXXXXXXXXXFYSLSKKALXLLXAXYTERKISFPAKXAKVIVASDTGLNFAKXTAX	1 800
Db	121	-----NGTFYTSLKADLIDLTVSGTERKISFSANGKRVITSDTGLNFAKXTAG	1 700
Qy	181	TNGDXTVHLNGIGSTLFDLXKXAXXXXXXXXXXXXTXXXXKRAASXKQVULNAGNIRGVKX	2 400
Db	171	TNGDPTVHLNIGISTLFDTLNTGATTNVTINDVNTDDEKRAASVKQVULNAGNIRKQVP	2 300
Qy	241	GXTYXXXXXXXXVFXVYTYDVEFLSADFTTYYNVBESKDNKXXTEVK IGAKTSVIREKDGKL	3 000
Db	231	GTT--ASDNVVFPTVYDVEFLSADFTTYYNVBESKDNKKEVEK IGAKTSVIREKDGKL	2 888
Qy	301	VTGKXKXKXNSSTOXGEGSLYTAKEVIDAVNAGKRMKTTTANCGTGADGFEPVYTSCTVY	3 600
Db	289	VTGKDKGNGSSDTGEBELVYTAKEVIDAVNAGKRMKTTTANCGTGADGFEPVYTSCTVY	3 488
Qy	361	TFASGXTTATVNSKDDGNIIVXADVVNNGDALANTNOQNSGWNLDKRAVAGSSGKTVISGN	4 200
Db	349	TFASGKGTATVNSDDGNIIVMTDVNNGDALANTNOQNSGWNLDKRAVAGSSGKTVISGN	4 088
Qy	421	VSPSGKADDEVYNINAGNNITIXNKGKNIDIATSMXKQFSSVLSIGACADAPTLTSDVXXXXA	4 800
Db	409	VSPSGKADDEVYNINAGNNIIEITRNGKNIDTASMTPOFSSVLSIGACADAPTLTSDV--GDA	4 672
Qy	481	LVNSGKXKXNRKVPRTTNVAPGVKEBDVYNVAQLKGVANLNXXIDNXYGMAKAGIAQAIAAT	5 400
Db	468	LVNSGKXKXNRKVPRTTNVAPGVKEBDVYNVAQLKGVANLNNRIDNVGNARAGIAQAIAAT	5 272
Qy	541	AGLXQAVLPGKSMAGIGXTYXGEGAYAGYSAISXKXGNMXIKKGTASGNSRGHFGKSAV	6 000
Db	528	AGLVQAVLPGKSMAGIGGTGTGEGAYAGYSAISDGGNMIKGTASGNSRGHFGKASAV	5 872
Qy	601	GYOM 604	
Db	588	GYOM 591	

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RESULT 10
US-09-377-155-21
: Sequence 21 Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 591
: TYPE: PRF
: ORGANISM: Neisseria meningitidis
US-09-377-155-21

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Query Match	89.3%;	Score 2230.5;	DB 4;	Length 591;
Best Local Similarity	77.6%;	Pred. No. 6.1e-214;		
Matches 469; Conservative	0;	Mismatches 122;	Indels 13;	Gaps 3;

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Oy      1 MNXKRIIWNLSLNAWVYSELFTPNHTKRASATVXAVALATLILATVAQAXXXXXXXXXXX 60
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNKIIRIIWNSLNAWVYSELFTPNHTKRASATVKRAVALATLLFATVQASANNEQEDEL 60
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Oy	61	XLXXYYRRXXYYXXXXXXXXXEGXXXXXXXKXXXXXXXXXXXXXXXXXXXXXTLAKADNLIKQ	120
Dd	61	YLDPEQRVAVLIYNDSKEGTGEKEKEEENSMDAIVNEGCVLARBITTLAKADNLIKQ	120
Oy	121	XXXXXXXXXXXXXXFFYSLKRLXALXVXYTEKLSFYANXXKVNIKSDTKGLNPAKXTAX	180
Dd	121	-----NGTFNTSLKKDLFDLISVGTEKLSFGSANKNKVITSDTGLNFAKETAG	170
Oy	181	TNGDXTHVLNIGSTLPDYLXXXXXXXXXXXXXTTXXXXRAASKRYVLAAGNNINGVKX	240
Dd	171	TNGDTPHALNIGSTLPDFTLNTGATTNVTDNVTDDEKRRAASVYKDVLAGNMINGVKP	230
Oy	241	GTXXXXXXNVDFVYTYPTVEFLSADTKTTTVYNVESKONGKXTEVIKIAKTSVIEKERDKL	300
Dd	231	GTT--ASNVDVPFRTYDTIVEFLSADTKTTTVYNVESKONGKTEVIKIAKTSVIEKERDKL	288
Oy	301	VTKKKXKENKSSTDJXGEGLYTAKEVIDAVNKAQNRMTTTTANGOTGOADKFETVTSCTYV	360
Dd	289	VTGRKGNGENSGSTDEGBELVTAKEVIDAVNKAQNRMTTTTANGOTGOADKFETVTSCTNV	348
Oy	361	TFPASGXGTTATVSKDDOGCNTVYXIDVANVGDALNVNOJONSGWILDSKAVAAGSSGKYISGN	420
Dd	349	TFPASRGKTATVASKDDOGNITVMADVNVGDALNVNOJONSGWMLDSKAVAAGSSGKYISGN	408
Oy	421	VSPSKGMDETVNJINAGNNIIEIXRNGKNIDIATSMXPQSFVSISLGACADAPTLISVQXXXA	480
Dd	409	VSPSKGMDETVNJINAGNNIIEITRNGKNIDIATSMTPQFSFVSISLGACADAPTLISV-DGA	467
Oy	481	LNVGSKXXNKEFVRTTNNAVPYKEGDEVTVNQOLKCAVNOLNNXIDNVYGNAIRAGIAQAIAAT	540
Dd	468	LNVGSKKNCKNFVRITTNNAVPGVKEGDEVTVNQOLKCAVNOLNNRIDNVYGNARAGIAQAIAAT	527
Oy	541	AGLXAOTVLPKGSMAIGGXTYXGGAGTAIGTSSIAXGGMXIKIGTASGNSRGHFGASASY	600
Dd	528	AGLYOATVLPKGSMAIGGTYRGEGAYTAIGTSSISDGGMIIKIGTASGNSRGHFGASASY	587
Oy	601	GYOW 604	
Dd	588	GYOW 591	

```

11 RESULT
11 US-09-669-974-11
11 Sequence 11, Application US/09669974
11 Patent No. 6333173
11 GENERAL INFORMATION:
11 APPLICANT: PEAK, Ian Richard Anselm
11 APPLICANT: JENNINGS, Michael Paul
11 APPLICANT: MOXON, E. Richard
11 TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
11 FILE REFERENCE: 065064/0128
11 CURRENT APPLICATION NUMBER: US/09/669,974
11 CURRENT FILING DATE: 2000-09-26
11 PRIOR APPLICATION NUMBER: US 09/377,155
11 PRIOR FILING DATE: 1999-08-19
11 PRIOR APPLICATION NUMBER: PCT/A098/01031
11 PRIOR FILING DATE: 1998-12-14
11 PRIOR APPLICATION NUMBER: GB 9726398.2
11 PRIOR FILING DATE: 1997-12-12
11 NUMBER OF SEQ ID NOS: 33
11 SOFTWARE: PatentIn Ver. 2.0
11 SEQ ID NO 11
11 LENGTH: 591
11 TYPE: PRT
11 ORGANISM: Neisseria meningitidis
11 US-09-669-974-11

```

Query Match	89.38;	Score 2230.5;	DB 4;	Length 591;
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Best Local Similarity	-77.68;	Pred. No. 6.1e-214;
Matches	469; Conservative	0; Mismatches 122; Indels 13; Gaps 3;

QY 1 MNXIXRIWNSALNAWVXVSELTNRNHTKRASATVXTAVLATLLXATVQAXXXXXXXXXX 60



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Db 1 MNEILRIIWNLSALNNAVYVSELTRNHTKRASATVKAVALATLLFATVQASANNEQEDL 60
Qy 61 XLXVYRXRXVXXXXXXXXXXGXXEXXXXXXXXXXXXXXXXXXXJTLKAGDNLIKQ 120
Db 61 YLDPVRLTVAVLIVNSDKGEGTEKEKEVEENSDMAVYFNEKGVLTAAREITLAKGDNLIKQ 120
Qy 121 XXXXXXXXXXXXXXXFTYSLKRLXLLXVYTERKLSFXANXXVNIJSDPTKGLNFAKETG 180
Db 121 -----NQTFTYSLKRLDLDLTSVGERKLSFXANXXVNIJSDPTKGLNFAKETG 170
Qy 181 TNGDXTVHLNGIGSTLTDLXAXXAXXXXXXXXXXXRAASXKDVINAGNINIGVX 240
Db 171 TNGDXTVHLNGIGSTLTDLXAXXAXXXXXXXXXXXRAASXKDVINAGNINIGVX 230
Qy 241 GXTXXXXXNVDFVXTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVYKEDGKL 300
Db 231 GTT--ASDNDVFRVRYDVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVYKEDGKL 288
Qy 301 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQIGQADKFETVTSCTYV 360
Db 289 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQIGQADKFETVTSCTYV 348
Qy 361 TFASGXTATVSKDDQGNITVYDVNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGN 420
Db 349 TFASGXTATVSKDDQGNITVYDVNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGN 408
Qy 421 VPSKGMDETVINAGNNEIETRNKNIDIAISMTPQSSVSLGAGADAPTLSDVXXXX 480
Db 409 VPSKGMDETVINAGNNEIETRNKNIDIAISMTPQSSVSLGAGADAPTLSDV-GDA 467
Qy 481 LNVGSKXKXKPRITNVAGVEGDTVNAOLKGVANLNNDXNDVXGNARAGIAQAIAT 540
Db 468 LNVGSKKDKPRITNVAGVEGDTVNAOLKGVANLNNDXNDVXGNARAGIAQAIAT 527
Qy 541 AGIXQATVLPKSMMAIGGTYXGEGYATGYSISXGXMMXIKGTASGNSRGHFGASASV 600
Db 528 AGIXQATVLPKSMMAIGGTYXGEGYATGYSISIDGGMWIIKGTASGNSRGHFGASASV 587
Qy 601 GYOW 604
Db 588 GYOW 591

RESULT 12
US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIORITY FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21
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Query Match 89.3%; Score 2230.5; DB 4; Length 591;  
Best Local Similarity 77.6%; Pred. No. 6.1e-214;

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Matches 469; Conservative 0; Mismatches 122; Indels 13; Gaps 3;
Qy 1 MNXIXRIIWNLSALNNAVYVSELTRNHTKRASATVKAVALATLLXATVQASANNEQEDL 60
Db 1 MNXIRIWNLSALNNAVYVSELTRNHTKRASATVKAVALATLLFATVQASANNEQEDL 60
Qy 61 XLXVYRXRXVXXXXXXXXXXGXXEXXXXXXXXXXXXXXXXXXXJTLKAGDNLIKQ 120
Db 61 YLDPVRLTVAVLIVNSDKGEGTEKEKEVEENSDMAVYFNEKGVLTAAREITLAKGDNLIKQ 120
Qy 121 XXXXXXXXXXXXXXXFTYSLKRLXLLXVYTERKLSFXANXXVNIJSDPTKGLNFAKETG 180
Db 121 -----NQTFTYSLKRLDLDLTSVGERKLSFXANXXVNIJSDPTKGLNFAKETG 170
Qy 181 TNGDXTVHLNGIGSTLTDLXAXXAXXXXXXXXXXXRAASXKDVINAGNINIGVX 240
Db 171 TNGDXTVHLNGIGSTLTDLXAXXAXXXXXXXXXXXRAASXKDVINAGNINIGVX 230
Qy 241 GXTXXXXXNVDFVXTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVYKEDGKL 300
Db 231 GTT--ASDNDVFRVRYDVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVYKEDGKL 288
Qy 301 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQIGQADKFETVTSCTYV 360
Db 289 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQIGQADKFETVTSCTYV 348
Qy 361 TFASGXTATVSKDDQGNITVYDVNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGN 420
Db 349 TFASGXTATVSKDDQGNITVYDVNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGN 408
Qy 421 VPSKGMDETVINAGNNEIETRNKNIDIAISMTPQSSVSLGAGADAPTLSDVXXXX 480
Db 409 VPSKGMDETVINAGNNEIETRNKNIDIAISMTPQSSVSLGAGADAPTLSDV-GDA 467
Qy 481 LNVGSKXKXKPRITNVAGVEGDTVNAOLKGVANLNNDXNDVXGNARAGIAQAIAT 540
Db 468 LNVGSKKDKPRITNVAGVEGDTVNAOLKGVANLNNDXNDVXGNARAGIAQAIAT 527
Qy 541 AGIXQATVLPKSMMAIGGTYXGEGYATGYSISXGXMMXIKGTASGNSRGHFGASASV 600
Db 528 AGIXQATVLPKSMMAIGGTYXGEGYATGYSISIDGGMWIIKGTASGNSRGHFGASASV 587
Qy 601 GYOW 604
Db 588 GYOW 591

RESULT 13
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIORITY FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9
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Query Match 89.2%; Score 2230; DB 4; Length 594;

Best Local Similarity 77.6%; Pred. No. 6.9e-214;  
Matches 469; Conservative 0; Mismatches 125; Indels 10; Gaps 4;

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QY 1 MNXIRIIMNSALNAMYVSELTFRNHTKRASATVYTAVALTLXATVOAAXXXXXXXXXX 60
  |||||||
Db 1 MNKIRIIMNSALNAMYVSELTFRNHTKRASATVATATLAFATVQA---STDDDDL 57
  61 XLXVXRXXXXXXEGEXEXXXXXXXXXXXXXXXXXXATLAKGNLIKQ 120
  58 YLEPQRTAAVLSRSPDEGTEKE-VTEDSNMGVFDKGVLTAGTITLAKGNLIKQ 116
QY 121 XXXXXXXXXXXXFTYSLKXXLXXVTEKLSFANAKKVINXSDTKLNAKKTAX 180
  |||||||
Db 117 ---NTNENTASSFTYSLKDLTDLTSVTEKLSFANSRKNVITSDTKLNAKKTAE 172
  181 TNGDXTVHLNIGSTLTDLXAXXXXXXXXXXXTAXXAXSKVDVLAAGNVIKGVX 240
  173 TNGDXTVHLNIGSTLTDLNTGATTVTNDNVTDEKKRAASVADVLAAGNVIKGV 232
QY 241 GXTXXXXXNDVFXTPDVEFLSADTKTTVNVESKNGKXTEVKGAKTSVIREKDKL 300
  |||||||
Db 233 GTT--ASDNVDFVRYTPDVEFLSADTKTTVNVESKNGKXTEVKGAKTSVIREKDKL 290
QY 301 VTGKXXKXNSSTDGEGVTAKEVIDAVNKAARMKTTTANGOTGADKEFTVSGTXV 360
  |||||||
Db 291 VTGKDKGENDSTDKGEGVTAKEVIDAVNKAARMKTTTANGOTGADKEFTVSGTXV 350
QY 361 TFASGKGTATVSKDDGNTVYXDVVNGDALNNOLNONGMNLDSKAVAGSSGKVISGN 420
  |||||||
Db 351 TFASGKGTATVSKDDGNTVYXDVVNGDALNNOLNONGMNLDSKAVAGSSGKVISGN 410
QY 421 VPSKGMDETVNINAGNIEIIXRKNIDATSMXPOFSSVSLGAGADAPTLSDVXXXA 480
  |||||||
Db 411 VPSKGMDETVNINAGNIEIIXRKNIDATSMXPOFSSVSLGAGADAPTLSDVDEGA 470
QY 481 LVNSGSKXNKRVRTTNAPGKEGDTVNVAKLKVQNLNIXDINVGXNARAGIAQAIAT 540
  |||||||
Db 471 LVNSGSKNANKVRITTNAPGKEGDTVNVAKLKVQNLNIXDINVGXNARAGIAQAIAT 530
QY 541 AGLXOAYLPKGSMAIGGTYXGAGYAIGYSSISXXGNMIXIKGTASGNSRGHFGXASV 600
  |||||||
Db 531 AGLVQAYLPKGSMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASAV 590
QY 601 GYQW 604
  ||||
Db 591 GYQW 594
```

RESULT 14  
US-09-669-974-9  
Sequence 9, Application US/09669974  
Patent No. 633173

GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669, 974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377, 155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 594  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 89.2%; Score 2230; DB 4; Length 594;

Best Local Similarity 77.6%; Pred. No. 6.9e-214;  
Matches 469; Conservative 0; Mismatches 125; Indels 10; Gaps 4;

```
QY 1 MNXIRIIMNSALNAMYVSELTFRNHTKRASATVYTAVALTLXATVOAAXXXXXXXXXX 60
  |||||||
Db 1 MNKIRIIMNSALNAMYVSELTFRNHTKRASATVATATLAFATVQA---STDDDDL 57
  61 XLXVXRXXXXXXEGEXEXXXXXXXXXXXXXXXXXXATLAKGNLIKQ 120
  58 YLEPQRTAAVLSRSPDEGTEKE-VTEDSNMGVFDKGVLTAGTITLAKGNLIKQ 116
QY 121 XXXXXXXXXXXXFTYSLKXXLXXVTEKLSFANAKKVINXSDTKLNAKKTAX 180
  |||||||
Db 117 ---NTNENTASSFTYSLKDLTDLTSVTEKLSFANSRKNVITSDTKLNAKKTAE 172
  181 TNGDXTVHLNIGSTLTDLXAXXXXXXXXXXXTAXXAXSKVDVLAAGNVIKGVX 240
  173 TNGDXTVHLNIGSTLTDLNTGATTVTNDNVTDEKKRAASVADVLAAGNVIKGV 232
QY 241 GXTXXXXXNDVFXTPDVEFLSADTKTTVNVESKNGKXTEVKGAKTSVIREKDKL 300
  |||||||
Db 233 GTT--ASDNVDFVRYTPDVEFLSADTKTTVNVESKNGKXTEVKGAKTSVIREKDKL 290
QY 301 VTGKXXKXNSSTDGEGVTAKEVIDAVNKAARMKTTTANGOTGADKEFTVSGTXV 360
  |||||||
Db 291 VTGKDKGENDSTDKGEGVTAKEVIDAVNKAARMKTTTANGOTGADKEFTVSGTXV 350
QY 361 TFASGKGTATVSKDDGNTVYXDVVNGDALNNOLNONGMNLDSKAVAGSSGKVISGN 420
  |||||||
Db 351 TFASGKGTATVSKDDGNTVYXDVVNGDALNNOLNONGMNLDSKAVAGSSGKVISGN 410
QY 421 VPSKGMDETVNINAGNIEIIXRKNIDATSMXPOFSSVSLGAGADAPTLSDVXXXA 480
  |||||||
Db 411 VPSKGMDETVNINAGNIEIIXRKNIDATSMXPOFSSVSLGAGADAPTLSDVDEGA 470
QY 481 LVNSGSKXNKRVRTTNAPGKEGDTVNVAKLKVQNLNIXDINVGXNARAGIAQAIAT 540
  |||||||
Db 471 LVNSGSKNANKVRITTNAPGKEGDTVNVAKLKVQNLNIXDINVGXNARAGIAQAIAT 530
QY 541 AGLXOAYLPKGSMAIGGTYXGAGYAIGYSSISXXGNMIXIKGTASGNSRGHFGXASV 600
  |||||||
Db 531 AGLVQAYLPKGSMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASAV 590
QY 601 GYQW 604
  ||||
Db 591 GYQW 594
```

RESULT 15  
US-09-377-155-7  
Sequence 7, Application US/09377155  
Patent No. 6197312

GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377, 155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 594  
TYPE: PRT  
ORGANISM: Neisseria meningitidis

US-09-377-155-7

## Query Match

89.0%; Score 2223; DB 4; Length 594;

Best Local Similarity 77.6%; Pred. No. 3.5e-213;

Matches 469; Conservative 0; Mismatches 125; Indels 10; Gaps 4;

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QY 1 MNXIRIINNSALNNAVXYSELTRNHTKRASATVTAVALATLILXATVQAXXXXXXXXXXXXXX 60
DB 1 MNKIYRIINNSALNNAVXYSELTRNHTKRASATVTAVALATLILFATVQA--NATDDDL 57
QY 61 XLXVXVXXXXVXXXXXXXXXXEXEXXXXXXXXXXXXXXXXXXXXXXTLKAGDNLKIQ 120
DB 58 YLEPVQRTAVVLSFRSDKEGTGEKE-CTEDSNMAVVFDEKRVLKACATILKAGDNLKIQ 116
QY 121 XXXXXXXXXXXXXFTYSLKKLXLXVYTERLSFXANXXKVNIXSDTKGLNFAKXTAX 180
DB 117 ---NTNENTNDSFYSLSKDLTDLTSVETERLSFGANGKNVNTSDTKGLNFAKETAG 172
QY 181 TNGDXTVHLNGISGTLTDLXAXXXXXXXXXXXXXXRAASXKXKDVNLNAGNINIKVXX 240
DB 173 TNGDPTVHLNGISGTLTDLTGLNTGATTNVTNDNVTDEKRRASVSKDVNLNAGNINIKVXP 232
QY 241 GATXXXXXNVDEVTYDVEFLSADTKTTVNYESKDNCKXTEVKIGAKTSVIERKDGKL 300
DB 233 GTT--ASDNVDFVRYDVEFLSADTKTTVNYESKDNCKKTEVKIGAKTSVIERKDGKL 290
QY 301 VTGKXKXKXSSSTDGEGVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTXY 360
DB 291 VTGKGDENGSSSTDGEGVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNY 350
QY 361 TPASGXTATATYSKDDQGNITVYDVNVDALNVLNOLNSGWNLDKAVAGSSGXVTSGN 420
DB 351 TPASGXTATATYSKDDQGNITVYDVNVDALNVLNOLNSGWNLDKAVAGSSGXVTSGN 410
QY 421 VSPSKGMDETVINAGNNIEIKRNKNIDIASMXPOFSVSLGAGADAPTLSPVXXXXA 480
DB 411 VSPSKGMDETVINAGNNIEIKRNKNIDIASMAPOFSVSLGAGADAPTLSPVDEGA 470
QY 481 LNVGSKXKXKPPVRIITVAVPGVKEGDTNVAOLKGVAQNLNNXIDNXXGNARAGIAQALAT 540
DB 471 LNVGSKDQTNKPVRIITVAVPGVKEGDTNVAOLKGVAQNLNNRIDNAGNARAGIAQALAT 530
QY 541 AGLXOAYLPGKSMMAIGXTYYGEAGYATGYSISXXGNMXIKGTASGNSRGHEGSASV 600
DB 531 AGLVQAYLPGKSMMAIGDITRGEAGYATGYSISDGNMILIKGTASGNSRGHFGASASV 590
QY 601 GYQW 604
DB 591 GYQW 594
```

Search completed: July 3, 2002, 08:10:23  
Job time: 535 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:32 ; Search time 95.27 Seconds  
(without alignments)  
609.194 Million cell updates/sec

Title: US-09-771-382-11

Sequence: 1 MNXIXRIIWSALNAMYVS.....TASGNSRGHFCXSASVGYOW 604

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_71:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2230.5	89.3	591	2	G81133
2	2221	88.9	592	2	A81888
3	465	18.6	298	2	I64138
4	326	13.0	1190	2	A82615
5	319	12.8	2059	2	D82671
6	299.5	12.0	1588	2	A86036
7	299.5	12.0	1588	2	H91188
8	287.5	11.5	658	2	AH0110
9	278.5	11.1	1107	2	AC0976
10	173	6.9	1004	2	C82672
11	154	6.2	365	2	AB3486
12	146.5	5.9	936	2	I40711
13	142.5	5.7	364	2	A81019
14	142.5	5.7	1567	2	S11672
15	142.5	5.7	1655	2	E97835
16	140	5.6	1300	2	S07575
17	138	5.5	1275	2	T33369
18	137.5	5.5	1335	2	T17508
19	137.5	5.5	1335	2	T31105
20	137	5.5	1052	2	AF2959
21	137	5.5	1341	2	H98323
22	136	5.4	585	2	F85809
23	136	5.4	5188	2	B85547
24	135.5	5.4	1430	2	AF0351
25	135	5.4	1651	2	JC1340
26	135	5.4	1910	2	AF0394
27	135	5.4	5291	2	F90696
28	134	5.4	585	2	F90961
29	133.5	5.3	1361	2	T03415

30	133	5.3	3013	2	AB0480	probable invasive y
31	131.5	5.3	3029	2	S76109	hypothetical prote
32	130.5	5.2	1477	2	B43855	high-molecular-wet
33	130	5.2	989	2	D89852	fibrinogen-binding
34	129.5	5.2	3705	2	AD0123	probable autotrans
35	129	5.2	1127	2	T25804	hypothetical prote
36	129	5.2	1536	2	A43855	high-molecular-wet
37	128.5	5.1	605	2	T33913	hypothetical prote
38	128.5	5.1	1369	2	T17504	hypothetical prote
39	127.5	5.1	2249	2	A41477	190k surface anti
40	127	5.1	1428	2	AC2224	hypothetical prote
41	127	5.1	4936	2	AH2515	hypothetical prote
42	126.5	5.1	1608	2	A28182	hemolysin A - Ser
43	125.5	5.0	1109	2	A56143	surface-array prot
44	125	5.0	893	2	A37284	circumsporozoite p
45	124	5.0	485	2	A60610	

## ALIGNMENTS

RESULT	1	
G81133		
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)		
C:Species: Neisseria meningitidis		
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001		
C:Accession: G81133		
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischman, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizzi, M. Science 287, 1809-1815, 2000		
A:Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MUID:2017575		
A:Accession: G81133		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-591 <RET>		
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AF41395.1; PID:g722		
A:Experimental source: serogroup B, strain MC58		
C:Genetics:		
A:Gene: NMB0992		
Query Match	89.3%;	Score 2230.5; DB 2; Length 591;
Best Local Similarity	77.6%;	Pred. No. 1.7e-149;
Matches 469; Conservative	0;	Mismatches 122; Indels 13; Gaps 3;
QY	1	MNXIXRIIWSALNAMYVSELTNRNHTKRASATVYTRAVLTLLXATVQAXXXXXXXX 60
DB	1	MNXIXRIIWSALNAMYVSELTNRNHTKRASATVYTRAVLTLLXATVQAXXXXXXXX 60
QY	61	XLXVXKXVXXXXXXEXXEXXXXXXXXXXXXXXTLAKADNLIKQ 120
DB	61	YLPVQFTVAVLLVNSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLAKADNLIKQ 120
QY	121	XXXXXXXXXXXXXXFTYSLKLLXLLXAXVTEKLSFRANKXKNIXSDTGLNFAKXTAX 180
DB	121	XXXXXXXXXXXXXXFTYSLKLLXLLXAXVTEKLSFRANKXKNIXSDTGLNFAKXTAG 170
QY	181	TGNDXTVHLNGISSTLDLXXXXXXKXXXXXXKXXXXXXRAASXKQVLAAGNNIKGVKX 240
DB	171	TGNDXTVHLNGISSTLDLTLNTGATTNVNDVTDDEKRRASVADVLAAGNNIKGVK 230
QY	241	GTXKXXXXXNDVFTYDTVEFLSADRTKTTVNESKDNKXTEVIGAKTSVIREKDKGL 300
DB	231	GTT--ASDNDVFTYDTVEFLSADRTKTTVNESKDNKXTEVIGAKTSVIREKDKGL 288
QY	301	VTRKXKXKXSTDXGEGVLAKEVIDAVKAKGRMTTANQOTGQADFEVTVSGTVX 360
DB	289	VTRKXKXKXSTDXGEGVLAKEVIDAVKAKGRMTTANQOTGQADFEVTVSGTVX 348
QY	361	TFSAGKTTATVSKDQGNITVXYDVNVGDALVNVQNSGMVLDKRAVAGSSGKTVISGN 420

Db 349 TFASGKGTATVSKDDQNTIVMYDVNVDALNVLQNLQNSGMNLSKAVASSGKRVISGN 408  
421 VSPSKGKMDDEVNINAGNNEIIRNGKNIDATSMXPOFSSVSLGAGADAPLISVDDXXA 480  
409 VSPSKGKMDDEVNINAGNNEIIRNGKNIDATSMXPOFSSVSLGAGADAPLISVDD- GDA 467  
481 LNVGSKKXNKKRVRITNVAPGVKEGDTVVAOLKGYAQMNNXIDNVKANARAGIAQAIAT 540  
468 LNVGSKKXNKKRVRITNVAPGVKEGDTVVAOLKGYAQMNNRINDVDCNARAGIAQAIAT 527  
541 AGLXOAYILPGKSMMAIGGXTYXGAGVAGYSSISXGNNXIKGTASGNSRGHFGASASV 600  
528 AGLVQAYILPGKSMMAIGGXTYXGAGVAGYSSISDGGNMIITGTASGNSRGHFGASASV 587  
601 GYOW 604  
588 GYOW 591

## RESULT 2

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)  
A:Accession: A81888  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jorgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84461.1; PID:9737989  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match 88.9%; Score 2221; DB 2; Length 592;  
Best Local Similarity 77.6%; Pred. No. 8, 2e-149;  
Matches 469; Conservative 0; Mismatches 123; Indels 12; Gaps 5;

1 MNXIXRIITNSALNMAVYSELTRNHTKRASATYATVATLTLATVQAAXXXXXXXX 60  
1 MNKIRIITNSALNMAVAVSELTRNHTKRASATYATVATLTLATVQA--NANDEDEE 58  
61 XLXVXRXXVXXXXXXEGXEXEXXXXXXXXXTLKAAGNLKTKQ 120  
59 ELESQVR-SVVGSIQASMEGSELE---TISLMTNDSEKPEVDPIYVTLKAGDLKTKQ 114  
121 XXXXXXXXXXKFTYSLKRXLLXVXTKELSEFANXKXVNIISDTKGINFAKXTAX 180  
115 ---NTNENNTNASSFTYSLKRDLTGLINVEETKLSFGANGKKNVITISPTKGLNFAKERT 170  
181 TNGDXTVHLNIGSTLNDLXKXXXXXXXXTXXXXXAAASKDVLNMGWNLKGTAX 240  
171 TNGDXTVHLNIGSTLNDLXKSSSHVDAGNOST--HYTPRAASIKDVLNMGWNLKGTAX 228  
241 GXTXXXXXANVDFVYTYDVEFLASDTKTFTVNVESKDNKGKTEVYIGAKTSVIRKEDGKL 300  
229 GSTTGOSFNVDVFRITDYVEFLASDTKTFTVNVESKDNKGKTEVYIGAKTSVIRKEDGKL 288  
301 VTGKXKXENKSSSTDGEGVLTAKEVIDAVNRKAGWEMKTTTANGQTDKFEVTSSTXV 360  
289 VTGKXKXENKSSSTDGEGVLTAKEVIDAVNRKAGWEMKTTTANGQTDKFEVTSSTXV 348  
361 TFASGKGTATVSKDDQNTIVMYDVNVDALNVLQNLQNSGMNLSKAVASSGKRVISGN 420  
349 TFASGKGTATVSKDDQNTIVMYDVNVDALNVLQNLQNSGMNLSKAVASSGKRVISGN 408

421 VSPSKGKMDDEVNINAGNNEIIRNGKNIDATSMXPOFSSVSLGAGADAPLISVDDXXA 480  
409 VSPSKGKMDDEVNINAGNNEIIRNGKNIDATSMXPOFSSVSLGAGADAPLISVDDXXA 468  
481 LNVGSKKXNKKRVRITNVAPGVKEGDTVVAOLKGYAQMNNXIDNVKANARAGIAQAIAT 540  
469 LNVGSKKXNKKRVRITNVAPGVKEGDTVVAOLKGYAQMNNRINDVDCNARAGIAQAIAT 528  
541 AGLXOAYILPGKSMMAIGGXTYXGAGVAGYSSISXGNNXIKGTASGNSRGHFGASASV 600  
529 AGLVQAYILPGKSMMAIGGXTYXGAGVAGYSSISDGGNMIITGTASGNSRGHFGASASV 588  
601 GYOW 604  
589 GYOW 592

## RESULT 3

164138  
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: 164138  
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vence  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: 164138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:91574588; PID:91574589; TIGR:HI1732

Query Match 18.6%; Score 465; DB 2; Length 298;  
Best Local Similarity 37.6%; Pred. No. 1, 2e-25;  
Matches 121; Conservative 26; Mismatches 129; Indels 46; Gaps 7;

1 MNXIXRIITNSALNMAVYSELTRNHTKRASATYATVATLTLATVQAAXXXXXXXX 60  
1 MNKIRIITNSALNMAVAVSELTRNHTKRASATYATVATLTLATVLSATVQA----- 49  
61 XLXVXRXXVXXXXXXEGXEXEXXXXXXXXXTXXXXXXXTLKAAGNLKTKQ 120  
50 -----INDAGTFVKVOSTEDIEDSAATKDDNKNQALKAGDTLLTLAGKMLAK- 98  
121 XXXXXXXXXXKFTYSLKRXLLXVXTKELSEFANXKXVNIISDTKGINFAKXTAX 173  
99 -----LDQGSVTFPALADLDVKTAKVSDTLTIGSNTFPAAGATKRVSTTSADSLK 151  
174 FAKTAXTNGDXTVHLNIGSTLNDLXKXXXXXXXXTXXXXXAAASKDVLNMGW 233  
152 LAK---GTNGDXTVHLNIGSTLNDLXKSSSHVDAGNOST--HYTPRAASIKDVLNMGW 207  
224 NIKGVR--XGTXXXXXXANVDFVYTYDVEFLASDTKTFTVNVESKDNKGKTEVYIGAKTS 291  
208 NIKGKAVAGGNT---ENVVDVAGIDNEFTGDKNTLDVLTAKENKTEVYIGAKTS 263  
292 VIKERKGLTVGKXKXENKSSST 313  
264 VIKDNNGKLTGKQLKDNATGT 285

## RESULT 4

surface protein xpr1981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq



A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSFDB:GN00145; UWGP:Z5029  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029

Query Match	12.0%;	Score 239.5;	DB 2;	Length 1586;
Best Local Similarity	-24.1%;	Pred. No. 3.7e-13;		
Matches 120;	Conservative 48;	Mismatches 177;	Indels 153;	Gaps 16;

```

0Y 149 VXTLELSTFXANXKXKXKXINISDPTKGL-----NFAKXTXJTGDXDVLHNGI-----GS 194
Db 1202 VGTDSBLANGAK-----TIVNGCKGJIGIGYALVDANALNGIATGSAOYIHNSTAIIGNGS 1257
0Y 195 TLTLDXLXXXXXXXXXXXXXTXKXXXXRAASKKDVLNMGWNITKGVKXGXTXXXXXNVDFVX 254
Db 1258 TTT-----RGAOTN-----YTAYNMDDAQNVSGEFVSASDAQOR 1291
0Y 255 TYDPVEFLSADPTKTTTVNVESEKDNKKXFEVKGAKTSVIRKDKGLVTKKKXENXSSTD 314
Db 1292 QITNVAAGSADPTDAVNG-----QKVTDAQVSQNTQSTITLMDNRVTNLDSTRVTN--IE 1343
0Y 315 XGEGLVTAKEVIDAVNKGWBRKTTTANGQTGAQDEFTVSGTXV-----TFASGXGT 368
Db 1344 NGIG-----DIYTGSTKYFKNTFDGVDASAQGKDSVAIGGSIAMAADNSVALGTGS 1395
0Y 369 TATV-----SKDDQGIT-VXYDVNNGDALNNOJONS-----GWNLDKRAVASSSGKVI 417
Db 1396 VATEENTISVGSSTJQRRTITNVAAGKNATDAVNAOLKSSAGGRRDYTK----- 1446
0Y 418 SGNSVPSKGMDETVNINAGNNIEIXRGNKNIDIATSMXPOFSSVSLGAGADAFTLSYDX 477
Db 1447 -----DGSID-----YSNITLGGGNGTT----- 1465
0Y 478 XXALNVGSKXXXXXKPVRLITNVAAPVKEGQDVTNVAOLKGAQ-----NLNNXIDNV 526
Db 1466 -----RISNVSAGVANNNDVNVYPAOLKOSVOETKQYTDORAVEMDNKLSKT 1510
0Y 527 XGNARAGIAQAIATAGLXQAVLPCKSMMAIGXYTXGEGAGYALIGYSSISXKXGNXKIXGTA 586
Db 1511 ESKLSGIGIASAMAMGTLPOAVTPGASVMAISIGGYTNCGESAVALVGSVMVSANGRMYRYLKQG 1570
0Y 587 SGNSRGHFGXASVGYQW 604
Db 1571 STNSGEGYSAALGAGIOW 1588

```

RESULT 7  
H91188  
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain R1MD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence.revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasasara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shitagawa, H.  
GenBank Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PUDN:BAR37903.1; PUD:gl3363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain R1MD 050952  
A:Genetics:  
A:Gene: ECS4480

Query Match	12.0%;	Score 299.5;	DB 2;	Length 1588;
Best Local Similarity	24.1%;	Pred. No. 3.7e-13;		
Matches 120;	Conservative 48;	Mismatches 177;	Indels 153;	Gaps 16;

[illegible]

RESULT 8  
 AH0110  
 Probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C:Accession: AH0110  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.  
 J.; Mo-Farrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
 L.; M. Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett  
 Nature 413, 523-527, 2001  
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; M0UD:21470413; PMID:11586360  
 A:Accession: AH0110  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-658 <KUR>  
 A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: YP00902

	Query Match	11.5%	Score 287.5;	DB 2;	length 658;
	Best Local Similarity	24.8%;	Pred. No.9.4e-13;		
	Matches 103;	Conservative 57;	Mismatches 185;	Indels 71;	Gaps 13;
QY	235	IKGVXGXGTXXXXXNVDPVXT-----YDPEFELASPTKTTTV--NYESKDNGKXTEV--	284		
		:	:   :	:	
Dd	268	ITGVAAGSASSADAVNAVQLTAVGDVOOANTANITSLSGRVTIEGSNAISLANGGVYFH	327		
QY	285	-----KIAGKTIVSIKEODKGLVTKKK-KENNSSTFDXGBGLTAKEVIDAVNKAGWRM	336		
	:	: : :	:   :	:	
Dd	328	ANSTGPDSVASGTINSVALIGPASLASGANALIASGAAVALIDPGAASAASADSGVALIGQG---	383		
QY	337	KTTTANQG-----TGQADKEFTVTSGSTVFPAESGXGTTATPYSKDDQGNITVXXDYDVANNGDA	391		
	:	:	:     :	:	



Db 384 ---SGDNGRGVENVYIGKYSNANSTSSGTVSVGNATGETRTVSNVADG-----LQATDA 434

Qy 392 LWNQNLQNGWMLDSKAVAGSSGKVIISGVNSPBGKMDETVINAGNNI-ELIKRCKNID 450

Db 435 VMLRQLDG-----IAASTVYENVNVSGLQNGCTDMFQVNNSSGLAKPSATANSA 484

Qy 451 I--ATSMXPOFSSVSLGACADAPTLIS-----VDXXXALNVGSKXXNKPVRITNVAP 499

Db 485 TGGAGSVASGNNSTAFSGAKKATTAANSALGANSVADRANSVSGVGER--QITNVAP 542

Qy 500 GYKGGDVTVNAOLKGYAQNMLNXXIDNVXGNAR-----AGIAQAIATAGLXQAVY 548

Db 543 ANQGTDAVNEFDQLKTSISNQTNAVYTNQRYSELKQDLKQNSVLSAGIASMSMASLTPPT 602

Qy 549 PGKSMATIGXHTYXGAGTAIGYSSISXXGNMXXIKGTASGNSRGHFGXSASVGYQW 604

Db 603 SSSMTTIGAMSYRGOSALSLGVSSISDSGRVWSKLOASSNTOGPGIGVGYQW 658

RESULT 9

AC0976

Probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhimurium

A:Note: This species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi C

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0976

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:q16504923; GSPDB:GN00176

C:Genetics:

A:Gene: sapB

Query Match 11.1%; Score 278.5; DB 2; Length 1107;

Best Local Similarity 25.3%; Pred. No. 7.3e-12;

Matches 102; Conservative 56; Mismatches 176; Indels 69; Gaps 14;

Qy 263 SADTKTTTVNVEKDKNGKXTEVK-----IGAKTVYKEK-DGKLVYTKKKXENXSSTD 315

Db 713 STREEDSLAVGTSLAMGAKTIVNADAGIGLNTLVMAALINGALISNARAHANSIAM 772

Qy 316 GEGLVYTAKEVIDAVNKAGRMKTT-----TANQGTQADFEYVSGTYTTFASGXG- 367

Db 773 GNGSQTTTREGA--QDTYTAVMMDTPONSVEFVSSESGDOR-QITNVAAASADTDVAVNQ 829

Qy 368 -----TTATTVSKDDQGNITVYDVN-----VGDALNNQNLQNSGNLD----- 405

Db 830 LKVTDAQVSRNTQSTLNTLTQVSNLDTRYTNIENGIGDITVTGSTRYFRTNTDGDADANAQ 889

Qy 406 -SKAVAGSSGKVIISGVNSPBGKMDETVINAGNNIEXR-----NGKNIDIA 452

Db 890 GADPSVAGSGSIAAENSVALGTNSVADENYSSVSTQQRITNVAVAGVNNITDAVNA 949

Qy 453 TSXKPOFSSVSLGACADAPTLISVDXXXALNVGSKXXNKPVRITNVAPGYKGGDVTVNAOL 512

Db 950 QLKASAGSVRYRETNDG---SVN-YSVNLGCD-GSGGTTTIGNVSAVADTDVAVNAOL 1004

Qy 513 KGYAQNMLNXXIDNVXGNAR-----GIAQAIATAGLXQAVYLPKSMATIGXHTY 561

Db 1005 KRSVEEANTYTTQDKWENNSKIKGLENKMSGGIASAMAAAGLPQAAVAPGANNMTSIAGTF 1064

Qy 562 XGEGAGTAIGYSSISXXGNMXXIKGTASGNSRGHFGXSASVGYQW 604

Db 1065 NGSNAVALIGVMSVSESGWVYKLGTSNSGQDVSAAIAGNFQW 1107

RESULT 10

C82672

Surface-exposed outer membrane protein Xf1516 [imported] - Xylella fastidiosa (strain surface-exposed outer membrane protein Xf1516 [imported]) - Xylella fastidiosa (strain surface-exposed outer membrane protein Xf1516 [imported])

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: C82672

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; PMID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82672

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <SIM>

A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN

A:Experimental source: strain 9abC

R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, N.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurama, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranca, E.C.; Miyaki, C.

Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R.V.; Sawa

M.; Tshukko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf1516

Query Match 6.9%; Score 173; DB 2; Length 1004;

Best Local Similarity 25.3%; Pred. No. 0.00017;

Matches 96; Conservative 55; Mismatches 148; Indels 80; Gaps 18;

Qy 274 ESKDNGKXTEVKIGAKTVYKEKDKLVYTKKKXE-NXSSTDGEGLV--TAKEVI----- 326

Db 139 QSANNG-----VALGSNTVSGVNSVALGAGSMASELNVISVGGDGVTPAAYRIVNVD 194

Qy 327 -----DAVNAKAGRMKTTTANQGTQADFEYV-----TSGYTTFASGXGTATVSKD 376

Db 195 GIGNNDVAVKSSOLDGVYASV--DVAASVKITALINQVYTGSSVASASGSESTAISS--- 248

Qy 377 QGNITVYXVYVNDALNVNQLQNSGNMLDSKAVAGSSGKVIISGVNSPBGKMDETVINAINA 436

Db 249 GAQAVADNTVAFEGRAIVANVAGSALGFSDSHAGINSTVYGTQVSLGQVSLGANSFV 308

Qy 437 G-----NNIEIXRNG-----KNIDATSMXPOFSSVSLGACADAPTLISVDXXXALNVGS-KX 487

Db 309 GEGSFNGLAGNSLVLLQVD-----SVALGSGMSAEPNV-----VSVSGDGS 353

Qy 488 XNRPV--RITNVAPGYKGGDVTVNAOLKGYAQNMLNXXIDNV-----XGNARAGIAQ 536

Db 354 LRGPAYRIVNVDGIGNNDVAVKSSOLDGVYASVNDVAVSVKNIAGAIQITGSGVASVSG 413

Qy 537 AIATAGLXQAVYLPKSMATIG-----GXHYXGAGTAIGYSSISXXGNMXXIKGTA-- 586

Db 414 QDSTAAGASQAAAGDSSIALGARSANALIGSALGVDAVGLGANSYALG---GSTAIS 469

Qy 587 -SGNSRGH---FGXSASV 601

Db 470 EGGSIGNSFVGSATNG 488

RESULT 11

AB3486

cell surface protein [imported] - Brucella melitensis (strain 16m)



QY 457 PQFSSVSLGADAPTLSDVXXXXALNVGSKXXNKPVRITNVAPGVKEGDTNVAOL-KGV 515  
 DB 226 -----AETPAKAEAAAGTANTADKAEVAAKATDTIDADIATNKADIAKNS 272  
 QY 516 AQ-MLNNXIDVYXGNARAGIAQAIATAGLXQAYLPKSKMM--AIGXTYXGEAGYAIQY 571  
 DB 273 ARISIDKNNVANLRKETROGLAEQALSGLFPQYVNGRNVNVAAGC--YKSSSAVAIG- 329  
 QY 572 SSSIXXGNMXIK-----GTASGNSRG-HFGXASVGYQW 604  
 DB 330 TGRFRTENFAKAGVAVGTSSGSSAAYHVG-----VNYEW 364

RESULT 14

S11672  
 Ice nucleation protein - Xanthomonas campestris  
 C:Species: Xanthomonas campestris  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 26-Aug-1999  
 C:Accession: S11672  
 R:Zhao, J.; Oser, C.S.  
 Mol. Gen. Genet. 223, 163-166, 1990  
 A:Title: Conserved repetition in the ice nucleation gene *inx* from *Xanthomonas campestris*  
 A:Reference number: S11672; MUID:91080859  
 A:Accession: S11672  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1567 <2NH>  
 A:Cross-References: EMBL:X52970; NID:948531; PIDN:CAA37140.1; PID:948532  
 C:Superfamily: Ice nucleation protein

Query Match 5.7%; Score 142.5; DB 2; Length 1567;  
 Best Local Similarity 19.2%; Pred. No. 0.04;  
 Matches 85; Conservative 55; Mismatches 235; Indels 67; Gaps 14;

QY 178 TAXTNGDXTHVHNGTSTLTDLXXXXXXXKXXXXXXRAASXKDVLMAGNNING 237  
 DB 865 TGTAGADSTL-ISGYSTOT-----AGSDSLTAGYGTOTARKSDVTAG---- 910  
 QY 238 VKXGTXXXXXXNVDFYVTEFLSADTKTTTVNVEKSKDNGKXTEVKIGAKTSVIKERD 297  
 DB 911 ---GSTGTAGADSTLTAGYGTOTSGSDSLTAGYGTOTARKSDMTAGYGTGTAGAD 967  
 QY 298 GKLVTGKXKXKXKXSTDXEGELVTAKEVIDAVNKKAGWRMKTTTANGCOTQADFEFTVSG 357  
 DB 968 STLIAGYGTOTSGS-----DSSLTAGYGTOTAREGSDVTAGYGTGTAG 1013  
 QY 358 TTVTFASGXTATATYSKDDQGNITVYDVNVDALNVNQLNSGWLDSKNAVAGSSGXYI 417  
 DB 1014 ADSTLIAGYGTOTAGSD--SSLTAGY---GSTGTARQSDVTAGYGTGTAGADSTLI 1067  
 QY 418 SGNVSPSKGMDETVAINAGNNIEIRNGKNIDI--ATSMKPOFSSVSLGAGADAPTL 474  
 DB 1068 AGYGTGTAGSDSLTAGYGT--GTARQSDITAGYGTGTAGADSDSLTAGYGS-TGTAG 1125  
 QY 475 VDXXXALNVGSKXXNKPVRITNVAPGVKEGDTNVAOLKGVANLNKXIDVYXGNARAGI 534  
 DB 1126 YDSNLTAGYGTOTAR-----EDSSLTAGYGTSTAGHDSLLIAGYGTGTAGY 1174  
 QY 535 AQAIATAGLXQAYLPKSKMMAIGCTYXGEAGY---AIGYSSISXXG--NMXIKGTASG 588  
 DB 1175 -NSILTTGSGTGTAGDESSSLTAGYGTSTAGYDSTLTLAGYGTGTAGYKSTLTLAGYGSN 1233  
 QY 589 NSRGH-----FGXSASVGYQ 603  
 DB 1234 STAGHESLLIAGYGTGTAGYE 1255

RESULT 15  
 E97835  
 hypothetical protein rompb [imported] - Rickettsia conorii (strain Malish 7)  
 C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
 C:Accession: E97835  
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;  
 Science 293, 2093-2098, 2001  
 A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.  
 A:Reference number: A97700; MUID:21442074; PMID:11557893  
 A:Accession: E97835  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1655 <KUR>  
 A:Cross-References: GB:AE006914; PIDN:AAL03623.1; PID:915620207; GSPDB:GN00173  
 C:Genetics:  
 A:Gene: rompb

Query Match 5.7%; Score 142.5; DB 2; Length 1655;  
 Best Local Similarity 23.5%; Pred. No. 0.043;  
 Matches 94; Conservative 50; Mismatches 183; Indels 73; Gaps 20;

QY 249 NDFVXTYD---TVEFLSADTKTTTVN-----VESKDN-----KXTEVKIGAKTSVIK 294  
 DB 430 NTAGVITFPANGTTLASASADANVATNNITALEASGAGVVOJSGTHAELRLGNAGSVK 489  
 QY 295 EKDGKLVTKGKXKXKXSTDXEGELVTAKEVIDAVNKKAGWRMKTTTANGCOTQADRF 351  
 DB 490 LADGVTINCKVNOTALVGCALAGTTTLDSATITTDIGNAG---GAALQGITTLANDAT 546  
 QY 352 ETVT-----SGTXVTFASGXTTATVSKDDQGNITVYXYDV-----NVGDALNVN 395  
 DB 547 KTLTLGAGNIGANGGTINFQANGCTIKLTS--TQNNIYVDFDLATDTQGTGVVDASSLT 604  
 QY 396 QLONSGWNLDKRAVAGSSGKVIISGNVSPSKGM-DETVAIN--AGNN--IEIXRGNIN 449  
 DB 605 NQOTLIRNKIGTGVANNKTLGQFNIGSSKTYLSDGDVAINELVYIGNNGAVOFAHNTYLI 664  
 QY 450 DIATSMXPO-----FSSV-----SLGAGADAPTLSDVXXXXALNVGSKXXNKPVRITNVAPG 500  
 DB 665 TRITNAGGKILTFNRYVNNNTLTATGNTUGS-ATPPLAEINFGSGAANVDTVLVNGVK 723  
 QY 501 VREGDTNVAOLKGVANLNKXIDVYXG-NARAGIAQAIATAGLXQ-----AYLPKGS 552  
 DB 724 VNL-VATNITTTDA---NVGSFIFNAGGTINIVG-----TVGGQGNKRFNFVALDNGTT 773  
 QY 553 MNAIGCTYXGEAGYAIIGYSSISXKXGNMXIKGTASGNSRG 592  
 DB 774 VKFLGNATFNNGNTTIAAN-STLIQIGNYADAFVASADGTG 812

Search completed: July 3, 2002, 08:12:36  
 Job time: 458 sec





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Db 58 YLEPVGATAPVLSFHADESGEKE-VIGNTNLGIYFDEKRVLAKGTTITLAKGDLKIKQ 116
Qy 121 XXXXXXXXXXXXXFTYSLKRLXLLXXVTEKLSFANXXKVNIXSDTGLNFAKKTAX 180
Db 117 NTDENTENTNASSFTYSLKRLDLTGLSVTEKLSFGANGKKNITSDTKLNAKKTAG 176
Qy 181 TNGDXTVHLNGIGSTLTDLXLLXXXXXXXXTXXXXXKRAASKVDLNAKGNIKGVXX 240
Db 177 TNGDXTVHLNGIGSTLTDLXLLXXXXXXXXTXXXXXKRAASKVDLNAKGNIKGVXX 234
Qy 241 GXTXXXXXNVDFVYTYDVEFLSADRTTTVNVESKNGKXTEVKGAKTSVIEKDKGL 300
Db 235 GSTGQSENVDFVYTYDVEFLSADRTTTVNVESKNGKXTEVKGAKTSVIEKDKGL 294
Qy 301 VTGKXKXENKSTDXGEGVLTAKEVIDAVNKAQKRMKTTTANGTGQADKFEYTSCTV 360
Db 295 VTGKXKXENKSTDXGEGVLTAKEVIDAVNKAQKRMKTTTANGTGQADKFEYTSCTV 354
Qy 361 TFAAGXTTATVSKDQGNITVXYDVNVGDALNVNOLNSGMDLSKAVAGSSGKVTISGN 420
Db 355 TFAAGXTTATVSKDQGNITVXYDVNVGDALNVNOLNSGMDLSKAVAGSSGKVTISGN 414
Qy 421 VSPSKGMDETVNIAGNIEIIXRNGKNIDATSMXPOFSSVSLGAGADAPTLISVDXXXA 480
Db 415 VSPSKGMDETVNIAGNIEIIXRNGKNIDATSMXPOFSSVSLGAGADAPTLISVDXXXA 474
Qy 481 LVNSKXKXNRPVRLTNNAPGKEDVTNNVQOLKVAQNLNXXIDNVYGNMNAAGIAQAIAT 540
Db 475 LVNSKXKXNRPVRLTNNAPGKEDVTNNVQOLKVAQNLNXXIDNVYGNMNAAGIAQAIAT 534
Qy 541 AGLXQAVLPGKSMALIGGXTYXGAGYALIGSSISXXGNMXXIKGTASGNSGHRGXSASV 600
Db 535 AGLVQAVLPGKSMALIGGXTYXGAGYALIGSSISXXGNMXXIKGTASGNSGHRGXSASV 594
Qy 601 GYQW 604
Db 595 GYQW 598

RESULT 2
Q9JPS5 ID Q9JPS5 PRELIMINARY: PRT: 600 AA.
AC Q9JPS5:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20175756; Pubmed=10710308;
RA Comanucci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.,
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.
RL Science 287:1816-1820(2000).
DR EMBL: AF226372; AAF42521.1; -.
SQ SEQUENCE 600 AA; 62606 MW; 13C35F1C46392524 CRC64;
```

Query Match 89.6%; Score 2240; DB 2; Length 600;  
Best local Similarity 77.5%; Pred. No. 8.9e-124;  
Matches 468; Conservative 0; Mismatches 132; Indels 4; Gaps 2;

```
Qy 1 MNXIXRIIMNSALNAMYVSELTRNHTKRASATYXAVLATLLXAFVQAXXXXXXXXXXX 60
Db 1 MNKIRIRIIMNIALNAMYVSELTRNHTKRASATYXAVLATLLSATVQA--NADEEDNE 58
Qy 61 XLXVXKXKXVXXXXXXEGXEXEXXXXXXXXKXXXXXXXKXKXKXKXKXKXKXKXKXKX 120
Db 59 DLEPVTAPVLSFHSDEKGEKEEVGASNLTVYFDKNVRLAKGTITLAKGDLKIKQ 118
Qy 121 XXXXXXXXXXXXXFTYSLKRLXLLXXVTEKLSFANXXKVNIXSDTGLNFAKKTAX 180
Db 119 NTNENTENTNASSFTYSLKRLDLTGLINTEKLSFGANGKKNITSDTKLNAKKTAG 178
Qy 181 TNGDXTVHLNGIGSTLTDLXLLXXXXXXXXTXXXXXKRAASKVDLNAKGNIKGVXX 240
Db 179 TNGDXTVHLNGIGSTLTDLXLLXXXXXXXXTXXXXXKRAASKVDLNAKGNIKGVXX 236
Qy 241 GXTXXXXXNVDFVYTYDVEFLSADRTTTVNVESKNGKXTEVKGAKTSVIEKDKGL 300
Db 237 GSTGQSENVDFVYTYDVEFLSADRTTTVNVESKNGKXTEVKGAKTSVIEKDKGL 296
Qy 301 VTGKXKXENKSTDXGEGVLTAKEVIDAVNKAQKRMKTTTANGTGQADKFEYTSCTV 360
Db 297 VTGKXKXENKSTDXGEGVLTAKEVIDAVNKAQKRMKTTTANGTGQADKFEYTSCTV 356
Qy 361 TFAAGXTTATVSKDQGNITVXYDVNVGDALNVNOLNSGMDLSKAVAGSSGKVTISGN 420
Db 357 TFAAGXTTATVSKDQGNITVXYDVNVGDALNVNOLNSGMDLSKAVAGSSGKVTISGN 416
Qy 421 VSPSKGMDETVNIAGNIEIIXRNGKNIDATSMXPOFSSVSLGAGADAPTLISVDXXXA 480
Db 417 VSPSKGMDETVNIAGNIEIIXRNGKNIDATSMXPOFSSVSLGAGADAPTLISVDXXXA 476
Qy 481 LVNSKXKXNRPVRLTNNAPGKEDVTNNVQOLKVAQNLNXXIDNVYGNMNAAGIAQAIAT 540
Db 477 LVNSKXKXNRPVRLTNNAPGKEDVTNNVQOLKVAQNLNXXIDNVYGNMNAAGIAQAIAT 536
Qy 541 AGLXQAVLPGKSMALIGGXTYXGAGYALIGSSISXXGNMXXIKGTASGNSGHRGXSASV 600
Db 537 AGLVQAVLPGKSMALIGGXTYXGAGYALIGSSISXXGNMXXIKGTASGNSGHRGXSASV 596
Qy 601 GYQW 604
Db 597 GYQW 600

RESULT 3
Q9JPS8 ID Q9JPS8 PRELIMINARY: PRT: 599 AA.
AC Q9JPS8:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20175756; Pubmed=10710308;
RA Comanucci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.,
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.
RL Science 287:1816-1820(2000).
DR EMBL: AF226364; AAF42513.1; -.
SQ SEQUENCE 599 AA; 62606 MW; 13C35F1C46392524 CRC64;
```

SQ SEQUENCE 599 AA: 62693 MW: 46C2E974AF78E9 CRC64:

Query Match

Best Local Similarity 89.6%; Score 2239.5; DB 2; Length 599;  
Matches 469; Conservative 0; Mismatches 130; Indels 5; Gaps 3;

1 MNXIXRIINNSALNMAWVYSELTRNHTKRASATVAVATLTLAATVQAAXXXXXXXX 60  
1 MNXIXRIINNSALNMAWVYSELTRNHTKRASATVAVATLTLAATVQAAXXXXXXXX 58  
61 XLXVYRXXVXXXXXXXXXXEEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX 120  
59 YLEPVKRTAVLVLSFRSDKGTGEKE-VTEDSHMGVYFDEKGLVLAAGTITLAKGDNLIK 117  
121 XXXXXXXXXXXXXFTYSLKKLXLLXVYTERKLSFXANXXVNIKXSDTKGLNFAKXTAX 180  
118 NTDEMTENTMNASFTYSLSKDLTDLTSVETELKSGANGKNVNTSDTKGLNFAKXTAG 177  
181 TNGDXTVHLNGISLTLDLXXXXXXXXTXXXXXRAASXKDVLAAGNINIGVXX 240  
178 TNGDXTVHLNGISLTLDLTLAAGSSASHVADAGNOST--HTTTRASIXDVLAAGNINIGV 235  
241 GXTXXXXXNVDFVXYDYVEFLSADTKTTTVNESKDNKXTEVKIGAKTSVIREKDKL 300  
236 GSTTQSENVDFVRYTDYVEFLSADTKTTTVNESKDNKXTEVKIGAKTSVIREKDKL 295  
301 VTGKXKXENXSSTDXEGGLVTAKEVIDAVNKAQMRKTTTANGQOTGADKFEFVTSCTYX 360  
296 VTGKXGGENSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGQOTGADKFEFVTSCTYX 355  
361 TFASGCGTATATYSKDOGNITVYDVNVDALVNOLQNSGNMLDSKAAVSSGKVISGN 420  
356 TFASGCGTATATYSKDOGNITVYDVNVDALVNOLQNSGNMLDSKAAVSSGKVISGN 415  
421 VSPSKGKMETVINAGNNIETIRNKNIDIAISMPPOFSVSLGAGADAPTLISVDEKGA 480  
416 VSPSKGKMETVINAGNNIETIRNKNIDIAISMPPOFSVSLGAGADAPTLISVDEKGA 475  
481 LVNGSKXXXKPVRTINVAPEKEDVTNVAQLKGVANLNKXIDNXXGNARAGIAQAIAT 540  
476 LVNGSKDANKPVRTINVAPEKEDVTNVAQLKGVANLNKXIDNXXGNARAGIAQAIAT 535  
541 AGLXQAYLPKSKMMAIGGTYXGEAGYAGYSISXKGMXIKGTASGNSRGHFGASASV 600  
536 AGLXQAYLPKSKMMAIGGTYXGEAGYAGYSISIDGGMWIKGTASGNSRGHFGASASV 595  
601 GYOM 604  
596 GYOM 599

RESULT 4  
09JPS3 PRELIMINARY: PRT: 590 AA.

AC 09JPS3: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN NCBI\_TaxID=487;  
RP SEQUENCE FROM N.A.  
RC STRAIN-NGE28;  
MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Balci L., Bartolini E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti R., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -  
SQ SEQUENCE 590 AA: 61661 MW: 8AA476AC300D80C8 CRC64:

Query Match

Best Local Similarity 89.4%; Score 2235; DB 2; Length 590;  
Matches 469; Conservative 0; Mismatches 121; Indels 14; Gaps 3;

1 MNXIXRIINNSALNMAWVYSELTRNHTKRASATVAVATLTLAATVQAAXXXXXXXX 60  
1 MNXIXRIINNSALNMAWVYSELTRNHTKRASATVAVATLTLAATVQAAXXXXXXXX 58  
61 XLXVYRXXVXXXXXXXXXXEEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX 120  
59 YLEPVKRTAVLVLSFRSDKGTGEKEVEENSDMAVYFNEKGVLAGTITLAKGDNLIK 118  
121 XXXXXXXXXXXXXFTYSLKKLXLLXVYTERKLSFXANXXVNIKXSDTKGLNFAKXTAX 180  
119 -----NGTFTYSLKKDLTDLTSVETELKSGANGKNVNTSDTKGLNFAKXTAG 168  
181 TNGDXTVHLNGISLTLDLXXXXXXXXTXXXXXRAASXKDVLAAGNINIGVXX 240  
169 TNGDXTVHLNGISLTLDLTLAAGSSASHVADAGNOST--HTTTRASIXDVLAAGNINIGV 235  
241 GXTXXXXXNVDFVXYDYVEFLSADTKTTTVNESKDNKXTEVKIGAKTSVIREKDKL 300  
229 GTT--ASDNVDFRYTDYVEFLSADTKTTTVNESKDNKXTEVKIGAKTSVIREKDKL 286  
301 VTGKXKXENXSSTDXEGGLVTAKEVIDAVNKAQMRKTTTANGQOTGADKFEFVTSCTYX 360  
287 VTGKXGGENSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGQOTGADKFEFVTSCTYX 346  
361 TFASGCGTATATYSKDOGNITVYDVNVDALVNOLQNSGNMLDSKAAVSSGKVISGN 420  
347 TFASGCGTATATYSKDOGNITVYDVNVDALVNOLQNSGNMLDSKAAVSSGKVISGN 406  
421 VSPSKGKMETVINAGNNIETIRNKNIDIAISMPPOFSVSLGAGADAPTLISVDEKGA 480  
407 VSPSKGKMETVINAGNNIETIRNKNIDIAISMPPOFSVSLGAGADAPTLISVDEKGA 466  
481 LVNGSKXXXKPVRTINVAPEKEDVTNVAQLKGVANLNKXIDNXXGNARAGIAQAIAT 540  
467 LVNGSKDANKPVRTINVAPEKEDVTNVAQLKGVANLNKXIDNXXGNARAGIAQAIAT 526  
541 AGLXQAYLPKSKMMAIGGTYXGEAGYAGYSISXKGMXIKGTASGNSRGHFGASASV 600  
527 AGLXQAYLPKSKMMAIGGTYXGEAGYAGYSISIDGGMWIKGTASGNSRGHFGASASV 586  
601 GYOM 604  
587 GYOM 590

RESULT 5  
09JPS3 PRELIMINARY: PRT: 598 AA.

AC 09JPS3: 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN NCBI\_TaxID=487;  
RP SEQUENCE FROM N.A.  
RC STRAIN-B210;

RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of *Neisseria meningitidis*."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157603; AK68864.1; -  
 SO SEQUENCE 598 AA; 62687 MW; 18CEFF6410A15DF CRC64;

Query Match 89.4%; Score 2235; DB 2; Length 598;  
 Best Local Similarity 77.6%; Pred. No. 1,7e-123;  
 Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

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QY 1 MNXIRIIMNSALNAMYVSELTNRNHTKRASATVATVLTATLKAIVQAXXXXXXXXXXXXXX 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MNKIRIIMNSALNAMYVSELTNRNHTKRASATVATVLTATLKAIVQAXXXXXXXXXXXXXX 57
QY 61 XLXVXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRX 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 58 YLEPVQRTAVVLSFRSDKEGTGEKE-GTEDSNMAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
QY 121 XXXXXXXXXXXXXFTYSLKKKLLXLLXXVTEKLSFYANXXKKVNIKSDTKGLNFAKXTAX 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 NTNENTMENTNDSFTYSLKKDLTDLTSLVEFEKLSFGANGKVNITSDTKGLNFAKXTAG 176
QY 181 TNGDXYHLNGIGSTLFDLXLLXAXXXXXXXXXXXTXXXXXRAASKDYLANAGNIKGVXX 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 177 TNGDPTVHLNGIGSTLFDLTLNTGATTNVTNDVTDDEKKRAASVKDYLANAGNIKGVKP 236
QY 241 GXTXXXXXNVDVXYTDTVEFLSADTKTTTVNVEKDKNGKXTEVKIGAKTSVIEKDGKL 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 GTT--ASDNVDFVTTYDTVEFLSADTKTTTVNVEKDKNGKXTEVKIGAKTSVIEKDGKL 294
QY 301 VTGKXKXENKSTDXGEGLYTAKAEVIDAVNKAQRMKTITANGOTGADKFEVTSCTVX 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 VTGKXGKENGSTDEGGLVYAKAEVIDAVNKAQRMKTITANGOTGADKFEVTSCTVX 354
QY 361 TFGAGXGTTATVSKDDGNTVXYDVNAGDALNVNOLNSGMNIDSKRAVAGSSGKVISGN 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 TFGAGNGTTATVSKDDGNTVXYDVNAGDALNVNOLNSGMNIDSKRAVAGSSGKVISGN 414
QY 421 VSPKGMKDEVTNINAGNIEITXRNKNIDTATSMXPOFSSVSLGAGADAPTLISVDXXXA 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 VSPKGMKDEVTNINAGNIEITXRNKNIDTATSMXPOFSSVSLGAGADAPTLISVDXXXA 474
QY 481 LVNSGKXKXNKFRITTNAPGVKEGDTVNAQLKGYAONLNMXIDNVXGNARAGIAQAIAAT 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 LVNSGSKDANKRVRTTNAPGVKEGDTVNAQLKGYAONLNMXIDNVXGNARAGIAQAIAAT 534
QY 541 AGLXQAVYLPKGSMAIGGXTYXGEGVYAGISYSISXGNMXXIKGTASGNSRGHFGXSASV 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 AGLXQAVYLPKGSMAIGGXTYXGEGVYAGISYSISDGTGNMVIKGTASGNSRGHFGTSASV 594
QY 601 GYQW 604
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 GYQW 598
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
O9JPT0 PRELIMINARY: PRT; 598 AA.
AC O9JPT0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;

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RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of vaccine candidates *Agalins* Serogroup B  
 RT Meningococcus by whole-genome sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226359; AAF42508.1; -  
 SO SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 89.4%; Score 2234; DB 2; Length 598;  
 Best Local Similarity 77.6%; Pred. No. 2e-123;  
 Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

```

QY 1 MNXIRIIMNSALNAMYVSELTNRNHTKRASATVATVLTATLKAIVQAXXXXXXXXXXXXXX 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MNKIRIIMNSALNAMYVSELTNRNHTKRASATVATVLTATLKAIVQAXXXXXXXXXXXXXX 57
QY 61 XLXVXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRX 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 58 YLEPVQRTAVVLSFRSDKEGTGEKE-GTEDSNMAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
QY 121 XXXXXXXXXXXXXFTYSLKKKLLXLLXXVTEKLSFYANXXKKVNIKSDTKGLNFAKXTAX 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 NTNENTMENTNDSFTYSLKKDLTDLTSLVEFEKLSFGANGKVNITSDTKGLNFAKXTAG 176
QY 181 TNGDXYHLNGIGSTLFDLXLLXAXXXXXXXXXXXTXXXXXRAASKDYLANAGNIKGVXX 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 177 TNGDPTVHLNGIGSTLFDLTLNTGATTNVTNDVTDDEKKRAASVKDYLANAGNIKGVKP 236
QY 241 GXTXXXXXNVDVXYTDTVEFLSADTKTTTVNVEKDKNGKXTEVKIGAKTSVIEKDGKL 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 GTT--ASDNVDFVTTYDTVEFLSADTKTTTVNVEKDKNGKXTEVKIGAKTSVIEKDGKL 294
QY 301 VTGKXKXENKSTDXGEGLYTAKAEVIDAVNKAQRMKTITANGOTGADKFEVTSCTVX 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 VTGKXGKENGSTDEGGLVYAKAEVIDAVNKAQRMKTITANGOTGADKFEVTSCTVX 354
QY 421 VSPKGMKDEVTNINAGNIEITXRNKNIDTATSMXPOFSSVSLGAGADAPTLISVDXXXA 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 TFGAGNGTTATVSKDDGNTVXYDVNAGDALNVNOLNSGMNIDSKRAVAGSSGKVISGN 414
QY 361 TFGAGXGTTATVSKDDGNTVXYDVNAGDALNVNOLNSGMNIDSKRAVAGSSGKVISGN 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 VSPKGMKDEVTNINAGNIEITXRNKNIDTATSMXPOFSSVSLGAGADAPTLISVDXXXA 474
QY 481 LVNSGKXKXNKFRITTNAPGVKEGDTVNAQLKGYAONLNMXIDNVXGNARAGIAQAIAAT 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 LVNSGSKDANKRVRTTNAPGVKEGDTVNAQLKGYAONLNMXIDNVXGNARAGIAQAIAAT 534
QY 541 AGLXQAVYLPKGSMAIGGXTYXGEGVYAGISYSISXGNMXXIKGTASGNSRGHFGXSASV 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 AGLXQAVYLPKGSMAIGGXTYXGEGVYAGISYSISDGTGNMVIKGTASGNSRGHFGTSASV 594
QY 601 GYQW 604
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 GYQW 598
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
O9JPS0 PRELIMINARY: PRT; 598 AA.
AC O9JPS0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.

```



OC Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxId=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGH15;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H15;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF226381; AAF42530.1; -;  
 DR EMBL: AF157607; AAK68868.1; -;  
 SQ SEQUENCE 598 AA: 62763 MW: E6C7AEF0BB8A63CB CRC64:

Query Match 89.4%; Score 2234; DB 2; Length 598;  
 Best Local Similarity 77.6%; Pred. No. 2e-123;  
 Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

OY 1 MNXIRIITNSALNANVYSELTRNHTKRASATVATLTLATLQVQAXXXXXXXX 60  
 DB 1 MNKIRIITNSALNANVYSELTRNHTKRASATVATLTLATLQVQAXXXXXXXX 57  
 OY 61 XLXVYRXXVXXXXXXGEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX 120  
 DB 58 YLEPQRTAVVLSFRSDKGTGEKE- GTEDSMWAYFDEKRLKAGATILKAGDNLKIQ 116  
 OY 121 XXXXXXXXXXXXXFTYSLKXLLXLYVTEKLSFXANXXKVNIXSDTKGLNFAKXTAX 180  
 DB 117 NTNENTNENTNDSFYSLSKDLTDLTSETEKLSFGANGKNVNTSDTKGLNFAKETAG 176  
 OY 181 TNGDXTVHLNGIGSTLTDLXXXXAXXXXXXXXTXXXXRAAXKDVNLAGNIGVXX 240  
 DB 177 TNGDPTVHLNGIGSTLTDLTLTGATTVNTDNDVTDDEKRRASVYDVLNAGNINIGVXP 236  
 OY 241 GXTXXXXXXNVDFYTYDYEFSLADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDGKL 300  
 DB 237 GTT--ASDNVDVRYTYDYEFSLADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDGKL 294  
 OY 301 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFETVTSCTYX 360  
 DB 295 VTGKGDENGSSTDGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFETVTSCTYX 354  
 OY 361 TPASGXTATYATYKDDQGNITVYDVNVDALNVLNOLNSGWLDSKRAVAGSSGKVISGN 420  
 DB 355 TPASGXTATYATYKDDQGNITVYDVNVDALNVLNOLNSGWLDSKRAVAGSSGKVISGN 414  
 OY 421 VPSKGMDETVINAGNNEIIRNGKNIDTATSMKPOFSVSLGAGADAPTLSTVYXXXA 480  
 DB 415 VPSKGMDETVINAGNNEIIRNGKNIDTATSMKPOFSVSLGAGADAPTLSTVYDEGA 474  
 OY 481 LNVGSKXKXNRPVITNVAVKEGDVTNVAOLKGVANLNKXIDNVXGNARAGIAQAIAT 540  
 DB 475 LNVGSKDANKPVITNVAVKEGDVTNVAOLKGVANLNKXIDNVXGNARAGIAQAIAT 534  
 OY 541 AGLXQAVYLPKSMALIGATYTGAGATYATGYSISXKXGNWIXKGTASGNSRGHFGASASV 600  
 DB 535 AGLAQAIVLPKSMALIGATYTGAGATYATGYSISIDTGMVWIKGTASGNSRGHFGASASV 594  
 OY 601 GYQM 604  
 ||||

DB 595 GYQM 598  
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 RESULT 8  
 O930Y1 ID 0930Y1 PRELIMINARY; PRT: 589 AA.  
 AC 0930Y1  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxId=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P20;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157610; AAK68871.1; -;  
 SQ SEQUENCE 589 AA: 61448 MW: 1FLA80CD610CB230 CRC64:

Query Match 89.3%; Score 2231.5; DB 2; Length 589;  
 Best Local Similarity 77.6%; Pred. No. 2.7e-123;  
 Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;

OY 1 MNXIRIITNSALNANVYSELTRNHTKRASATVATLTLATLQVQAXXXXXXXX 60  
 DB 1 MNKIRIITNSALNANVYSELTRNHTKRASATVATLTLATLQVQAXXXXXXXX 58  
 OY 61 XLXVYRXXVXXXXXXGEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX 120  
 DB 59 ELESVARSAVLYQFLMDKENGELIE- STGDIGSITYYDDHNTLHGATVTLKAGDNLKIQ 117  
 OY 121 XXXXXXXXXXXXXFTYSLKXLLXLYVTEKLSFXANXXKVNIXSDTKGLNFAKXTAX 180  
 DB 118 -----SGKDFYSLSKELKDLTSETEKLSFGANGKNVNTSDTKGLNFAKETAG 167  
 OY 181 TNGDXTVHLNGIGSTLTDLXXXXAXXXXXXXXTXXXXRAAXKDVNLAGNIGVXX 240  
 DB 168 TNGDPTVHLNGIGSTLTDLTLTGATTVNTDNDVTDDEKRRASVYDVLNAGNINIGVXP 236  
 OY 241 GXTXXXXXXNVDFYTYDYEFSLADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDGKL 300  
 DB 226 GSTTGSSENVDFRYTYDYEFSLADTKTTTVNVEKDKNGKTEVKIGAKTSVYKEKDGKL 285  
 OY 301 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFETVTSCTYX 360  
 DB 286 VTGKGDENGSSTDGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFETVTSCTYX 345  
 OY 361 TPASGXTATYATYKDDQGNITVYDVNVDALNVLNOLNSGWLDSKRAVAGSSGKVISGN 420  
 DB 346 TPASGXTATYATYKDDQGNITVYDVNVDALNVLNOLNSGWLDSKRAVAGSSGKVISGN 405  
 OY 421 VPSKGMDETVINAGNNEIIRNGKNIDTATSMKPOFSVSLGAGADAPTLSTVYXXXA 480  
 DB 406 VPSKGMDETVINAGNNEIIRNGKNIDTATSMKPOFSVSLGAGADAPTLSTVYDEGA 465  
 OY 481 LNVGSKXKXNRPVITNVAVKEGDVTNVAOLKGVANLNKXIDNVXGNARAGIAQAIAT 540  
 DB 466 LNVGSKDANKPVITNVAVKEGDVTNVAOLKGVANLNKXIDNVXGNARAGIAQAIAT 525  
 OY 541 AGLXQAVYLPKSMALIGATYTGAGATYATGYSISXKXGNWIXKGTASGNSRGHFGASASV 600  
 DB 526 AGLAQAIVLPKSMALIGATYTGAGATYATGYSISIDTGMVWIKGTASGNSRGHFGASASV 585  
 OY 601 GYQM 604  
 ||||

Db 586 GYOW 589

## RESULT 9

ID 09JPR8 PRELIMINARY: PRT: 599 AA.

AC 09JPR8; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHA OUTER MEMBRANE PROTEIN).

GN GNA992 OR NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=NGH38;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).

RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=H38;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226383; AAF42532.1; -;  
DR EMBL: AF157608; AAK68869.1; -;  
SQ SEQUENCE 599 AA; 62844 MW; BBA16BPF3C1970C CRC64;

Query Match 89.38; Score 2231.5; DB 2: Length 599;  
Best Local Similarity 77.68; Pred. No. 2.8e-123;  
Matches 469; Conservative 0; Mismatches 130; Indels 5; Gaps 3;

QY 1 MNXIXRIIMNSALNAAWYVSELTNRNHTKRASATVATVATLATAVQAAXXXXXXXXXX 60  
DB 1 MNKTYRIIMNSALNAAWYVSELTNRNHTKRASATVATVATLATAVQA--NATDEDEE 58

QY 61 XLXVYRXXVXXXXXXXXXXEGXEXXXXXXXXXXXXXXXXXXXXXTLKAGNLIKQ 120  
DB 59 ELEPVVNSALVLOFMIDKEGNGENE-STGNIGWSIYYDNHTLGCATVTLKAGNLIKQ 117

QY 121 XXXXXXXXXXXXXFTYSLKXXLXXLVYTEKLSFANXXKKVINXSTPKLNAKKTAX 180  
DB 118 NTNKNNTNENTDSSEFTYSLKLDLTLSVETEKLSFGANGKRVNITSOTKGLNFAKETAG 177

QY 181 TNGDXTVHLNGIGSTLDPDLKXXXXXXAXXXXXXXXXXXRAASKVDVLAAGNINIKGYKX 240  
DB 178 TNGDXTVHLNGIGSTLDPDLKXXXXXXAXXXXXXXXXXXRAASKVDVLAAGNINIKGYKX 237

QY 241 GXTXXXXXNVDFVYTYDVEFLSADTKTTTVNVEKDKGKXTEVYIGAKTSVIREKDKL 300  
DB 238 GTT--ASDNVDFVHTYDVEFLSADTKTTTVNVEKDKGKXTEVYIGAKTSVIREKDKL 295

QY 301 VTGKXKXKXNASTXGSGELVTAKEVYDAVNKAAGRMKTTTANGGTGQADKRETYTSGTXY 360  
DB 296 VTGKXKXKXNASTXGSGELVTAKEVYDAVNKAAGRMKTTTANGGTGQADKRETYTSGTXY 355

QY 361 TFAAGXGTTAVVNSKDDGNTVYXVDVNGDALNVNOLNSGMNLDKSKAVASSSGKVISGN 420  
DB 356 TFAAGXGTTAVVNSKDDGNTVYXVDVNGDALNVNOLNSGMNLDKSKAVASSSGKVISGN 415

QY 421 VSPSKGMDETVINAGNNIEIKRNGKNIDIASMKXPOFSSVSLGAGADAPTLSDVXXXX 480  
DB 416 VSPSKGMDETVINAGNNIEIKRNGKNIDIASMKXPOFSSVSLGAGADAPTLSDVXXXX 475  
QY 481 LVNSKXKXNKPVRITVAVPGVEGDTVNAOLKGVANLNINXIDNYXGNARAGIAQAIAT 540  
DB 476 LVNSKXKXNKPVRITVAVPGVEGDTVNAOLKGVANLNINXIDNYXGNARAGIAQAIAT 535  
QY 541 AGLXOAVLPKSMMAIGKXTYXGAGYATGSSISXKXNMKXIGTASGNSRGHFGASAV 600  
DB 536 AGLXOAVLPKSMMAIGKXTYXGAGYATGSSISXKXNMKXIGTASGNSRGHFGASAV 595

## RESULT 10

ID 09JPIO PRELIMINARY: PRT: 589 AA.

AC 09JPIO; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.

GN Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=NGP165, 90/18311, AND 93/4286;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).

DR EMBL: AF226384; AAF42533.1; -;  
DR EMBL: AF226362; AAF42511.1; -;  
DR EMBL: AF226363; AAF42512.1; -;  
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match 89.38; Score 2230.5; DB 2: Length 589;  
Best Local Similarity 77.68; Pred. No. 3.1e-123;  
Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;

QY 1 MNXIXRIIMNSALNAAWYVSELTNRNHTKRASATVATVATLATAVQAAXXXXXXXXXX 60  
DB 1 MNKTYRIIMNSALNAAWYVSELTNRNHTKRASATVATVATLATAVQA--NATDDEDE 58

QY 61 XLXVYRXXVXXXXXXXXXXEGXEXXXXXXXXXXXXXXXXXXXXXTLKAGNLIKQ 120  
DB 59 ELEPVVNSALVLOFMIDKEGNGEIE-STGDIGWSIYYDNHTLGCATVTLKAGNLIKQ 117

QY 121 XXXXXXXXXXXXXFTYSLKXXLXXLVYTEKLSFANXXKKVINXSTPKLNAKKTAX 180  
DB 118 -----SGKDFYTSLKRELDTLSVETEKLSFGANGKRVNITSOTKGLNFAKETAG 167

QY 181 TNGDXTVHLNGIGSTLDPDLKXXXXXXAXXXXXXXXXXXRAASKVDVLAAGNINIKGYKX 240  
DB 168 TNGDXTVHLNGIGSTLDPDLKXXXXXXAXXXXXXXXXXXRAASKVDVLAAGNINIKGYKX 225

QY 241 GXTXXXXXNVDFVYTYDVEFLSADTKTTTVNVEKDKGKXTEVYIGAKTSVIREKDKL 300  
DB 226 GSTTGQSENVDVFRITVYDVEFLSADTKTTTVNVEKDKGKXTEVYIGAKTSVIREKDKL 285

Db	171	TNGDTTVHLNIGSLPTDPTLLNTGATTTVTDNTVTDDEKRAASVKOVLANGMRIKGVK	230
Qy	241	GATXXXXXNVDPVXTYDTVEFLSADPTKTTVNVESKONGKXTEVYIGAKTSVYKEKDGL	300
Db	231	GTT--ASNVDVFPVRTDYVEELISADTKTTVNVESKONGKTEVYIGAKTSVYKEKDGL	288
Qy	301	VTGKXKXENXSSTQDEGLVNAKEVYDAVYKAGRMKTTTNGSGTGADKFEYVTSCTHY	366
Db	289	VTGKXKXENXSSTQDEGLVNAKEVYDAVYKAGRMKTTTNGSGTGADKFEYVTSCTHY	348
Qy	361	TFASAGKGTATVYAKDQGNITVYXDVNVGDALANTNOIUNGSMNDSKAVAGSSGKTVISGN	420
Db	349	TFASAGKGTATVYAKDQGNITVYXDVNVGDALANTNOIUNGSMNDSKAVAGSSGKTVISGN	408
Qy	421	VSPSKGKMDFTVNIAGNNIEITXRNKGNIDIATSMXPOFSSVSIGAGADAPTLISVDXXXA	480
Db	409	VSPSKGKMDFTVNIAGNNIEITXRNKGNIDIATSMTPQFSSVSIGAGADAPTLISVD--GDA	467
Qy	481	LNVGSKXXXXNPKVRIITNVAAGVKEGDTVVAOLKCAVQNLNIXIDNXYGNMAGITAOAIAT	540
Db	468	LNVGSKKDNKPKVRIITNVAAGVKEGDTVVAOLKCAVQNLNRIIDNVGNMAAGITAOAIAT	522
Qy	541	AGLXGAVLPGKSMMAIGGXTYXGEGAVYIGVSSISXXGNMXXIKGTASGNSRGHRGXSASV	600
Db	528	AGLVGAVLPGKSMMAIGGCTYRGEGAVYIGVSSISDGMNIIKGTASGNSRGHRGXSASV	587
Qy	601	GYOW 604	
Db	588	GYOW 591	
RESULT 12			
ID	Q93QY3	PRELIMINARY;	PRT; 591 AA.
AC	Q93QY3;		
DT	01-DEC-2001 (Tremblrel. 19, Created)		
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)		
DE	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
GN	NHHA OUTER MEMBRANE PROTEIN.		
OS	NHHA.		
OC	Neisseria meningitidis.		
OX	NHHA_TaxID=487;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=E6329;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RL	membrane protein of Neisseria meningitidis.";		
DR	Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.		
SO	EMBL: AF157606; AAK68867.1;--		
	SEQUENCE 591 AA: 62048 MW: CODC600798859C65 CRC64;		

[illegible]

QY	241	GTXXXXXXXNDPFXATDPTVEEFSADQKTTTANNVESKDCKXTVEKIGAKTSYIKEDGKL	300
Db	231	GTT--ASDNVDFPRITDPTVEEFSADQKTTTANNVESKDCKTEVIGAKTSYIKEDGKL	288
QY	301	VTGKXXKXENXSSTDJSEGLVTAAKEVIDAIVNKAQWKRKTTTANGOTGOADKETVTYSTXV	360
Db	289	VTGKDKGENSSDDEEGGLVTAKEVEIDAIVNKAQWKRKTTTANGOTGOADKETVTYSTXV	348
QY	361	TFPAGXGXTATVSKDDQGNITYYVDVNGDALNVNDLNSGNNLDSKAVAGSSGIVISGN	420
Db	349	TFPAGKKTPTVTSKDDQGNITYYVDVNGDALNVNDLNSGNNLDSKAVAGSSGIVISGN	408
QY	421	VSPSKGMDETVNIANGNNIETIRKNCNIDIATSMKPPQSSVSLGADAPILSVXXXXA	480
Db	409	VSPSKGMDETVNIANGNNIETIRKNCNIDIATSMTPQSSVSLGADAPILSTD--GDA	467
QY	481	LNVGSKXXNKPVRITVAVPQVEGDTVYVAQLKGYAQNINXNDVYXGNARAGIAQAIAAT	540
Db	468	LNVGSKKDNKPVRLITVAVPQVEGDTVYVAQLKGYAQNINRNDVNDGARAGIAQAIAAT	527
QY	541	AGLXQATLPKSMMAATIGGXTYXGEAGATAGYSSISXGXGWAATKGTASGNSRHFEXKASV	600
Db	528	AGLVAQALPPEKSMMAATIGGXTYXGEAGATAGYSSISDGGWIIKGTASGNSRHFEXASV	587
QY	601	GYOW	604
Db	588	GYOW	591
RESULT	13		
Q9JRI8			
IC	09JRI8	PRELIMINARY;	PRT: 591 AA.
ID	09JRI8		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).		
GN	GNA992 OR NMB0992 OR NHHA.		
OS	Neisseria meningitidis (serogroup B).		
OC	Neisseria meningitidis (serogroup B).		
OX	Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxId=487, 491;		
NP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRATIN-MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;		
RX	MDLINE=20175756; PubMed=10710308.		
RA	Pizza M., Scariato V., Mesigiani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolotti E., Capecci B.,		
RA	Galeotti C.L., Iazzi E., Maretti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.";		
RL	Science 287:1816-1820(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRATIN-MC58 / SEROGROUP B;		
RX	MDLINE=20175755; PubMed=10710307;		
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,		
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,		
RA	Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,		
RA	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T., Clecko A., Parksey D.S., Blair E., Cillone H., Clark E.B.,		
RA	Cotton M.D., Uetebach T.R., Khouri H., Qin H., Yamatchevan J.,		
RA	Smith J., Scarlato V., Mesigiani V., Pizza M., Grandi G., Sun L.,		
RA	Galli H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;		
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain		
RT	MC58.";		
RL	Science 287:1809-1815(2000).		

RN	[3]
RP	SEQUENCE FROM N.A.
RC	SPECIES=N.meningitidis; STRAIN=EMC21;
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT	"Identification and characterization of a gene encoding a novel outer
RT	membrane protein of Neisseria meningitidis.";
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF226375; AAF42524.1; -;
DR	EMBL; AE002450; AAF41395.1; -;
DR	EMBL; AF226367; AAF42516.1; -;
DR	EMBL; AF226370; AAF42519.1; -;
DR	EMBL; AF226374; AAF42523.1; -;
DR	EMBL; AF157611; AAK68872.1; -;
DR	TIGR; NMB0992; -;
KM	Complete proteome.
SO	SEQUENCE 591 AA; 62112 MW; 7C22P3CAE7F73EC6 CRC64;

Query Match	89.38;	Score 2230.5;	DB 16;	Length 591;
Best Local Similarity	77.68;	Pred. No. 3.1e-123;		
Matches 469; Conservative	0;	Mismatches 122;	Indels 13;	Gaps 3;

QY	1	MNXXIRITMNSALNAAWXYVSLTFNTHNRKRSATVXTVLATFLTXATFQAQXXXXXXXXXXXX	60
Db	1	MNKYIRITMNSALNAAWVSELTFRNTHRRASATVKTAVLTFLTFATFQAQSANNEDEEDL	60
QY	61	XLXXVXXRXXVXXXXXXXXXXEGXXEXXXXXXXXXXXXXXXXXXXXXXXXTLAKGDNLIKQ	120
Db	61	YLDPVQRTVAVLIYNSDKEGTEGEKEKVEENSDMAVYFNEKGVLTJAREITLTKAGDNLIKQ	120
QY	121	XXXXXXXXXXXXXXXXFYVSLKKKLLXXVXTEKLSFPAKXKXVNIASDITGLNFAKXTAX	180
Db	121	-----NGTFRTYSLKKDLTDLTSVGETEKLSFSAKXKXVNIITSDITGLNFAKXTAG	170
QY	181	TNGDXTHVHLNGISGTLTUDLXXXXXXXXXXXXXXXXXXXXXKXVLAAGNMIKGVXX	240
Db	171	TNGDTFVHLNGISGTLTDLTLNGATTTNVTNDNVTDDEKRRASVXKVLNAGNMIKGVK	230
QY	241	GXTXXXXXXXXNVDFVXTYDTVEFLSADTKTTTVNVESSKDNKXTEVKGAKTSVIREKDGKL	300
Db	231	GTT--ASDNVDFVARTYDTVEFLSADTKTTTVNVESSKDNKXTEVKGAKTSVIREKDGKL	288
QY	301	VTGKXXXXENASSTDXXGEGVLTAKEVIDAVNKKAGRRMKTTTTANGOTGQADKFEYVTSSTXV	360
Db	289	VTGKDXKDENGSSTDEGEGVLTAKEVIDAVNKKAGRRMKTTTTANGOTGQADKFEYVTSSTNV	348
QY	361	TFASGXGTTTAVVSKDDOGNTIVXYDVAVNGDALVANOJONGSMNIDSKAVAGSSGKTVSGN	420
Db	349	TFASGKGTGTTAVVSKDDOGNTIVMYDVAVNGDALVANOJONGSMNIDSKAVAGSSGKTVSGN	408
QY	421	VSPSKGKMDETVINAGNNIEIXHNGKNIDIAVSMXPQFSSVSLGAGADAPTLSDVXXXXA	480
Db	409	VSPSKGKMDETVINAGNNIEITRNGKNIDIAVSMTPQFSSVSLGAGADAPTLSDV--GDA	467
QY	481	LNVSSKXXXNKVVRTTNAVAPGYKBEEDVTNVQOLKVAQNLNXXIDNVYGNARRAGIAQAIAT	540
Db	468	LNVSSKXDNKRVRTTNAVAPGYKBEEDVTNVQOLKVAQNLNRRIDNVYGNARRAGIAQAIAT	527
QY	541	AGLQOAVTLPGKSMMAIGGXTYXGAGTAIGSSISXXGNXXIKGTASGNSRGHFGXSASV	600
Db	528	AGLQOAVTLPGKSMMAIGGCTTRGEGTAIGTSSISDGGNMIKGTASGNSRGHFGXSASV	587
QY	601	GYQW 604	
Db	588	GYQW 591	
RESULT	14		
ID	Q93QY4		
AC	Q93QY4	PRELIMINARY;	PRT; 594 AA.
DT	01-DEC-2001 (TremBurel. 19, Last sequence update)		

01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EG327;  
 RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157605; AAK68866.1; -  
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 89.2%; Score 2230; DB 2; Length 594;  
 Best Local Similarity 77.6%; Pred. No. 3.4e-123;  
 Matches 469; Conservative 0; Mismatches 125; Indels 10; Gaps 4;

0Y 1 MNXIRIINWNSALNMAWVAVSELTRNHTKRASATVATATLTLKATVQAXXXXXXXXXXXXXX  
 1 MKKIRIINWNSALNMAWVAVSELTRNHTKRASATVATATLTLKATVQAXXXXXXXXXXXXXX  
 61 XLXVYRXXVXXXXXXXXXXGEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
 58 YLEPQRTAPVLSFNSDKEGTGEKE-VTEDSMNGVYFDKKGVLTAAGTITLTKADNLIKIKO 116  
 121 XXXXXXXXXXXXXXXXEFYSEKXKXLLXVYXTEKLSFXANXXKXNIXSDPTKGLFAKXTAX 180  
 117 ----NTNEMTANSSFTYSLAKDLTDLTSGTEKLSFANSKNVITSDTKGLNFAKKTAE 172  
 0Y 181 TNGDXTVHLNGIGSTLTDLXKXXXXXXXXXXXXXRAASXKDVLAAGNINIKVXX 240  
 173 TNGDXTVHLNGIGSTLTDLTNTGATTVNTNDVTDEKKRAASVADVLNAGNINIKVXX 232  
 0Y 241 GXTXXXXXVNDVFXVYDYEFELSAADTKTTTVNVEESKDNKKTVEKIGAKTSVAKEDGKL 300  
 233 GTT--ASDNDVFRYDYEFELSAADTKTTTVNVEESKDNKKTVEKIGAKTSVAKEDGKL 290  
 0Y 301 VTGKXKXENXSSTDXGEGVLTAKEDVDAVNAKGMRAKTTTANGOTGADKFEVTSCTYX 360  
 291 VTGKXGEMDSSTDXGEGVLTAKEDVDAVNAKGMRAKTTTANGOTGADKFEVTSCTYX 350  
 0Y 361 TFAAGXGTTATVSKDQGNITVYXVNDVGDALVNLQNSGMNLSKAVAGSSGKVISGN 420  
 351 TFAAGXGTTATVSKDQGNITVYXVNDVGDALVNLQNSGMNLSKAVAGSSGKVISGN 410  
 0Y 421 VPSKGMDETVINAGNNEIETRNKNIDTATSMKPOSSVSLGAGADPTLSVDEGXA 480  
 411 VPSKGMDETVINAGNNEIETRNKNIDTATSMKPOSSVSLGAGADPTLSVDEGXA 470  
 0Y 481 LVNGSKXXKPRITVAVPVEKEDVTNVAOLKGVANLNKXIDNXXGNARAGIAOAIAT 540  
 471 LVNGSKDANKPRITVAVPVEKEDVTNVAOLKGVANLNKXIDNXXGNARAGIAOAIAT 530  
 0Y 541 AGLXQAVLPKGSMAIGXATYXGEGAGTAIGSSISXGXNMXIKGTASGNSRGHFGASASV 600  
 531 AGLVQAVLPKGSMAIGXATYXGEGAGTAIGSSISXGXNMXIKGTASGNSRGHFGASASV 590  
 0Y 601 GYQW 604  
 591 GYQW 594

RESULT 15  
 ID 09DPI3 PRELIMINARY; PRT; 594 AA.  
 AC 09DPI3;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)

OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NG3/88, AND B232;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.M., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226376; AAF42525.1; -  
 EMBL: AF226369; AAF42518.1; -  
 SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 89.2%; Score 2228; DB 2; Length 594;  
 Best Local Similarity 77.6%; Pred. No. 4.4e-123;  
 Matches 469; Conservative 0; Mismatches 125; Indels 10; Gaps 4;

0Y 1 MNXIRIINWNSALNMAWVAVSELTRNHTKRASATVATATLTLKATVQAXXXXXXXXXXXXXX  
 1 MKKIRIINWNSALNMAWVAVSELTRNHTKRASATVATATLTLKATVQAXXXXXXXXXXXXXX  
 61 XLXVYRXXVXXXXXXXXXXGEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
 58 YLEPQRTAPVLSFNSDKEGTGEKE-VTEDSMNGVYFDKKGVLTAAGTITLTKADNLIKIKO 116  
 121 XXXXXXXXXXXXXXXXEFYSEKXKXLLXVYXTEKLSFXANXXKXNIXSDPTKGLFAKXTAX 180  
 117 ----NTNEMTANSSFTYSLAKDLTDLTSGTEKLSGANKKNVITSDTKGLNFAKKTAE 172  
 0Y 181 TNGDXTVHLNGIGSTLTDLXKXXXXXXXXXXXXXRAASXKDVLAAGNINIKVXX 240  
 173 TNGDXTVHLNGIGSTLTDLTNTGATTVNTNDVTDEKKRAASVADVLNAGNINIKVXX 232  
 0Y 241 GXTXXXXXVNDVFXVYDYEFELSAADTKTTTVNVEESKDNKKTVEKIGAKTSVAKEDGKL 300  
 233 GTT--ASDNDVFRYDYEFELSAADTKTTTVNVEESKDNKKTVEKIGAKTSVAKEDGKL 290  
 0Y 301 VTGKXKXENXSSTDXGEGVLTAKEDVDAVNAKGMRAKTTTANGOTGADKFEVTSCTYX 360  
 291 VTGKXGEMDSSTDXGEGVLTAKEDVDAVNAKGMRAKTTTANGOTGADKFEVTSCTYX 350  
 0Y 361 TFAAGXGTTATVSKDQGNITVYXVNDVGDALVNLQNSGMNLSKAVAGSSGKVISGN 420  
 351 TFAAGXGTTATVSKDQGNITVYXVNDVGDALVNLQNSGMNLSKAVAGSSGKVISGN 410  
 0Y 421 VPSKGMDETVINAGNNEIETRNKNIDTATSMKPOSSVSLGAGADPTLSVDEGXA 480  
 411 VPSKGMDETVINAGNNEIETRNKNIDTATSMKPOSSVSLGAGADPTLSVDEGXA 470  
 0Y 481 LVNGSKXXKPRITVAVPVEKEDVTNVAOLKGVANLNKXIDNXXGNARAGIAOAIAT 540  
 471 LVNGSKDANKPRITVAVPVEKEDVTNVAOLKGVANLNKXIDNXXGNARAGIAOAIAT 530  
 0Y 541 AGLXQAVLPKGSMAIGXATYXGEGAGTAIGSSISXGXNMXIKGTASGNSRGHFGASASV 600  
 531 AGLVQAVLPKGSMAIGXATYXGEGAGTAIGSSISXGXNMXIKGTASGNSRGHFGASASV 590  
 0Y 601 GYQW 604  
 591 GYQW 594

Mon Jul 8 07:47:27 2002

us-09-771-382-11.std.rspt

Page 10

Search completed: July 3, 2002, 08:28:49  
Job time: 1170 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:30:20 ; Search time 48.34 Seconds  
(Without alignments)  
483.794 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 2499  
Sequence: 1 MNXIRIIMNSALNMYXVS.....TASGNSRGHFGXSASVGYOW 604

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	142.5	5.7	1567	1	P18127 xanthomonas
2	142.5	5.7	1655	1	09K833 r outer mem
3	140	5.6	1300	1	P14914 rickettsia
4	140	5.6	1654	1	Q53047 r outer mem
5	129	5.2	1148	1	Q30611 pseudomonas
6	128	5.1	1196	1	Q33479 pseudomonas
7	127.5	5.1	2249	1	P15921 rickettsia
8	126.5	5.1	1608	1	P15320 serralia ma
9	124	5.0	1322	1	P20469 pantoea ana
10	123.5	4.9	933	1	P35827 campylobact
11	122.5	4.9	581	1	P11818 human adeno
12	122.5	4.9	1656	1	Q06653 r outer mem
13	122.5	4.9	2021	1	Q52657 rickettsia
14	122	4.9	575	1	P22252 campylobact
15	121.5	4.9	1953	1	P25927 salmonella
16	121	4.8	1200	1	P06620 pseudomonas
17	119.5	4.8	1025	1	P35828 caulobacter
18	119	4.8	1034	1	Q47879 pantoea ana
19	119	4.8	1210	1	P09815 pseudomonas
20	119	4.8	1258	1	P16239 erwinia her
21	118.5	4.7	930	1	Q92393 chlamydia p
22	118.5	4.7	1645	1	P36989 r outer mem
23	118	4.7	444	1	P35829 lactobacilli
24	114	4.6	1861	1	P38536 t amylolipuli
25	113.5	4.5	575	1	P22252 campylobact
26	113	4.5	1577	1	P16466 proteus mir
27	112	4.5	948	1	P36867 deinoxococcus
28	112	4.5	2003	1	P33666 escherichia
29	111.5	4.5	2329	1	Q09624 caenorhabdit
30	111.5	4.5	2334	1	Q07833 bacillus su
31	111	4.4	484	1	P21171 listeria mo
32	111	4.4	1286	1	Q03155 escherichia
33	110.5	4.4	455	1	P31489 yersinia en

34	110	4.4	1039	1	AG43_ECOLI	P39180 escherichia
35	109.5	4.4	762	1	SLAP_ACEKI	P22258 acetogenium
36	109.5	4.4	1325	1	YDEK_ECOLI	P32051 escherichia
37	109	4.4	512	1	FLAA_HELPF	Q9358 helicobacte
38	109	4.4	1153	1	PVDB_PLAKN	P50493 plasmodium
39	109	4.4	1398	1	TOP2_PLAFK	P41001 plasmodium
40	108.5	4.3	550	1	FLIC_SHIFL	Q08860 shigella fl
41	108	4.3	666	1	MUR2_ENTHR	P39046 enterococu
42	108	4.3	1036	1	HP12_DEIRA	P13126 deinoxococcus
43	108	4.3	1848	1	CBPA_CLOCL	P38058 clostridium
44	107.5	4.3	389	1	SERI_BOMMO	P07856 bombyx mori
45	107.5	4.3	1643	1	OMP_RICPR	Q53020 r outer mem

## ALIGNMENTS

```

RESULT 1
ICEN_XANCT STANDARD: PRT: 1567 AA.
AC P18127 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X565;
RX MEDLINE=9108059; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT *Conserved repetition in the ice nucleation gene inax from
RT Xanthomonas campestris pv. translucens.
RL Mol. Gen. Genet. 223:163-166(1990).
CC -!- FUNCTION: ICE NUCLEATION PROTEIN ENABLE BACTERIA TO NUCLEATE
CC -!- CRYSTALLIZATION IN SUPERCOOLED WATER. (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC -!- NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
CC
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CC
CC EMBL: X52970; CAA37140.1; -
CC PIR: S11672; S11672.
CC HSSP: P06620; 11NA.
CC InterPro: IPR000258; Ice_nucleatn.
CC Pfam: PF00818; Ice_nucleatn; 81.
CC PRINTS: PR00327; ICENUCLEATN.
CC PROSITE: PS00314; ICE_NUCLEATION; 57.
CC Ice nucleation. Repeat: Outer membrane.
CC
CC SEQUENCE 1567 AA; 152548 MW; CGB451D959ECAD63 CRC64;

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Query Match 5.7%; Score 142.5; DB 1; Length 1567;  
Best Local Similarity 19.2%; Pred. No. 0.017;  
Matches 85; Conservative 55; Mismatches 235; Indels 67; Gaps 14;  
Qy 178 TAXTNGDVTYHLNGISGTLTDLXXXXXXAXXXXXXXRAASKYDVLNAGNINIK 237

```

Db 865 TGTAGADSTL-1SGYGTGT-----AGSDSLTAGYGTGTARKGSDVTAAGY---- 910
OY 238 VKXGTXXXXXXXNDFEYDVEFLSADTKTTTNNVESKDNCKXTEPVKCAKTSVKEKD 297
Db 911 ---GSGTGAAGSTLTAGYGTGTSDSLTAGYGTGTARKGSDMTAGYGTGTAGAD 967
OY 298 GKLVTKKXKXKXKXSTDXEGELVTAKEVIDAVNKKAGMRKTTTANGOGQADKFTVTS 357
Db 968 STLIAGYGTGTSGS-----DSSLTAGYGTGTARKGSDVTAAGYGTGTAG 1013
OY 358 TXYTFASGXTATATVSKDDQGNITVYDVNVDALNVQLNSGMNLDSKAVAGSSGKYI 417
Db 1014 ASSTLIAGYGTGTAGSD--SSLTAGY---GSTGTARQSGDVTAGYGTGTAGADSTLI 1067
OY 418 SGNVSPSKKMDKDEYVNNANNEIIXRNKNIDI--ATSKMPPSSVSLAGACAPTL 474
Db 1068 AGYGTGTAGSDSLTAGYGTGT--GTARQSGDVTAGYGTGTAGSDSLTAGYGTGTAG 1125
OY 475 VDXXXALANGSKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 534
Db 1126 YDSNLTAGYGTGTGTAR-----EDSSLTAGYGTGTSTAGHSDSLTAGYGTGTAGY 1174
OY 535 AQAATAGLXQAVLPKSKMMALIGKXTYXGEAGY---AIGYSISXG--MKXIGTASG 588
Db 1175 -NSILTTGSGTGTAESSSLTAGYGTGTSTAGYGTGTAGYGTGTAGYKSTLTAGYGSN 1233
OY 589 NSRGH-----FGXSAVYQ 603
Db 1234 SPAGHSSLTAGYGTGTAGYE 1255

RESULT 2
OMP_RICCN STANDARD; PRT; 1655 AA.
ID OMP_RICCN
AC 09KKA3; 09KKA3; 09KKA3;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scat) (OMP B)
DE (omp B) (Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).
GN OMPB OR RCL085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barde V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RT Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=2033643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein ompb (ompb)";
RT Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR

```

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CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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CC -----
DR EMBL; AE008659; AAL03623.1; -
DR EMBL; AF123721; AAF34124.1; -
DR EMBL; AF123726; AAF34129.1; -
DR EMBL; AF149110; AAD39533.1; -
DR InterPro: IPR003858; OMPA_ompb.
DR Pfam: PF02708; ompb_ompb; 1.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334
FT CHAIN 1335 1655
FT VARIANTE 61 61
FT VARIANTE 75 75
FT VARIANTE 78 78
FT VARIANTE 251 251
FT VARIANTE 413 413
FT VARIANTE 959 959
FT VARIANTE 988 988
FT VARIANTE 1139 1139
FT CONFLICT 353 354
FT CONFLICT 776 776
FT CONFLICT 1159 1159
FT CONFLICT 1177 1177
FT CONFLICT 1492 1492
FT CONFLICT 1655 AA; 168342 MW; E49E19377D5FCB37 CRC64;
SQ SEQUENCE

Query Match 5.7%; Score 142.5; DB 1; Length 1655;
Best Local Similarity 23.5%; Pred. No. 0.018;
Matches 94; Conservative 50; Mismatches 183; Indels 73; Gaps 20;

OY 249 NDFEYDVEFLSADTKTTTNNVESKDNCKXTEPVKCAKTSVKEKD 294
Db 430 NTAGVITFDANGTLASASADAVNVTNNITALEASGAVVQLSGTHAELRLGNAGSVK 489
OY 295 EKDKLVTKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 351
Db 490 LADGYIANGVNTALVAGLAAAGTTTLDGSKATITTDIGNAG--GAALOGTTLANDYT 546
OY 352 ETVT-----SGTXVTFASGXTATVSKDDQGNITVYDVNVDALNVQLNSGMNLDSK 395
Db 547 KTLTLGANGITANGGTINFGANGTIFIKLTS--TQNNIVDDDLAATFGQGVVASSLT 604
OY 396 QLQNSGMNLDSKAVAGSSGKYISGNVSPSKGM-DETVAIN--AGNN--IIXRNKNI 449
Db 605 NAOFTLTINKIGTGVANNKTLGOFNIGSSKTVLSDVDVAINELVYNGGAQVFAHNTYLI 664
OY 450 DIATSKPKP-----FSSV-----SLGAGADAPTLSDVXXALNVGSKXKXKXKXKXKX 500
Db 665 TPTTNAAGGKLIIFNVVANNNTLTATGTNLGS-ATNPPLAINEFGSKGAANDVTYLVNGKG 723
OY 501 VKEGDTNVAQLKGVAAQNNXIDNVXG-NARAGTAQALATAGLXQ-----ATLPKGS 552
Db 724 VNL-VATNITTTDA---NVGSFIFNAGGTINIVSG-----TVGGGQGGKKNFTVALDNGTT 773
OY 553 MMAIGKXTYXGEAGYAGYSSISXGKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 592
Db 774 VKFLGNATPNTTNTTAAAN-STLQIGCNTATDFVVASADGTG 812

```



RESULT 3  
ID 120K\_RICRI STANDARD: PRT: 1300 AA.  
AC P14914;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE 120 kDa surface-exposed protein.  
GN P120.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiellae; Rickettsia.  
OX NCBI\_Taxid=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";  
RT Mol. Microbiol. 3:1579-1586(1989).  
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES  
CC CONFERRING ANTIGENICITY TO THE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIA OMPA/OMPB FAMILY.  
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CC -----  
DR EMBL: X16353; CAA34402.1; -;  
DR PIR: S07575; S07575.  
DR InterPro: IPR003858; romPA\_OMPb.  
KW Antigen; Glycoprotein; Cell wall; S-layer.  
FT CARBOHYD 7 N-LINKED (POTENTIAL).  
FT CARBOHYD 66 66 N-LINKED (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (POTENTIAL).  
FT CARBOHYD 268 268 N-LINKED (POTENTIAL).  
FT CARBOHYD 330 330 N-LINKED (POTENTIAL).  
FT CARBOHYD 375 375 N-LINKED (POTENTIAL).  
FT CARBOHYD 415 415 N-LINKED (POTENTIAL).  
FT CARBOHYD 424 424 N-LINKED (POTENTIAL).  
FT CARBOHYD 430 430 N-LINKED (POTENTIAL).  
FT CARBOHYD 436 436 N-LINKED (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (POTENTIAL).  
FT CARBOHYD 515 515 N-LINKED (POTENTIAL).  
FT CARBOHYD 547 547 N-LINKED (POTENTIAL).  
FT CARBOHYD 593 593 N-LINKED (POTENTIAL).  
FT CARBOHYD 655 655 N-LINKED (POTENTIAL).  
FT CARBOHYD 698 698 N-LINKED (POTENTIAL).  
FT CARBOHYD 710 710 N-LINKED (POTENTIAL).  
FT CARBOHYD 799 799 N-LINKED (POTENTIAL).  
FT CARBOHYD 800 800 N-LINKED (POTENTIAL).  
FT CARBOHYD 826 826 N-LINKED (POTENTIAL).  
FT CARBOHYD 844 844 N-LINKED (POTENTIAL).  
FT CARBOHYD 861 861 N-LINKED (POTENTIAL).  
FT CARBOHYD 879 879 N-LINKED (POTENTIAL).  
FT CARBOHYD 920 920 N-LINKED (POTENTIAL).  
FT CARBOHYD 926 926 N-LINKED (POTENTIAL).  
FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).  
FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).

FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).  
FT CARBOHYD 1146 1146 N-LINKED (POTENTIAL).  
FT CARBOHYD 1211 1211 N-LINKED (POTENTIAL).  
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;  
Query Match 5.6%; Score 140; DB 1; Length 1300;  
Best Local Similarity 21.44; Pred. No. 0.021;  
Matches 89; Conservative 58; Mismatches 163; Indels 106; Gaps 22;  
OY 249 NVDFVXTVD---TVEFLSADRTKTTVN---VESKDC-----KTEVKIGAKTSYIK 294  
DB 76 NTAGYITFDANGTLESASADANVAVTNNITAIASGAGVVLGTHAEIRLGNAGSIFK 135  
OY 295 EKDGLVYTGKKKXEXXSTDXGEGLYT---AKEVIDAVNKGWR---MKTTANGQTGQA 348  
DB 136 LADGTVINGKVQNALVGCALAAAGTITLDGSAVTITGDIIGNAGAAALORTILAN----- 189  
OY 349 DKFEVTSGTXYTFASGXT-----TATSKDQGNITVXYDVNVG-DALNVN 395  
DB 190 DAKKTLITLGGANITIGAGGTTDLQANGTITKLTST-----QNNIVDFDLAIATDQGV- 243  
OY 396 OLQNSGMNLSKAVAGSSGKVISGNVSPSKGMDTV-NINAGNIEIXRNG-----KIID 450  
DB 244 -----VDASLTNNAGTLITNGKIG-TIGANNKTLGQFNIGSSKTVLSGNVAINELY 294  
OY 451 IATSKXPPF-----SSVIGAGADAPTLSDVXXALNVG 484  
DB 295 IONDGAVQFAHDYTLITRTNNAAGGKLIENPVANNGTLLAGTNGS-ATNPPLAENFG 353  
OY 485 SKXXNKPVRITVAPGKREGDVTNVAQLKGVANLNINIDNYXG-NARAGIAQAIAATAGL 543  
DB 354 SGGVNVDY-VLVNGEYVNL-YATNITTTDA---NVGSFVFNAGNINYSG-----TVGG 402  
OY 544 XO-----AYLPKSMMAIGXYXGEGVYAIIGYSSISXGNMXIKIGTASNSNG 592  
DB 403 QQGNKFNVALENGTIVKFLGNATFNGNTTIAN-STLDIGNNTADCVASADGTG 457  
RESULT 4  
ID OMPB\_RICRI STANDARD: PRT: 1654 AA.  
AC 053047;  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rompB)  
DE (romp B) [contains: 120 kDa surface-exposed protein (surface protein  
DE antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].  
GN OMPB.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiellae; Rickettsia.  
OX NCBI\_Taxid=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;  
RT "The 120 kilodalton outer membrane protein (romp B) of Rickettsia  
RT rickettsii is encoded by an unusually long open reading frame:  
RT evidence for protein processing from a large precursor.";  
RT Mol. Microbiol. 5:2361-2370(1991).  
RN [2]  
RP SEQUENCE OF 279-1654 FROM N.A.  
RC STRAIN=R;  
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";  
RT Mol. Microbiol. 3:1579-1586(1989).  
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR

Query Match	5.6%	Score 140	DB 1	Length 1654
Best Local Similarity	21.4%	Pred. No. 0.027		
Matches 89	Conservative 58	Mismatches 163	Indels 106	Gaps 22

RESULT	5	
ICCK_PSEX		
ID	ICCK_PSEX	STANDARD;
00001		PRT; 1148 AA

	RA	Jung H.C., Pan J.-G.,
	RL	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
	CC	- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
	CC	CRYSTALLIZATION IN SUPERCOOLED WATER.
	CC	- SUBCELLULAR LOCATION: Outer membrane (By similarity).
	CC	- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
	CC	OCAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
	CC	REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
	CC	- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
	CC	FAMILY.
	CC	-----
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	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
	CC	or send an email to license@isb-sib.ch).
	CC	-----
	DR	EMBL; AF013159; AAB66891.1; .
	DR	HSSP; P06620; IINA.
	DR	InterPro; IPRO00258; Ice_nucleatn.
	DR	Pfam; PF00818; Ice_nucleation; 57.
	DR	PRINTS; PR00327; ICENUCLEATN.
	DR	PROSITE; PS00314; ICE_NUCLEATION; 38.
	KW	Ice nucleation; Repeat; Outer membrane.
	FT	DOMAIN 161 POLY-ALA.
	FT	DOMAIN 180 1099 OCTAPEPTIDE PERIODICITY.
	SQ	SEQUENCE 1148 AA; 113811 MW; BA0109CF02FAE224 CRC64;
		-----
		Query Match 5.2%; Score 129; DB 1; Length 1148;
		Best Local Similarity 19.0%; Pred. No. 0.11;
		Matches 87; Conservative 50; Mismatches 248; Indels 74; Gaps 14;
		-----
QY	152	EKLSEKXAXXXVNIIXSDRKLNFAXXTXNTGDHXVHLNGTGSTLTLDLXXXXXXX 211
DB	230	EDSSLTAIYGSTQTQAQEGSNLTAGYGSTGTAGSDSLIAGIGSTQT-----SGDS 280
QY	212	XXXXXXXXXXRAASKDVLTNAGMNIRGVKKGXTXXXXXNVDPVTVDVEFLSADTKTTTV 271
DB	281	SLTFAGYGSTQTQAQEGSNLTAGY-----GSNGTAGVDSLIAGYGSQTSGSDSALTAG 333
QY	272	NVESKDNGKATREVIKGAITSYIKEDGKLVYGGKXXEXXSSTDKEGLVTAKEVIDAVNK 331
DB	334	YGSTQTQAQEGSNLTAGYGSTGTAGSDSSLIAGYGSTQTS-----DSSLT 379
QY	332	AGMFMKTTTANQGOTGOADKFETVTSGRVTVPASGCTPAFVSKDQGNITVYDVNWDA 391
DB	380	AGYSTQTQAQEGSNLTAGYGSTGTAGVDSLIAGYGSTQTSGBDA--LTAGY---GST 433
QY	392	LNVQOLGSGNNLDSKAVAGSSGYISGNVSPSKGMDETVNINAGNIEIXRNKNIDI 451
DB	434	QTAQEGSNLTAGYGSTGTAGADSSLIAGYGSTQTSGBSSSLTAGYGSF-QTAREG---- 487
QY	452	ATSMXPQESSVLACGADAPTLSDVDDXXAALWVGSKXXMKPRITNVAVG----VKESDVT 507
DB	539	TSGYGSTQTAGAANL-----TTGYGSGT-----TAGHSSFIIAGYGSTQTAGHKSL 586
QY	508	---NVAQLKGVAQNLLNNXIDNVYGNARAGIAOAIATGLAQVALPGKSMAIGGXTYXG 563
DB	564	EAGYAIGYSSLSXXGNMXIKGTASGNSRGHGXSASVY 602
QY	587	TAGY--GSTQTARDGSYLIAGYGSGTAGS--GSSLIAGY 622
RESULT	6	
ID	ICEV_PSESX	STANDARD:
AC	033479;	PRT; 1196 AA.
DT	15-DEC-1998 (Rel. 37, Created)	

DR 15-DEC-1998 (Rel. 37, Last sequence update)  
 DR 16-OCR-2001 (Rel. 40, Last annotation update)  
 DE Ice nucleation protein.  
 GN INAV.  
 OS Pseudomonas syringae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=317;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=INAV.  
 RX MEDLINE=97462815; PubMed=9323042;  
 RA Schmid D., Pridmore D., Capitani G., Battistutta R., Neeser J.-R.,  
 Jan A.;  
 RT "Molecular organization of the ice nucleation protein Inav from  
 Pseudomonas syringae."  
 RT FEBS Lett. 414:590-594(1997).  
 CC -1- FUNCTION: ICE NUCLEATION PROTEIN ENABLE BACTERIA TO NUCLEATE  
 CC -1- CRYSTALLIZATION IN SUPERCOOLED WATER.  
 CC -1- SUBUNIT: MEMBRANE ENVIRONMENT OR AGGREGATION SEEMS TO BE REQUIRED  
 CC -1- FOR ICE NUCLEATION ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).  
 CC -1- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS  
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A  
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AJ001086; CA04521.1; -  
 DR HSSP: P06620; 11NA.  
 DR InterPro: IPR000258; Ice\_nucleatn.  
 DR Pfam: PF00818; Ice\_nucleation; 61.  
 DR PRINTS: PR00327; ICNDCLEATN.  
 DR PROSITE: PS00314; ICE\_NUCLEATION; 42.  
 KW Ice nucleation; Repeat; Outer membrane.  
 FT DOMAIN 172 1147 OCTAPEPTIDE PERIODICITY.  
 FT SEQUENCE 1196 AA; 117991 MW; C9E9974CB1/31E68 CRC64;

Query Match 5.1%; Score 128; DB 1; Length 1196;  
 Best Local Similarity 18.4%; Pred. No. 0.13; 222; Indels 78; Gaps 11;  
 Matches 79; Conservative 50; Mismatches 222; Indels 78; Gaps 11;

OY 181 TNGDXYVHLNGISLTLDLXXXXXXXRAASXKDVLAGNINIKVKKX 240  
 DB 259 TACSDSLIAGYGTQ-----SGEDSLIAGYGTQAOEGSNLAGY----- 302  
 OY 241 GXTYXXXXXNDPXYTVEFLSADTKTTVNVESKDNKXTEVKGAKTSVKENDGKL 300  
 DB 303 GSTGTAGSDSLIAGYGTQSGDSSLTGTAGYGTQAOEGSNLTSGYGTGTAGAGASSL 362  
 OY 301 VTGXXXXXKNSSTDXGGLVTAKEVIDAVNKGWRMKTMTANSGTQADGFETVSTGYX 360  
 DB 363 IAGGSGTQSGS-----DSALTAGYGTQAOEGSNLTAGGSGTGTAGSDS 408  
 OY 361 TFASGXTATVSKDQGNITVYXVNVGDALNVNOLNSGWNLSKAVAGSSGKVIISGN 420  
 DB 409 SLIAGYGTQSGSD--SSLTGY-----GSTQAOEGSNLTAGYGTGTAGVDSLLIAGY 462  
 OY 421 VSPKGMDETVINAGNNIETXRNGKNIDTATSMAPQSSVSLGADADPTLSVDXXA 480  
 DB 463 GSTGTSGSDSLTGYG-----STQTAOEGSNLTAGYGTGTGTAGDSSLI 507  
 OY 481 LNVGSKXXNKRVTITNVAQVKGEDVTNVAOLKGVAAONLNNXIDNVAGNARAGTAAQ--- 537

DB 508 AGYGTQTS-----GSESSLFAGYGTQTAAREGSTLTAGYGTGTAGADSS 553  
 OY 538 -IATAGLXQAVLPCKSMATIGCTYXGAGTAV--GYSSISXKNWMIKGTASNGSHF 594  
 DB 554 LIAGYGTQTSQSDSLIAGYGTQTAQAGSVLNSGYSQTQAG-----AASNLITGY 606  
 OY 595 GXASAVGYO 603  
 DB 607 GSTGTAGHE 615

RESULT 7

OMPA\_RICRI STANDARD; PRT: 2249 AA.  
 AC P15921;  
 DR 01-APR-1990 (Rel. 14, Created)  
 DR 01-APR-1990 (Rel. 14, Last sequence update)  
 DR 16-OCR-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
 DE antigen) (rOmpA) (rOmp A).  
 GN OMPA.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=90354033; PubMed=2117568;  
 RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
 RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
 RT repeated, near-identical sequences."  
 RL Infect. Immun. 58:2760-2769(1990).  
 CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- PTM: GLYCOSYLATED (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: M31227; AAA26380.1; -  
 DR PIR: A41477; A41477.  
 DR InterPro: IPR003858; rOmpA\_rOmpB.  
 DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
 KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
 FT CHAIN 1 28  
 FT DOMAIN 212 1180  
 FT REPEAT 212 286  
 FT REPEAT 287 358  
 FT REPEAT 359 430  
 FT REPEAT 431 505  
 FT REPEAT 506 577  
 FT REPEAT 578 652  
 FT REPEAT 653 724  
 FT REPEAT 725 799  
 FT REPEAT 800 874  
 FT REPEAT 875 949  
 FT REPEAT 950 1021  
 FT REPEAT 1022 1093  
 FT REPEAT 1094 1165  
 FT REPEAT 1166 1180  
 FT SEQUENCE 2249 AA; 224333 MW; A9D646C089F087 CRC64;

Query Match 5.1%; Score 127.5; DB 1; Length 2249;



CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).  
CC -1- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS  
CC OCTAPEPTIDE A-G-Y-G-S-T-X-T. FURTHER ON A 16-RESIDUE AND A  
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
CC FAMILY.  
CC -----  
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CC -----  
DR EMBL: X17316; CA35194.1; -.  
DR PIR: S07053; S07053.  
DR HSRP: P06620; 11NA.  
DR InterPro: IPR000258; Ice\_nucleatn.  
DR Pfam: PF00818; Ice\_nucleation; 69.  
DR PRINTS: PR00327; ICENUCLEATN.  
DR PROSITE: PS00314; ICE\_NUCLEATION; 49.  
KW Ice nucleation; Repeat; Outer membrane.  
FT DOMAIN 162 1281 OCTAPEPTIDE PERIODICITY.  
SQ SEQUENCE 1322 AA; 131094 MW; 89B0EE24AA837039 CRC64;  
  
Query Match 5.0%; Score 124; DB 1; Length 1322;  
Best Local Similarity 20.5%; Pred. No. 0.28;  
Matches 88; Conservative 52; Mismatches 192; Indels 98; Gaps 17;  
  
OY 181 TNGDVTNHLNGISLTDLXXXXXXXKXXXXXXRAASKKDVLAAGNKGKX 240  
DB 339 TAGESTGTAGGSGTGT-----AOKGSDTLTAGY----- 356  
OY 241 GYXXXXXXNVDFYVEFLADPTKTTVNVESKDNKXTEVKIGAKTSYKEDGL 300  
DB 357 GSTGTAGDSSLIAGYGTGTAGEDSSLTAGYGTGTAKGSDLTAGYGTGTGADSSL 416  
OY 301 VTGKXKXENXSSTDXGEGLVTAKEVIDAVNKAQWKKTTTANGOTGQADKFTVTSY 360  
DB 417 IAGYGTGT-----TAG-----ESTGTAGYGTGTAKGSDLTAGYGTGTAGDSS 462  
OY 361 TTAGSGCTATATYKSDQCNITTYVYVNGDALNVNOLNKGMLDSKAVAGSGKATY 420  
DB 463 SLIAGYGTGTAKG--SPLTAGY-----GSTTAGYESSLIAGY 500  
OY 421 VPSKGGKMDETVINAGNNEIEXRNGKNIDI--ATSMXKPOFSSVSLGAGADAPTLSV 477  
DB 501 GSTGTAGYGTGTAGYGTGT--GTANBESDLITGYGTGTAGANSSLIAGYGT--TOTA 558  
OY 478 XXALNVGSKXXKPVRTNVAPVKEG--DVTNVAQLKGYAQNLMNXXIDNVXGNARAG 536  
DB 559 VLTAGYGT-----TQTA---REGSDLTAGYGTGTAGDSSLIAGYGTGTAG--AD 605  
OY 537 ALATAGLXALYLPG-KSMMAIG-GATYXGEAG--YATGSSISXXGNMXIKGTASGNS 592  
DB 606 SSLIAGYGTGTAGYGTGTAGYGTGTAEKSDLTAGYGTGTAG-----ADSSLIA 658  
OY 593 HFGXSASVGY 602  
DB 659 GYGSTGTAGY 668  
  
RESULT 10  
ID SLAP CAMFE STANDARD; PRT; 933 AA.  
AC P35827;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE S-layer protein (Surface array protein) (SAP).  
GN SAPA.

OS Campylobacter fetus.  
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_Taxid=196;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN-84-32 / 23D;  
RX MEDLINE-90354448; PubMed-2387868;  
RA Blaser M.J., Gotschlich E.C.;  
RT "Surface array protein of Campylobacter fetus. Cloning and gene  
RT structure.";  
RL J. Biol. Chem. 265:14529-14535(1990).  
RN [2]  
RP ERRATUM.  
RX MEDLINE-91035477; PubMed-2229082;  
RA Blaser M.J., Gotschlich E.C.;  
RL J. Biol. Chem. 265:19372-19372(1990).  
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
CC CRITICAL FOR VIRULENCE.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
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CC -----  
DR EMBL: J05577; AAA23032.1; -.  
KW Cell wall; S-layer.  
SQ SEQUENCE 933 AA; 96757 MW; F88C729BABA5B1E9 CRC64;  
  
Query Match 4.9%; Score 123.5; DB 1; Length 933;  
Best Local Similarity 21.6%; Pred. No. 0.2; Mismatches 179; Indels 99; Gaps 15;  
Matches 90; Conservative 49;  
  
OY 215 TYXXXXXRAASKKDVLAAGN-----IKGYKXGTXXXXXNVDFV--X 254  
DB 440 TAAIDKSASTLNLINSVNGPKHLYSSKRRYCKFKRAAKYKLTNTATDQVTLKANA 499  
OY 255 TYDVEFLADPTKTTVNESKDNKXTEVKIGAKTSYKEDGLVTKKXKXENXSSTD 314  
DB 500 TNSLEFDSATAKTSVT--ASGSGKTLVIK--GAEEVETLVNID----- 539  
OY 315 XDEGLVTAKEVIDAVNKAQWKKTTTANGOTGQADKFTVTSYVTFASGXTTATY 374  
DB 540 -----TTAFNALQSV-----SFGKGTGGKGF--SVKGTGTGDKLEFVGTTLTEGS 582  
OY 375 --DDGQNIIVXYDVNVDALNVNOLNKGMLDSKAVAG--SSGKVISGNVSPSKGMD 429  
DB 583 VIDAPENDTIAMKSAALTSANFTMIKNIENVAISDAVATADLSSAFKXSVIITTEAD 642  
OY 430 ETVNINAGNNEIEXRNGKNIDIATSMXKPOFSSVSLGAGADAPTLVSDXXALNVGSK 489  
DB 643 TLTITNKDQVI-----NFTAADAGSVKLTIVKLN---DVTALMTIVKIVILDAAKD-- 690  
OY 490 KPVRTNVAPVKEG-----VTNVAQL-----KGVANQNLNNXXIDNVXGNARAG 533  
DB 691 -----TNIALGTAAADKALVIDGTGIELTLNTSLVKATSPETTANTVNAKLTDTV 745  
OY 534 IAAQIATAGLXALYLPKSKMMAIGGATYXGEAGYATGYSISXXGNMXIKGTASGNS 590  
DB 746 MQITLGHAGTAGDYSKYSVMIDASAL-----KAGLTFDASALITLGNAMATIKGSGGANS 798  
  
RESULT 11  
ID FIBP\_ADE05 STANDARD; PRT; 581 AA.  
AC F1B18;  
DT FIBP\_ADE05  
GN F1B18;



```
Db      556 ---IISANGGINQANGGTTKLTLS--TÖNNIVYDCDLALATDGTGVVDASSL----- 604

Oy      402 WMLDSKAVAGSSGKVISGNVSPSK---GKMDETVN-----IN--ACNN--IEIXRGNK 448
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      605 -NAOTLITSGITIGILCANNTTLGOFNIGSSKTTLGCNGVAINELVIGNNSVOFAHNTYL 663
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      449 IDINTSMKPQ-----ESSV-----SLGADAPFLTSVDXXXALNVGSXKKPKRITVPAR 499
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      664 ITRPTNAAGOKIIIFNPVNNNTTLAAGTNGLS-AAAPLAEINGSGSGABARDT-VLNWGE 721
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      500 GVEEGEDVTYNVOLTKGVAQNLNKNXIDNYXG-NARAGIAQAIALTAGLXO-----AYLPKG 551
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      722 GVNL-YATNIITTDA---NWGSFVFENAGKNIVSG-----TYGGOGGKNKFNTVALDNGT 771
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy      552 SMAAIGCTTYXGEGCIVAICGISJSJXXGNMXIKRTAGSCNSRG 592
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      772 TVKELGNATFNNGNTTIAAN-STLODSGYNTADFIASDGTG 811
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

## RESULT 13

ID OMPA\_R1CNC STANDARD; PRT: 2021\_AA.  
AC 056567; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
AC Q52670; Q52674;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
antigen) (OMP<sub>A</sub>) (OMP A).  
GN OMPA OR R01273.  
OS Rickettsia conorii.  
OC Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.  
NCBI\_taxid=781;  
TX

RP SEQUENCE FROM N.A.  
RC STRAIN-Malish 7;  
RX MEDLINE=94171067; PubMed=0125327;  
RA Croquet-Valdes P.A., Weiss R., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia  
RL conorii (Malish 7 strain).";  
RN Gene 140:115-119(1994).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Malish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Rudifren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Rault D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
RL Science 293:2095-2098(2001).  
[3]  
RP SEQUENCE OF 8-204 FROM N.A.  
RC STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan;  
RX MEDLINE=97015921; PubMed=0862558;  
RA Roux V., Fournier P.E., Rault D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and  
RT analysis of restriction fragment length polymorphism of PCR-amplified  
RT DNA of the gene encoding the protein rompa.";  
RL J. Clin. Microbiol. 34:2058-2065(1996).  
[4]  
RP SEQUENCE OF 953-2012 FROM N.A.  
RC STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan;  
RA Rault D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study  
RT of the outer surface protein ompA.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PTM: GLYCOSYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

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```
DR EMBL: U01028; AAA17405.1; -.
DR EMBL: AE008674; AAI03811.1; -.
DR EMBL: U43794; AAB49549.1; -.
DR EMBL: U43798; AAB49550.1; -.
DR EMBL: U43806; AAB49551.1; -.
DR EMBL: U45244; AAB49566.1; -.
DR EMBL: U46918; AAB86663.1; -.
DR EMBL: U83440; AAC35176.1; -.
DR EMBL: U83443; AAC35179.1; -.
DR EMBL: U83448; AAC35184.1; -.
DR EMBL: U83453; AAC35189.1; -.
DR InterPro: IPR003858; COMPACTOMP.
```

KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;  
KW Complete proteome.

FT	SIGNAL	1	38	POTENTIAL.
FT	CHAIN	39	2021	OUTER MEMBRANE PROTEIN A.
FT	CHAIN	39	2021	OUTER MEMBRANE PROTEIN A.

FT	DOMAIN	238	946	THR-RICH.
FT	DOMAIN	1424	1528	THR-RICH.
FT	VARIANT	60	60	N -> NN (TN SMPRN INDIAN TTRC TYPHUS)

	R -> H (IN STRAIN INDIAN TICK TYPHUS).
VARIANT	86 MISSING (IN STRAIN M1).
VARIANT	76
FT	86
FT	137
VARIANT	86
VARIANT	86
VARIANT	86

FT	VARIANT	126	133	MISSING (IN STRAIN MOROCCAN).
FT <td>VARIANT <td>953 <td>954 <td>VT -&gt; II (IN STRAIN INDIAN TICK TYPHUS).</td> </td></td></td>	VARIANT <td>953 <td>954 <td>VT -&gt; II (IN STRAIN INDIAN TICK TYPHUS).</td> </td></td>	953 <td>954 <td>VT -&gt; II (IN STRAIN INDIAN TICK TYPHUS).</td> </td>	954 <td>VT -&gt; II (IN STRAIN INDIAN TICK TYPHUS).</td>	VT -> II (IN STRAIN INDIAN TICK TYPHUS).

FT	VARIANT	1245	1245	D -> A (IN STRAINS INDIAN TICK TYPHUS, M1 AND MOROCCAN).
FT				

FET	VARIANT	1308
N ->	H (IN STRAIN MOROCCAN).	
FET	VARIANT	1877
M ->	I (IN STRAIN INDIAN TICK TYPHUS).	
COUNTING		10
	(2ND SER.	1)

FT	CONFLICT	10	Q -> K (IN REF. 1).
FT <th>CONFLICT</th> <th>92</th> <th>I -&gt; V (IN REF. 1).</th>	CONFLICT	92	I -> V (IN REF. 1).
FT <th>CONFLICT</th> <th>126</th> <th>V -&gt; T (IN REF. 1).</th>	CONFLICT	126	V -> T (IN REF. 1).

FT	CONFLICT	126	V > I (IN REF. 1).
FT	CONFLICT	126	T -> N (IN REF. 1).
FT	CONFLICT	137	G -> D (IN REF. 1).
FT	CONFLICT	157	

FT	CONFLICT	368	369	IS -> VN (IN REF. 1).
FT	CONFLICT	374	388	KATLGAIKATTTK -> LLOVOGVVAKANTIN (IN

FT		REF. 1).
FT		N -> D (IN REF. 1).
CONFLICT	640	640

FT	CONFLICT	669	V -> I (IN REF. 1).
FT	CONFLICT	793	N -> D (IN REF. 1).

FT	CONFLICT	803	804	FN -> IS (IN REF. 1).
FT	CONFLICT	809	823	LLRVGGVVKSNITIN -> KATLGAIKATTTK (IN

FT	898	REF. 1).
FT	898	D -> Y (IN REF. 1).
FT	908	P -> N (IN REF. 1).
CONFLICT	908	
CONFLICT	908	

FT	CONFLICT	1009	L -> S (IN REF. 1).
FT	CONFLICT	985	N -> K (IN REF. 1).
FT	CONFLICT	986	F -> K (IN REF. 1).

FT	CONFLICT	1013	1013	Y -> S (IN REF. 1).
FT	CONFLICT	1182	1182	K -> Q (IN REF. 1).

FT	CONFLICT	1314	1314	N -> Y (IN REF. 4).
FT	CONFLICT	1451	1451	H -> N (IN REF. 1).

FT	CONFLICT	1624	G -> D (IN REF. 1).
FT <td>CONFLICT</td> <td>1628</td> <td>E -&gt; G (IN REF. 1).</td>	CONFLICT	1628	E -> G (IN REF. 1).
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	1872	1875	1879	MS - 210 (IN REF. 1)
FT	CONFLICT	18/2	18/2	A -> V (IN REF. 1)
FT	CONFLICT	1875	1875	T -> P (IN REF. 1)
FT	CONFLICT	1879	1879	
FT	CONFLICT	1879	1879	

E1	CONFLICT	1978	M3 > L6 (IN REF. 1).
FT	CONFLICT	1936	E -> A (IN REF. 1).
FT	CONFLICT	1965	MTALBP -> ITPPLS (IN REF. 1).

FT	CONFLICT	1997	1997	G -> R (IN REF. 1).
SQ	SEQUENCE	2021 AA;	203328 MM;	327FC42D7CB24668 CRC64;

Query Match	4.98;	Score 122.5;	DB 1;	Length 201;
Best Local Similarity	22.28;	Pred. No. 0.56;		

Matches	94;	Conservative	44;	Mismatches	152;	Indels	133;	Gaps	22;
---------	-----	--------------	-----	------------	------	--------	------	------	-----







RC STRAIN-LT2;  
 RX MEDLINE-91100301; PubMed-1987123;  
 RA Wu J.Y., Siegel L.M., Kredich N.M.;  
 RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
 requirement for a cloned cystG plasmid to overcome limiting streptococcal  
 cofactor";  
 RL J. Bacteriol. 173:325-333(1991).  
 CC -! CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
 in positions 414 and 732.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: AF133696; AAD39458.1; -  
 DR EMBL: AE008859; AAL22340.1; -  
 DR EMBL: M64606; AAA27042.1; ALT\_FRAME.  
 DR EMBL: M64606; AAA27043.1; ALT\_FRAME.  
 DR PIR: C39200; C39200.  
 DR PIR: D39200; D39200.  
 DR StyGene: SG10437; bigA.  
 DR Virulence: Repeat; Signal; Complete proteome.  
 KM SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 1953 PUTATIVE SURFACE-EXPOSED VIRULENCE  
 FT  
 FT DOMAIN 101 252 PROTEIN BIGA.  
 FT REPEAT 101 103 15 X 11 AA TANDEM REPEATS.  
 FT REPEAT 104 113 1 (INCOMPLETE).  
 FT REPEAT 114 122 2 (INCOMPLETE).  
 FT REPEAT 123 133 3 (INCOMPLETE).  
 FT REPEAT 134 144 4.  
 FT REPEAT 145 155 5.  
 FT REPEAT 156 166 6.  
 FT REPEAT 167 177 7.  
 FT REPEAT 178 188 8.  
 FT REPEAT 189 199 9.  
 FT REPEAT 200 210 10.  
 FT REPEAT 211 221 11.  
 FT REPEAT 222 232 12.  
 FT REPEAT 233 243 13.  
 FT REPEAT 244 252 14.  
 FT CONFLICT 207 207 15 (INCOMPLETE).  
 FT CONFLICT 514 514 D -> DRGDDVTTPDD (IN REF. 1).  
 FT CONFLICT 1698 1698 A -> R (IN REF. 3).  
 FT CONFLICT 1795 1798 D -> N (IN REF. 1).  
 FT CONFLICT 1836 1837 OYLE -> ITLO (IN REF. 1).  
 FT CONFLICT 1836 1837 SA -> T (IN REF. 1).  
 SO SEQUENCE 1953 AA; 200150 MW; 61B3F1C954D91AE CRC64;

Query Match 4.9%; Score 121.5; DB 1; Length 1953;  
 Best Local Similarity 21.6%; Pred. No. 0.63;  
 Matches 86; Conservative 48; Mismatches 162; Indels 103; Gaps 19;

OY 223 ASXKDVNLNAGNIKGVKXKXIXXXXXNDEYVYDTVEFL-SADTKYTTVNESKDNCRX 281  
 DB 301 ADGKTLNVTGMVDTANAAVIEGTQEN-GLYWKYDSRGYLIADNDTVIISGDDQAHNSD 359  
 OY 282 TEVKIGAKTSVKEKDKLYTG-----KXKXENXSSTDGEGLYTAKEVIDAVNKAQMRMK 337  
 DB 360 RGMDSIG-----QDRGTVIISGDRVTNLTGDSVYTDGATGMV----- 397  
 OY 338 TTANGOTQADKFEVTVISGTVTFASGXGTATATSKD---DQGNITVXYDVNVDALNV 394  
 DB 398 -ISGCGTTNTISGHTVDNATG-ALISGNGTTTNFAGDLAIVSGGATIIIDGDNATIKMT 455  
 OY 395 NOLNSGWNLOSKAIVAGSGKIVISGNVSPSKMDETVINAGNNIEIXRNGKNIDIATS 454  
 DB 456 GTSDISG-----AGSTGTVIDGNNAFVNNDGDMTIT-DGCTGCHITGDNVVIDNAGS 506

OY 455 MXPQFSSVSLGAGADAPTLSDVXXAL--NVGSKXXNKPVRITNVAPGVK-EGD---VTN 508  
 DB 507 -----TTVS---GADATATXIEDNALVINEGNOT-----ISGCAVGTIRIDGDHHTTN 552  
 OY 509 VAQLKGVAQNLNNXIDNVXGNARAGIAQAIATAGLQAVLPKSMMAIGGXTYXGEAGYA 568  
 DB 553 TGDY-----AVDGAASAIVIIINGDN-----GSLTQAGDLLVT 584  
 OY 569 IGYSSISXXGNXIKGTASGNSKGFHGXSA-----SVGY 602  
 DB 585 DGAMGIIYTG-----TGNEAKNTGNATVRDADSVGF 615

Search completed: July 3, 2002, 08:30:26  
 Job time: 1197 sec







Query Match 89.4%; Score 2235; DB 22; Length 598;  
Best Local Similarity 77.6%; Pred. No. 3.6e-183;  
Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

QY 1 MNXIXRIIWNLSLNAVXVSELTNRHTKRASATVXTAVLATLXATVQAXXXXXXXXXXXXXX  
DB 1 mkiisrllwnslnavvsvseltrnhlkrasatvatlatllfavega---natdddl 57  
QY 61 XLXVYRXXXVXXXXXXXXXXEXEXXXXXXXXXXXXXXXXXXXXXXTLKAGDNLIKQ 120  
DB 58 ylepvqrlavlsfrsdegtege-atedsmnavyfdelkrvllkagatclikagdnlikq 116  
QY 121 XXXXXXXXXXXXXFTYSLKXKXLLXVXTKLSFXANXXVNIISDTRKGNFAKXTAX 180  
DB 117 ntenntentndstfyslkkdltdltsveteklsfngankvnltstdckglnfaketa 176  
QY 181 TNGDXTVHLNIGISTLTDLXXXXXXXKXXXXXXRAASXKDVLAGMNIKGVKX 240  
DB 177 tngdptvhlngisltldcllntgatlnvtnndvlddekkraasvkvlnagwnlkqvnp 236  
QY 241 GXTXXXXXNVDFVXTYDVEFLSADTKTTTVNESKDNCKXTVEKIGATSVIKEDGKL 300  
DB 237 gtlc--asdnvdfvrltydveflsadtclttvneskdngklevkigatvlikekdgkl 294  
QY 301 VTGKXKXENXSSTDGEGVTAKEVIDAVNKAQWBMKTTTANGQOTGOADKFEVTSGTYX 360  
DB 295 vtgkkgkngensstdgegeglvtakevidavnkagwrmkttlangqgqadkfetvsgtkv 354  
QY 361 TFAAGXGTTATVSKDDQGNITVXYDVNVDALVNQOLNSGWNLDKAVAGSSGKVISGN 420  
DB 355 tfasnggtlatvskddqgnltvkvdyvngdalinvglnqsgwnldskavagssgkvisgn 414  
QY 421 VPSKGMDETVNINAGNIEIXRNCKNIDITSMKPPQSSVSLGAGADPTLSVDXKXA 480  
DB 415 vpspgkmdetvnlagnnleltltnkgndlatlsmtpqfssvslgagadapclsvddeg 474  
QY 481 LNVGSKXKXKPRITNVAVGVEGDTVNAOLKGVANLNKXIDNVXGNARAGIAQAIAIT 540  
DB 475 lnvgskdankpvlritnvavpvegdvtnvaqlkyvaqnlmntldvngnaraglaqat 534  
QY 541 AGLXQAYLPKGSMAIGXTYXGEAGYAIGYSSISXKXNMWIKGTASGNSRGHFGXSASV 600  
DB 535 aglaqaylpkgmma1gg9tlyrgeagya1gyslsdtgnwlvkgtasgnsrghfgtsaav 594  
QY 601 GYQW 604  
DB 595 gyqw 598

RESULT 3  
AA23742  
ID AA23742 standard; Protein: 598 AA.  
XX  
AC AA23742;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN MO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
XX  
DR N-PSDB: AAX85794.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PS Claim 1: Page 108-110; 132pp; English.  
XX  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

Sequence 598 AA:

Query Match 89.4%; Score 2234; DB 20; Length 598;  
Best Local Similarity 77.6%; Pred. No. 4.4e-183;  
Matches 469; Conservative 0; Mismatches 129; Indels 6; Gaps 3;

QY 1 MNXIXRIIWNLSLNAVXVSELTNRHTKRASATVXTAVLATLXATVQAXXXXXXXXXXXXXX  
DB 1 mkiisrllwnslnavvsvseltrnhlkrasatvatlatllfavega---natdddl 57  
QY 61 XLXVYRXXXVXXXXXXXXXXEXEXXXXXXXXXXXXXXXXXXXXXXTLKAGDNLIKQ 120  
DB 58 ylepvqrlavlsfrsdegtege-atedsmnavyfdelkrvllkagatclikagdnlikq 116  
QY 121 XXXXXXXXXXXXXFTYSLKXKXLLXVXTKLSFXANXXVNIISDTRKGNFAKXTAX 180  
DB 117 ntenntentndstfyslkkdltdltsveteklsfngankvnltstdckglnfaketa 176  
QY 181 TNGDXTVHLNIGISTLTDLXXXXXXXKXXXXXXRAASXKDVLAGMNIKGVKX 240  
DB 177 tngdptvhlngisltldcllntgatlnvtnndvlddekkraasvkvlnagwnlkqvnp 236  
QY 241 GXTXXXXXNVDFVXTYDVEFLSADTKTTTVNESKDNCKXTVEKIGATSVIKEDGKL 300  
DB 237 gtlc--asdnvdfvrltydveflsadtclttvneskdngklevkigatvlikekdgkl 294  
QY 301 VTGKXKXENXSSTDGEGVTAKEVIDAVNKAQWBMKTTTANGQOTGOADKFEVTSGTYX 360  
DB 295 vtgkkgkngensstdgegeglvtakevidavnkagwrmkttlangqgqadkfetvsgtkv 354  
QY 361 TFAAGXGTTATVSKDDQGNITVXYDVNVDALVNQOLNSGWNLDKAVAGSSGKVISGN 420  
DB 355 tfasnggtlatvskddqgnltvkvdyvngdalinvglnqsgwnldskavagssgkvisgn 414  
QY 421 VPSKGMDETVNINAGNIEIXRNCKNIDITSMKPPQSSVSLGAGADPTLSVDXKXA 480  
DB 415 vpspgkmdetvnlagnnleltltnkgndlatlsmtpqfssvslgagadapclsvddeg 474  
QY 481 LNVGSKXKXKPRITNVAVGVEGDTVNAOLKGVANLNKXIDNVXGNARAGIAQAIAIT 540  
DB 475 lnvgskdankpvlritnvavpvegdvtnvaqlkyvaqnlmntldvngnaraglaqat 534  
QY 541 AGLXQAYLPKGSMAIGXTYXGEAGYAIGYSSISXKXNMWIKGTASGNSRGHFGXSASV 600  
DB 535 aglaqaylpkgmma1gg9tlyrgeagya1gyslsdtgnwlvkgtasgnsrghfgtsaav 594  
QY 601 GYQW 604  
DB 595 gyqw 598

Accession	Protein	Region	Sequence
AAU06177	standard; Protein: 598 AA.		
AAU06177			
24-OCT-2001	(first entry)		
N. meningitidis H15	surface antigen NhaA polypeptide sequence.		
Surface antigen NhaA	meningococcal disease; meningitis vaccine.		
Neisseria meningitidis strain H15.			
Key	Location/Qualifiers		
Region	1..50		
Region	/label= C1		
Region	/note= "Conserved region 1"		
Region	51..104		
Region	/label= V1		
Region	/note= "Variable region 1"		
Region	105..116		
Region	/label= C2		
Region	/note= "Conserved region 2"		
Region	117..130		
Region	/label= V2		
Region	/note= "Variable region 2"		
Region	131..194		
Region	/label= C3		
Region	/note= "Conserved region 3"		
Region	195..216		
Region	/label= V3		
Region	/note= "Variable region 3"		
Region	217..235		
Region	/label= C4		
Region	/note= "Conserved region 4"		
Region	236..242		
Region	/label= V4		
Region	/note= "Variable region 4"		
Region	243..598		
Region	/label= C5		
Region	/note= "Conserved region 5"		
MO200155182-A1.			
02-AUG-2001.			
25-JAN-2001; 2001WO-AU00069.			
25-JAN-2000; 2000US-0177917.			
(UOQU ) UNIV QUEENSLAND.			
Peak IRA, Jennings MP;			
WPI: 2001-488774/53.			
N-PSDB: AAS09167.			
New NhaA surface antigen polypeptides and polynucleotides from			
Neisseria meningitidis, useful in producing vaccines for treating or			
preventing broad spectrum of Neisseria meningitidis -			
Claim 9; Fig 1; 91pp; English.			

Query Match	89.4%;	Score 2234;	DB 22;	Length 598;
Best Local Similarity	77.6%;	Pred. No. 4,4e-183;		
Matches 469;	Conservative 0;	Mismatches 129;	Indels 6;	Gaps 3;
CC	immunise against a broader spectrum of <i>N. meningitidis</i> strains than			
CC	would be expected from a corresponding wild-type surface antigen.			
CC	The present sequence representing the wild type surface antigen NhaA			
CC	from <i>N. meningitidis</i> strain H15 is 1 of 10 NhaA polypeptide sequences			
CC	(AA06171-AA06180) from 10 different <i>N. meningitidis</i> strains given in			
CC	the present invention.			
XX				
SO	Sequence	598 AA;		
QY	1 MNXIXRITMNSALNANWYVSELTRNHRRAATYXTAVLATLRLAATVQAXXXXXXXXXXX	60		
DB	1 mkllyrllwnsalnawvvselltrnhkrraatavataclllfatvga---naldaddl	57		
QY	61 XLXVYRXRXVYXXXXXXEGEXXXXXXXXXXXXXXXXXXXXXXXTLAAGDLRKTKQ	120		
DB	58 yleprqraavvlslfsdkegtgeke-gtedsnwavyfiekvllkagaitllkagadllkllq	116		
QY	121 XXXXXXXXXXXXXXXXFTVYSLKRLXLLXVXTYKLSFXNAXXKVNIXSDPTKGLNFAKXTAX	180		
DB	117 ntntentnenrtndstctyglkklcdltcvtcekeklsfgnqghkvntlstcklfnakecaag	176		
QY	181 TNGDXTVHLNGIGSTLVDLXXXXAXXXXXXXXTXXXXXRAASKVDYLANGMWIKGVXX	240		
DB	177 tngdptvlhnglgslltldtllntgatltvndnyddekkrasavkdvlnagwnlkgykp	236		
QY	241 GXTXXXXNNVDFVYTYDVEFLSADTKTNTYNVESKONGKKTBYKIGAKTSVIREKDGKL	300		
DB	237 gtc--asdnvdfvtlydveflsadtcltynveskngklevkigaktsvirkexdgl	294		
QY	301 VTGKXXKXENKXSTFDXEGELVTAKKEYIDAVNKAQWPMKTTTANGOTGQADKEETVTSCTYV	360		
DB	295 vtgfygkdeugsstdegeglvtakeyiaevnkagymktttngtqtgqadkftetvsgtkv	354		
QY	361 TFAAGXGTTATVSKDDGNTVYXYDVNVDALNVNQLONSGMNLDKRAVAGSSGKVISGN	420		
DB	355 tfaasngtlatvskddgntlcvkydvnvgdalnvynqldnsqwnldskavagssgkvisgn	414		
QY	421 VSPSGKMKDEEVNINAGNNIETLXRNGKIIDATSMXPEFSSVSLSGAGDAPTLSDVXXXA	480		
DB	415 vspsgkmkdeevnlnagnnietlcnrgknidatlsmtpfjssvslsagadapcltjlvddgea	474		
QY	481 LNVSGSKXNKKFVRIITNNVAPGVKEGDVTWAOCLKVAOQLNNXIDNVXGNARAGIAQAIAT	540		
DB	475 lnvsgskanbkpriltlnvapykvegdvtrnvagllkyvaqglnmrindvngnaratagatlat	534		
QY	541 AGLXQAVLPFGSKMAIGXITYXGEAGVAGIYGSYSIXXGMWIKGTASGNSRGHFGXSASV	600		
DB	535 aglaqaylpgksmmaiggytyrgeagyaigysslsadctgnwllkgylaasngsrghfgasasv	594		
QY	601 GYQW 604			
DB	595 gyqw 598			
RESULT 5				
AAI23745				
ID	AAI23745 standard; Protein; 589 AA.			
XX				
XX	AAI23745;			
DT	08-SEP-1999 (first entry)			
XX				
DE	A surface protein of <i>Neisseria meningitidis</i> .			
XX				
KW	Surface protein; surface glycoprotein; infection; vaccine;			
XX	immunoreactive peptide.			
OS	<i>Neisseria meningitidis</i> .			

XX WO931132-A1.  
 PN  
 XX 24-JUN-1999.  
 PD  
 XX 14-DEC-1998; 98WO-AU01031.  
 PF  
 XX 12-DEC-1997; 97GB-0026398.  
 PR  
 XX (ISTS-) ISIS INNOVATION LTD.  
 PA (UYOU) UNITV QUEENSLAND.  
 XX  
 XX Jennings MP, Moxon ER, Peak IRA;  
 PI  
 XX WPI: 1999-418754/35.  
 DR N-PSDB: AAS85797.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 PS  
 XX Claim 1: Page 122-124; 132pp; English.  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX  
 SQ Sequence 589 AA:

Query Match 89.3%; Score 2231.5; DB 20; Length 589;  
 Best Local Similarity 77.6%; Pred. No. 7.1e-183;  
 Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;

QY 1 MAXXIRITNSLNMVAVXSELRNHTKRASATVXTAVLATLXATVQAXXXXXXXX 60  
 DB 1 mmkilyrlwnsalnawvvselttrhbkraatavatlalsatvg--natldede 58  
 QY 61 XLXVYRXRXVXXXXXXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX 120  
 DB 59 elsesarsalvqfmdkegeie-stgdlwsiydhntlhgactvclkgadnklkq 117  
 QY 121 XXXXXXXXXXFTYSLKRLXLLXVYXTEKLSFXANXVNIKSDPRGLFAKXTAX 180  
 DB 118 -----sgkdfyslkkelkdltsveteklsfgangknvntsdckglnfaketa 167  
 QY 181 TNGDXTVHLNGIGSTLTDXLXXXXXXXXXXXXXXRAASXKDVINAGNKGVRX 240  
 DB 168 tngdprvhlnglgsstltdtclagsasahvdagngst--hytraaslkdvlnagvnlkgykt 225  
 QY 241 GXTXXXXXWVDFVYTDYEFPLSADTKTTVNVESKDNKTEVKGAKTSVYKEDGL 300  
 DB 226 gsetlqgsenvdfrvydvlveflsadcclttvneskdngkrevkigaktvylkedqk 285  
 QY 301 VTGKXKXENXSSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQOTGOADKFETVSGTYX 360  
 DB 286 vtgkxkxengsstdegeglvtakevidavnkagwrmkcttanqsgqadkfetvsgtkv 345  
 QY 361 TFSAGGTATYTKDQGITVXYDVNVDALNVLNOLQNSGMNLDSKAVAGSGKVISGN 420  
 DB 346 tfsaggtatvskddqgnltvkvdydvgdalnvnqlqnsywnldskavagsgkvysgn 405  
 QY 421 VSPSKGKMETVINAGNIEIIXRGNKNIDTSMXPOSSVSLGAGAPRTSVXXXXA 480  
 DB 406 vpskxkxmetvlnagngieitlrngknidatlsmpgissvslgagadapltsvddeg 465  
 QY 481 LNVGSKXKXKPRITNVAPVKEGDTNVQOLKGVANLNKNIIDNVXGNARAGIAQAIAT 540  
 DB 540 lnvgsxkxkpritnvapvkegdtnvqolkgvannlnkniidnvxgnaragiaqaiat 540

DB 466 lnvgsdankpvriltvnapvkegdvtvnaqjkyvaqnlmnrldvngnragiaqalat 525  
 QY 541 AGLXQAVYLPFGKSMATGATYXGEAGYATGYSISXKXGWWXIKGTASGSRGFGXSASV 600  
 DB 526 aqlaqaylpqksmma199gltlylgeagyalgysisdltgnwvlkqtsagnsrghfgtsa 585  
 QY 601 GYQW 604  
 DB 586 gyqw 589  
 RESULT 6  
 AAU06173  
 ID AAU06173 standard: Protein; 589 AA.  
 XX  
 AC AAU06173;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis P20 surface antigen Nhma polypeptide sequence.  
 XX  
 KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain P20.  
 FH  
 FT Key Location/Qualifiers  
 FT Region 1..50 /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..105 /label= V1  
 FT /note= "Variable region 1"  
 FT 106..117 /label= C2  
 FT /note= "Conserved region 2"  
 FT 118..121 /label= V2  
 FT /note= "Variable region 2"  
 FT 122..185 /label= C3  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 186..205 /label= V3  
 FT /note= "Variable region 3"  
 FT 206..224 /label= C4  
 FT /note= "Conserved region 4"  
 FT 225..233 /label= V4  
 FT /note= "Variable region 4"  
 FT 234..589 /label= C5  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 PN  
 PD WO20015182-A1.  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 PF  
 PR 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU) UNITV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI  
 DR WPI: 2001-488774/53.  
 DR N-PSDB: AAS09163.  
 XX  
 PT New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9, Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel *Neisseria*  
 CC meningitidis mutant polypeptides of the surface antigen NHA  
 CC (AAU06182-AAU06186). The modified or mutant NHA polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of *N. meningitidis*, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of *N. meningitidis* strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen NHA  
 CC from *N. meningitidis* strain P20 is 1 of 10 NHA polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
 CC the present invention.

XX Sequence 589 AA;

Query Match 89.3%; Score 2231.5; DB 22; Length 589;

Best Local Similarity 77.6%; Pred. No. 7.1e-183;  
 Matches 469; Conservative 0; Mismatches 120; Indels 15; Gaps 4;

YY 1 MNXIRIIMNSALNAMYVSELTFRNHTKRSATVYTAVALTLKATVQAXXXXXXXXXXXXX 60  
 YY 1 mkiyriimsalnwvsvseltrnhlkrasatavalatlissatvga--natldede 58  
 YY 61 XLXVXXX 120  
 YY 59 elsvarsalavlqfmldkegngele--stgdiysviydhnlhgtatclhagdnllkagdnllkq 117  
 YY 121 XXXXXXXXXXXXXXXXFFYSLKRLXLLXXVTEKLSFYANXXKVNIXSDTGLNPAKXTAX 180  
 YY 118 -----sgkdfytslkelkdlsveteksifangnkvnltsdtkglntafeketag 167  
 YY 181 TNGDXYHLNGIGSTLFDXLLXXXXXXXXTXXXXXRAASXKDYLANGMKIKYKX 240  
 YY 168 tngdptvhlnglsgtlcltclagssasahvdagngst--hytraasikdvlnagwnlkgykt 225  
 YY 241 GXTXXXXXNDVFYTPVTEFLSADTKTTYNVESKNGKTEKIGAKTSVIREKQKX 300  
 YY 226 gxtgsgenvdflvtlytelisadtkcltwnveskdngrklevklgaktsvlkekqkl 285  
 YY 301 VTGKXKXKXNSTDNGEGLVTAKEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTXV 360  
 YY 286 vtgkygkngsgstdegeglvtakevidavnkagymktttngtqgadtrettsqtkv 345  
 YY 361 TPASGXTTATVSKDDGNTVXYDVNVGALNVLNQLONGSMNLSKRAVAGSGKVTISGN 420  
 YY 346 tfasngtlatvskddgntlvkvdvngdalnvngqlngsgwnlidskavagssgkvlsgn 405  
 YY 421 VSPSGKMKDEVNINAGNNIETXRNKKIDTATSMXPOFSSVSIGAGADAPTLISVXXXXX 480  
 YY 406 vspsgkmddevninaagmnieitrnngknidatmtbpjssvsigagadaptlisvddaga 465  
 YY 481 LNVSSKXKXKXNVRTTNVAPVKEGDDVTNVAQLKGAQNLNXXIDNVXNANAGIAQAAT 540  
 YY 466 lnvsskdknkvpriitnvapvkegdvtnvaqlkgaqnlmriidvngnatragatlat 525  
 YY 541 AGLXQAVTLPGKSMATIGGXTYXGEGYATGYSSISXKXNMXIKTGASNSGKHFGXSASV 600  
 YY 526 aglxaqaylpgkssmaigggytlygeagyaigyssisldtgnwlikgaasngsrghfsgsasv 585  
 YY 601 GYQW 604  
 YY 586 gyqw 589

RESULT 7  
 AA57045  
 ID AA57045 standard; Protein: 591 AA.  
 XX

AA57045;

21-FEB-2000 (first entry)

BASB029 amino acid sequence from *N. meningitidis* strain H44/76.

BASB029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;  
 infection; treatment; prevent; antibacterial drug.

*Neisseria meningitidis*.

Key Location/Qualifiers

Misc-difference 90 /note= "Encoded by AAT"

Misc-difference 92 /note= "Encoded by GAT"

Misc-difference 98 /note= "Encoded by AAC"

Misc-difference 108 /note= "Encoded by AATC"

Misc-difference 123 /note= "Encoded by ACA"

Misc-difference 269 /note= "Encoded by AAA"

Misc-difference 389 /note= "Encoded by CGT"

WO958683-A2.

18-NOV-1999.

07-MAY-1999; 99MO-EP03255.

13-MAY-1998; 98GB-0010276.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J.

WPI; 2000-053103/04.

N-PSDB; AA239865.

New polypeptide from *Neisseria meningitidis* useful for diagnosis,

treatment or prevention of bacterial infections in mammal

Claim 4; Fig 2; 74pp; English.

This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
 serogroup B strain H44/76. The BASB029 protein is homologous to the  
 Hemophilus influenzae surface fibrin (HSF) protein. The invention  
 relates to BASB029 polynucleotide sequences (AA239864-239865) and  
 polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.  
 BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 meningitidis infection in a mammal. Compositions containing BASB029  
 polynucleotides and polypeptides are useful for generating an immune  
 response in an animal. A therapeutic composition comprising an antibody  
 directed against BASB029 is useful in treating humans with *Neisseria*  
 meningitidis disease. The polynucleotide is useful in the diagnosis of  
 the stage of infection, type of infection, susceptibility to an  
 infection which results from increased or decreased expression of the  
 polynucleotide, and for therapeutic or prophylactic purposes,  
 particularly genetic immunisation. Antibodies against BASB029  
 polynucleotides and polypeptides are also useful for treating infections  
 particularly bacterial infections. The protein is useful in the  
 screening and development of antibacterial drugs. Fused recombinant  
 protein is useful for the stimulation of the immune system of an organism  
 receiving the protein.

Sequence 591 AA;

Query Match 89.3%; Score 2231.5; DB 21; Length 591;  
 Best Local Similarity 77.6%; Pred. No. 7.2e-183;



PI	Jennings MP, Moxon ER, Peak IRA;
XX	WP1; 1999-418754/35.
DR	N-PsDB; AAX85795.
XX	
PT	Neisseria meningitidis surface proteins useful for treating N.
PS	meningitidis infections
XX	
XX	Claim 1; Page 114-115; 132pp; English.
CC	
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for
CC	the detection or diagnosis of N. meningitidis infection in humans.
CC	The N. meningitidis surface glycoproteins can also be used to
CC	prevent or treat N. meningitidis infection in humans, especially
CC	in the form of vaccines. The proteins and antibodies can also
CC	be used to identify immunoreactive peptides.
CC	
XX	
SQ	Sequence . 599 AA;
	Query Match 89.3%; Score 2231.5; DB 20; Length 599;
	Best Local Similarity 77.6%; Pred. No. 7.3e-183;
	Matches 469; Conservative 0; Mismatches 130; Indels 5; Gaps
	3;
QY	1 MNXIRIIMNSALNMAWVSELTFRNHTRASATVTAVLATLTXATVOAXXXXXXXXXX 60
Dd	1 mmklyrllmnsalnawavaseltrnhktraatatvtlatlftctvga--natdedee 58
QY	61 XLXVYXRXXVXXXXXXXEGXXEXXXXXXXXKXXXXXXXXXXTLKAGDLTKIQ 120
Dd	59 eleprvsralvlqfmldkegngene-stgnlgwsilydnhnllbhagatvllkagdnlklq 117
QY	121 XXXXXXXXXXXXXHTFYSLKRLXLLXAVTPEKLSFXANXXKVNI XSDFTKGTFPKRTAX 180
Dd	118 ntnknhtenlnsdstfclskkdltal fsevelakisfgangnvnltstdtqlntakeleg 177
QY	181 TNGDXTVHLNIGISGLTLOLXXXXXXXKXXXXXXXXRRASAKDVLNMGWNIKGVXX 240
Dd	178 tngdtvhlngisgltlcrtlntgatctvndnrddkkkraasakdvlnegwnlkgykrp 237
QY	241 GTXXXXXXNVDFVXTYTDFEFLSADTKTTVNVESKDNKGKTVEKIGAKTSYIKERDKL 300
Dd	238 gtc--asnvdflvhlydtveflsadtkcttvnveskdngrktevrkigaktsvikekgkl 295
QY	301 VTGKKKXNNKSTDDGEELVTAKEVIDAVNKRAGMFKTTTTANGOTGGADKFETVTSGTYV 360
Dd	296 vtgkkgkngssdtegegjlvtakevidavnkagwtmtktlanqgtgqdakfetvsgtlv 355
QY	361 TFASGSGGTAAVSKDDGNITFYXYVVNNGDALNVNQOLNSGNILDSKRVAVSSGGSVISGN 420
Dd	356 fltasgkgtlatraskddgniltvkdyvnnvgdalnvnglqnsgvnlidskavaagssgkvvisgn 415
QY	421 VSPSKGKADEFVNINAGNNIEIXRNGKNIDIAITSKXPFFSVSLGAGADAPLSTVDXXXXA 480
Dd	416 vspskghndeetvnlagnnielttrngkhidiatcmtpgfsvslgaqadaprlsvddkga 475
QY	481 LNVGSKXXNKPVRITNVAPGVKEGDVTVAQLKGYAQLNNKXIDNVXGNARAGIAQAIIAT 540
Dd	476 lnvsgkdkanbpvrltnvapgvkgegdvtnvaqlkygaqplnnrlidvndgnaraglaqaalat 535
QY	541 AGLGAAVLPBGSMNIGGXTRYXGEGVVALGVSSITXGXGWMXIKGNASGSRGHPCXSASY 600
Dd	536 aglvayalpbgsmnalggtyrgeagyalgyssisdggnwllkgtlasnstrghftgasasv 595
QY	601 GYQM 604
Dd	596 gyqw 599
RESULT	9

AAU06176  
ID AAU06176 standard; Protein; 599 AA.  
XX  
AC AAU06176;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis H38 surface antigen NhbA polypeptide sequence.  
XX  
KW Surface antigen NhbA; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain H38.  
XX  
FH Key  
FH Location/Qualifiers  
FH 1..50  
FH /label= C1  
FH /note= "Conserved region 1"  
FH 51..105  
FH /label= V1  
FH /note= "Variable region 1"  
FH 106..117  
FH /label= C2  
FH /note= "Conserved region 2"  
FH 118..131  
FH /label= V2  
FH /note= "Variable region 2"  
FH 132..195  
FH /label= C3  
FH /note= "Conserved region 3"  
FH 196..217  
FH /label= V3  
FH /note= "Variable region 3"  
FH 218..236  
FH /label= C4  
FH /note= "Conserved region 4"  
FH 237..243  
FH /label= V4  
FH /note= "Variable region 4"  
FH 244..599  
FH /label= C5  
FH /note= "Conserved region 5"  
XX  
PN W0200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PE 25-JAN-2001; 2001W0-AU00069.  
XX  
PR 25-JAN-2000; 2000U05-0177917.  
XX  
PA (UYOU ) UNIT QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI: 2001-488774/53.  
DR N-PSDB; AAS09166.  
XX  
PT New NhbA surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen NhbA  
CC (AAU06182-AAU06186). The modified or mutant NhbA polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen NhbA  
CC from N. meningitidis strain H38 is 1 of 10 NhbA polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 599 AA;  
Query Match 89.3%; Score 2231.5; DB 22; Length 599;  
Best Local Similarity 77.6%; Pred. No. 7.3e-183;  
Matches 469; Conservative 0; Mismatches 130; Indels 5; Gaps 3;  
OY 1 MNXIXRIITNSALNAMYVSSELTFRNHTKRASATYTAVALTLAATVQAXXXXXXXXXXXXXX  
DB 1 mkiyriilmsalnwavasseittrnhtkrasatvktavlatllfatvga--natedeese 58  
OY 61 XLXVYKRXKXVXXXXXXXXXEGXEXXXXXXXXXXXXXXXXXXXXXXTLKAGDNLKIKQ 120  
DB 59 elepyvrsalvlgfmidkegngene-stgnlqwslyydhntlhqatvllkagdnlikq 117  
OY 121 XXXXXXXXXXXXXPTYSLKXKXLLXVXTXKLSFXANXXXKVNIXSDPTKGLNFAKXTAX 180  
DB 118 ntukntneutndsstfyslkkdlcltsveteklsfgangknvntsdtkglnfaketaq 177  
OY 181 TNGDXTVHLNGIGSTLTDLXAXXXXXXXXXXXXXXRAASXKDYLNAGWNIKGVKX 240  
DB 178 tngdtvhlnglgsfcltdlIntgatntvndvddkkkraasvkdvlmagwnlkvyp 237  
OY 241 GXTXXXXXNDFVXTYDVEFLSADTKTTTYNVNESKDNKKTVEKIKGKTSYIREKDKL 300  
DB 238 glt--asdnvdfvlnhdyelvsadtkltlvnveskdngkrtvevlgatsvixekdgl 295  
OY 301 VTGKKKXENXSSTDGEGELVTAKEVIDAVNKAQGMKTTTANNGTQADKFEFTVSGTXV 360  
DB 296 vtgkkgengsstdegeglvtakevidavnkagvrmktlttngtqgqgdktelvtsgtlnv 355  
OY 361 TFASGXTTATVSKDDGNTIVXYDVNVGDALNVNQLONSGNLDSKAVAGSSGKVIISGN 420  
DB 356 tfasgxttatvskddgntlvkydvngdalinvnqlnsgwnlidskavagssgvlsign 415  
OY 421 VPSKSGKMDENVNINAGNNIEIXRGNKIDTATSMXPOFSSVSIGAGADAPTLISVXXXXA 480  
DB 416 vpsksgkmdenvninaagnlcltrngknidatstmcptfssvsigagadapltlsvdddga 475  
OY 481 LNVGSKXXXKRPVRLTNVAPVKEGCDVTNVAOLKGYAQLNNXIDNVXGNABAGIAOAATAT 540  
DB 476 lnvsgkdanbkpyrltnvapgvykegdvtlnvaqlkygaqnlmnrldnvdgtnaragaialat 535  
OY 541 AGLXQAVLPGRSMWATIGGXTYXGEGVAGVAGYSISIXXGNMXXIKGTASGNSRGHFGXSASV 600  
DB 536 aglvqaylpgkemmaigqgtyrgeagyaigyssisdggnwlkgtasgnsrghfgsasv 595  
OY 601 GYQW 604  
DB 596 gyqw 599  
RESULT 10  
AAZ27202  
ID AAZ27202 standard; Protein; 591 AA.  
XX  
AC AAZ27202;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
KW bacterial infection; treatment.  
XX  
OS Neisseria meningitidis.  
XX  
PN W09936544-A2.

XX 22-JUL-1999.  
 PD 14-JAN-1999; 99WO-IB00103.  
 XX  
 PF 09-OCT-1998; 98GB-0022143.  
 XX PR 14-JAN-1998; 98GB-0000760.  
 PR 01-SEP-1998; 98GB-0019015.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Grandi G, Maignani V, Pizsa M, Rappuoli R, Scarlato V;  
 XX  
 DR WPI: 1999-444400/37.  
 N-PSDB; AAX99124.  
 XX  
 PT New protein and its nucleotide sequence, useful in vaccines or  
 PT diagnostic compositions for treating and/or preventing Neisseria  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 62; 123pp; English.  
 XX  
 CC The invention provides proteins (AAY27201-245) from Neisseria  
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
 CC encoding the proteins. Compositions comprising the protein, nucleic acid  
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
 CC vaccine composition or a diagnostic composition. The composition is also  
 CC useful for treating or preventing an infection due to Neisseria  
 CC bacteria, especially Neisseria meningitidis.  
 XX  
 SQ Sequence 591 AA:

Query Match 89.3%; Score 2230.5; DB 20; Length 591;  
 Best Local Similarity 77.6%; Pred. No. 8.7e-183;  
 Matches 469; Conservative 0; Mismatches 122; Indels 13; Gaps 3;

QY 1 MNXIXRIINNSALNMAVYXSELRNHTKRASATVYTAVALTLXATVQAXXXXXXXXXX 60  
 DB 1 mkiyrlfimsalnawvvseltlnhtkrasatvktavlatllfatvgasanneegeeql 60  
 QY 61 XLXVYVRRXXXXXXEGXEXEXXXXXXXXXXXXXXXXXXXXXTLKAQDNKIRQ 120  
 DB 61 yldpvyqtravavlinsdkegtekekeveensdwayfnekyvltareitlkgadnklkq 120  
 QY 121 XXXXXXXXXXXXXFTYSLKKLXLXVYXTEKLSFXANXXKVNIXSDTKGLNFAKXTAX 180  
 DB 121 -----ngntfyslkkdltltsvgteklfsangknvltstckglnfaketaq 170  
 QY 181 TNGDXTVHLNGIGSTLTDLXXXXXXXXTXXXXXRAASXKDVIAGNNTIGVAX 240  
 DB 171 tngdltvhlnglsgstldtlnhtgactnvlndvltdekkrtasavdlinaqnlkgvvp 230  
 QY 241 GXTXXXXXNVDPEYXYDYTEFLSADTKTTVNVESKDNCKYTEVKTGATSVYKEKDKL 300  
 DB 231 gtt--asdvndvfyrdvteflsadtclttvnveskdncktevkigtatsvylkedgkl 288  
 QY 301 VTGKXXKXKXSTDXGEGLVTAKEVIDAVNKAQWRMKTTPANGQTGQADKFETVTSYXV 360  
 DB 289 vtgkdkgensstdegeglvtakevidavnkagwrmtcttanqgtgqadkfetvtsqtnv 348  
 QY 361 TPASAGGTATATYKDOGNITVXYDVNVDALNVNOLNONGWMLDSKAVAAGSSGKATISGN 420  
 DB 349 tlasggtatavskddqgnltvmydvndgdaInvnqlqnsqwnldskavagssgkvisgn 408  
 QY 421 VSPSKGMDPVTINAGNIEIIRNKNIDITSMXPOFSSVSLGAGAPLTSLVDXXXXA 480  
 DB 409 vspskgmdetvtninaqnieltngknldiatstmpqfssvslgsagadapltslvd-gda 467  
 QY 481 LVVGSKXXKXKXPRITNVAPGKVEGDTVNAOLKGAQONLNKXIDNVXGNARAGIAQAIAT 540  
 DB 468 lvvgskdkkpkpritnvapgvkegdvtnvaqlkyvaqnnlnrindvngnaraglaqaiat 527

QY 541 AGLXQAVLPKSKMAIGXTYXGEGAYIAGYSISXXGNWIKIGTASGNSRGHFGXASAY 600  
 DB 528 aglvqaylpgksmma1gg9ltyrgeayalgyssisdggnwilkgtasgnrghfgasay 587  
 QY 601 GYQW 604  
 DB 588 gyqW 591

## RESULT 11

AAY23741  
 ID AAY23741 standard; Protein; 591 AA.

AC AAY23741;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;  
 immunoreactive peptide.

OS Neisseria meningitidis.

PN WO9931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PI (UYOU ) UNITV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.

DR N-PSDB; AAX85793.

PT Neisseria meningitidis surface proteins useful for treating N.

PS meningitidis infections  
 Claim 1; Page 104-106; 132pp; English.

CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

SQ Sequence 591 AA:

Query Match 89.3%; Score 2230.5; DB 20; Length 591;  
 Best Local Similarity 77.6%; Pred. No. 8.7e-183;  
 Matches 469; Conservative 0; Mismatches 122; Indels 13; Gaps 3;

QY 1 MNXIXRIINNSALNMAVYXSELRNHTKRASATVYTAVALTLXATVQAXXXXXXXXXX 60  
 DB 1 mkiyrlfimsalnawvvseltlnhtkrasatvktavlatllfatvgasanneegeeql 60  
 QY 61 XLXVYVRRXXXXXXEGXEXEXXXXXXXXXXXXXXXXXXXXXTLKAQDNKIRQ 120  
 DB 61 yldpvyqtravavlinsdkegtekekeveensdwayfnekyvltareitlkgadnklkq 120  
 QY 121 XXXXXXXXXXXXXFTYSLKKLXLXVYXTEKLSFXANXXKVNIXSDTKGLNFAKXTAX 180  
 DB 121 -----ngntfyslkkdltltsvgteklfsangknvltstckglnfaketaq 170



Key	Location/Qualifiers
Peptide	1..51
	/label= Signal_peptide
Region	1..50
	/label= C1
Region	/note= "Conserved region 1"
	51..108
	/label= V1
Protein	/note= "Variable region 1"
	52..591
	/label= Mature_Nhha
	/note= "Predicted mature protein, specifically claimed in claim 12"
Region	109..120
	/label= C2
	/note= "Conserved region 2"
Region	121..124
	/label= V2
	/note= "Variable region 2"
Region	125..188
	/label= C3
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	/note= "Conserved region 5"
WO200155182-A1.	
02-AUG-2001.	
25-JAN-2001; 2001WO-A000069.	
25-JAN-2000; 2000US-0177917.	
(UYOU ) UNIV QUEENSLAND.	
Peak IRA, Jennings MP;	
WPI: 2001-488774/53.	
N-PSDB; AAS09161.	
New Nhha surface antigen polypeptides and polynucleotides from	
Neisseria meningitidis, useful in producing vaccines for treating or	
preventing broad spectrum of Neisseria meningitidis -	
Claim 9; Fig 1; 91pp; English.	
The present invention relates to the isolation of novel Neisseria	
meningitidis mutant polypeptides of the surface antigen Nhha	
(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are	
characterised by deletions of non-conserved amino acids, particularly	
the deletion of variable regions. The deletion mutants are useful in	
diagnostics, therapeutic and prophylactic vaccines against a broader	
spectrum of N. meningitidis, and in designing and/or screening of	
medicaments. The mutant proteins when used as a vaccine can effectively	
immunise against a broader spectrum of N. meningitidis strains than	
would be expected from a corresponding wild-type surface antigen.	
The present sequence representing the wild type surface antigen Nhha	
(AAU06171-AAU06180) from 10 different N. meningitidis sequences	
the present invention.	

Query Match	Similarity	89.3%	Score 2230.5	DB 22	Length 591
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Db	61		120		
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QY	231	glt--asdvdfvrcydvelfsadtclttvveskdhgklevkigaktsvikekgkL	288		
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Db	301		360		
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QY	421	VSPSGKMDIYVINAAGNIEIXRNGKNIDITSMXPPQSSVSLGAGADAPLISDXXXXA	480		
Db	421		480		
QY	481	LNVGSKXKXKPRIRINNVAPGVKEGQVTNVNOLKGYAONLNKXIDNVXGNARAGIAQATAT	540		
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Db	541		600		
QY	601	GIQW 604			
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XX	24-OCT-2001	(first entry)			
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XX	Surface antigen Nhma: meningococcal disease: meningitis vaccine.				
XX	Neisseria meningitidis strain EG329.				
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XX	/note= "Variable region 1"				
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FT      /label= C5
FT      /note="Conserved region 5"

MO200155182-A1.
XX      02-AUG-2001.
XX      PD
XX      25-JAN-2001; 2001MO-A000069.
XX      PE
XX      25-JAN-2000; 2000US-0117917.
XX      PR
XX      (UYOU ) UNIV QUEENSLAND.
XX      PA
XX      Peak IRA, Jennings MP;
XX      PI
XX      WPI; 2001-48874/53.
XX      DR
XX      N-PSDB; AAS09165.

PT      New Nhha surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis .
XX      XX
XX      Claim 9; Fig 1; 91pp; English.
XX      XX
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhha
XX      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      The present sequence representing the wild type surface antigen Nhha
XX      from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
XX      SO
XX      Sequence 591 AA;

Query Match      89.3%; Score 2230.5; DB 22; Length 591;
Best Local Similarity 77.6%; Pred. No. 8,7e-183;
Matches 469; Conservative 0; Mismatches 122; Indels 13; Gaps 3;

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QY      421 VSPSKGKMEFTVNTNGNNIEIXRNGKNIDATSMXQFSSVSLGAGADAPTLSDVXXA 480
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QY      481 LNVGSKXXNRPVRTTNVAPGVKEGDYTNVAOLKGVAOQLNNXIDNVXGNARAGIAQAIAT 540
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QY      601 GYQW 604
Db      588 gyqw 591

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XX      AC
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XX      DT
XX      08-SEP-1999 (first entry)
XX      DE
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XX      KW
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX      OS
XX      Neisseria meningitidis.
XX      PN
XX      WO9931132-A1.
XX      PD
XX      24-JUN-1999.
XX      PE
XX      14-DEC-1998; 98WO-AU01031.
XX      PR
XX      12-DEC-1997; 97GB-0026398.
XX      PA
XX      (ISIS-) ISIS INNOVATION LTD.
XX      PA
XX      (UYOU ) UNIV QUEENSLAND.
XX      PI
XX      Jennings MP, Moxon ER, Peak IRA;
XX      WPI; 1999-418754/35.
XX      DR
XX      N-PSDB; AAX85792.
XX      PT
XX      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX      PS
XX      Claim 1; Page 100-101; 132pp; English.
XX      CC
XX      The present sequence represents a surface protein of Neisseria
XX      meningitidis which is approximately 62 kDa. The N. meningitidis

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:24:09 ; Search time 14.71 Seconds  
(without alignments)  
1002.927 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 604

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Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	9.8	589	4	US-09-377-155-19
2	59	9.8	589	4	US-09-669-974-19
3	59	9.8	591	4	US-09-377-155-11
4	59	9.8	591	4	US-09-377-155-21
5	59	9.8	591	4	US-09-669-974-11
6	59	9.8	591	4	US-09-669-974-21
7	59	9.8	592	4	US-09-377-155-2
8	59	9.8	592	4	US-09-377-155-17
9	59	9.8	592	4	US-09-669-974-2
10	59	9.8	592	4	US-09-669-974-17
11	59	9.8	594	4	US-09-377-155-7
12	59	9.8	594	4	US-09-377-155-9
13	59	9.8	594	4	US-09-669-974-7
14	59	9.8	594	4	US-09-669-974-9
15	59	9.8	598	4	US-09-377-155-5
16	59	9.8	598	4	US-09-377-155-13
17	59	9.8	598	4	US-09-669-974-5
18	59	9.8	598	4	US-09-669-974-13
19	59	9.8	599	4	US-09-377-155-15
20	59	9.8	599	4	US-09-669-974-15
21	19	3.1	658	1	US-08-409-995-5
22	19	3.1	658	3	US-08-685-467-5
23	19	3.1	658	4	US-08-913-942-5
24	19	3.1	1098	1	US-08-409-995-2
25	19	3.1	1098	3	US-08-685-467-2
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28	19	3.1	1098	4	US-09-669-974-32	Sequence 32, Appl
29	19	3.1	1098	4	US-09-268-347-44	Sequence 44, Appl
30	17	2.8	1094	4	US-09-268-347-32	Sequence 32, Appl
31	13	2.2	1912	1	US-08-409-995-4	Sequence 4, Appl
32	13	2.2	1912	3	US-08-685-467-4	Sequence 6, Appl
33	13	2.2	2353	4	US-08-913-942-33	Sequence 33, Appl
34	13	2.2	2353	4	US-08-913-942-33	Sequence 33, Appl
35	13	2.2	2353	4	US-09-669-974-33	Sequence 33, Appl
36	13	2.2	2354	4	US-09-268-347-33	Sequence 33, Appl
37	13	2.2	2411	4	US-09-268-347-36	Sequence 36, Appl
38	12	2.0	607	1	US-08-409-995-6	Sequence 6, Appl
39	12	2.0	607	3	US-08-685-467-6	Sequence 6, Appl
40	12	2.0	607	4	US-08-913-942-6	Sequence 6, Appl
41	10	1.7	679	4	US-08-913-942-15	Sequence 15, Appl
42	10	1.7	679	4	US-09-268-347-26	Sequence 26, Appl
43	9	1.5	36	4	US-09-268-347-54	Sequence 54, Appl
44	9	1.5	1002	4	US-09-268-347-24	Sequence 24, Appl
45	9	1.5	1004	4	US-09-268-347-30	Sequence 30, Appl

#### ALIGNMENTS

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RESULT 1
US-09-377-155-19
; Sequence 19, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
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; ORGANISM: Neisseria meningitidis
US-09-377-155-19

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DB 369 YDVNVGDALNVQLONSGNMLDSKAVAGSSGRVISCNVSPPSKGKMDFTVINAGNNIEI 427

RESULT 2
US-09-669-974-19
; Sequence 19, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
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PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 19  
LENGTH: 589  
TYPE: PRF  
ORGANISM: Neisseria meningitidis  
US-09-669-974-19

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OY 384 YDVAVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEI 442  
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RESULT 3  
US-09-377-155-11  
Sequence 11, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 11  
LENGTH: 591  
TYPE: PRF  
ORGANISM: Neisseria meningitidis  
US-09-377-155-11

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Best Local Similarity 100.0%; Pred. No. 9,1e-48;  
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RESULT 4  
US-09-377-155-21  
Sequence 21, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 21

LENGTH: 591  
TYPE: PRF  
ORGANISM: Neisseria meningitidis  
US-09-377-155-21

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Best Local Similarity 100.0%; Pred. No. 9,1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVAVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEI 442  
DB 372 YDVAVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEI 430

RESULT 5  
US-09-669-974-11  
Sequence 11, Application US/09669974  
Patent No. 633173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 11  
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ORGANISM: Neisseria meningitidis  
US-09-669-974-11

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Best Local Similarity 100.0%; Pred. No. 9,1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVAVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEI 442  
DB 372 YDVAVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEI 430

RESULT 6  
US-09-669-974-21  
Sequence 21, Application US/09669974  
Patent No. 633173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
APPLICANT: MOXON, E. Richard  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 21  
LENGTH: 591

TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 9.8%; Score 59; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 9.1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 372 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 430

RESULT 7  
US-09-377-155-2

Sequence 2, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 9.8%; Score 59; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 9.1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 373 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 431

RESULT 8  
US-09-377-155-17

Sequence 17, Application US/09377155  
Patent No. 6197312  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/377,155  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-377-155-17

Query Match 9.8%; Score 59; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 9.1e-48;  
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OY 384 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 442  
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RESULT 9  
US-09-669-974-2

Sequence 2, Application US/09669974  
Patent No. 633173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 9.8%; Score 59; DB 4; Length 592;  
Best Local Similarity 100.0%; Pred. No. 9.1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 373 YDVNVDALNVNQLNSGMNLDKRAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 431

RESULT 10  
US-09-669-974-17

Sequence 17, Application US/09669974  
Patent No. 633173  
GENERAL INFORMATION:  
APPLICANT: PEAK, Ian Richard Anselm  
APPLICANT: JENNINGS, Michael Paul  
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
FILE REFERENCE: 065064/0128  
CURRENT APPLICATION NUMBER: US/09/669,974  
CURRENT FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/377,155  
PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: PCT/AU98/01031  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: GB 9726398.2  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-09-669-974-17

Query Match 9.8%; Score 59; DB 4; Length 592;

Best Local Similarity 100.0%; Pred. No. 9.1e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 442  
Db 372 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 430

## RESULT 11

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 9.8%; Score 59; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 9.2e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 442  
Db 374 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 432

## RESULT 12

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 9.8%; Score 59; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 9.2e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 442  
Db 374 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 432

Db 374 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 432

## RESULT 13

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 9.8%; Score 59; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 9.2e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 442  
Db 374 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 432

## RESULT 14

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 9.8%; Score 59; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 9.2e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 442  
Db 374 YDVNVGDALNVNOLQNSGMWLDKRAVAGSSGKYISGNVSPSKGMDETVINAGNNIEI 432

RESULT 15  
 US-09-377-155-5  
 ; Sequence 5, Application US/09377155  
 ; Patent No. 6197312  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PEAK, Ian Richard Anselm  
 ; APPLICANT: JENNINGS, Michael Paul  
 ; APPLICANT: MOXON, E. Richard  
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
 ; FILE REFERENCE: 065064/0128  
 ; CURRENT APPLICATION NUMBER: US/09/377, 155  
 ; CURRENT FILING DATE: 1999-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: GB 9726398. 2  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria meningitidis  
 US-09-377-155-5

Query Match 9.88; Score 59; DB 4; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-48;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 384 YDVNNGDALNNTGNSGWNLDKRAVAGSGKVTSGNVPSPKGMDETWINAGNNIEI 442  
 Db 378 YDVNNGDALNNTGNSGWNLDKRAVAGSGKVTSGNVPSPKGMDETWINAGNNIEI 436

Search completed: July 3, 2002, 08:30:34  
 Job time: 385 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:30:29 ; Search time 34.27 Seconds

(without alignments)  
3048.991 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 604  
Sequence: 1 MNXIRLIMNSALNANVXVS.....TASGNSRGRGXSASVGYQW 604

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	9.8	526	2	Q9JPS4 neisseria m
2	59	9.8	530	2	Q9JPS1 neisseria m
3	59	9.8	589	2	Q9JPI0 neisseria m
4	59	9.8	589	2	Q9JQY1 neisseria m
5	59	9.8	590	2	Q9JPS3 neisseria m
6	59	9.8	591	2	Q9JPS7 neisseria m
7	59	9.8	591	2	Q9JQY3 neisseria m
8	59	9.8	591	16	Q9JRI8 neisseria m
9	59	9.8	592	2	Q9AOF0 neisseria m
10	59	9.8	592	2	Q9JPS9 neisseria m
11	59	9.8	592	2	Q9JQY2 neisseria m
12	59	9.8	592	16	Q9JQW4 neisseria m
13	59	9.8	594	2	Q9JPI3 neisseria m
14	59	9.8	594	2	Q9JPS2 neisseria m
15	59	9.8	594	2	Q9JPH7 neisseria m
16	59	9.8	594	2	Q9JQY4 neisseria m

17	59	9.8	595	2	Q9JPH0 neisseria m
18	59	9.8	598	2	Q9JPI0 neisseria m
19	59	9.8	598	2	Q9JPI9 neisseria m
20	59	9.8	598	2	Q9JPI7 neisseria m
21	59	9.8	598	2	Q9JPS0 neisseria m
22	59	9.8	598	2	Q9JQY5 neisseria m
23	59	9.8	599	2	Q9JPS8 neisseria m
24	59	9.8	599	2	Q9JPI8 neisseria m
25	59	9.8	600	2	Q9JPS6 neisseria m
26	59	9.8	600	2	Q9JPS5 neisseria m
27	19	3.1	1098	2	Q48152 haemophilus
28	13	2.2	2353	2	P71401 haemophilus
29	8	1.3	438	16	Q91664 pseudomonas
30	8	1.3	498	16	Q92087 rhizidium m
31	8	1.3	574	17	Q26815 methanother
32	8	1.3	1755	17	Q26812 methanother
33	8	1.3	3301	11	Q91210 mus musculu
34	8	1.3	3312	4	Q9NYQ7 homo sapien
35	8	1.3	3313	11	Q88278 rattus norv
36	8	1.3	3546	2	Q9F830 micromosp
37	7	1.2	88	9	Q21889 bacterioph
38	7	1.2	93	2	Q921X9 borrelia bu
39	7	1.2	94	17	Q96X74 sulfolobus
40	7	1.2	120	17	Q28622 archaeoglob
41	7	1.2	157	16	Q9RU00 delnoccocus
42	7	1.2	159	2	Q92621 salmonella
43	7	1.2	173	16	Q9KCO4 bacillus ha
44	7	1.2	179	11	Q9JLM8 mus musculu
45	7	1.2	180	5	Q18085 caenorhabdi

#### ALIGNMENTS

RESULT 1

Q9JPS4 PRELIMINARY: PRT: 526 AA.

AC Q9JPS4: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DI 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE UPPER MEMBRANE PROTEIN GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NG6/88;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masiagnani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;

RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";

RT Science 287:1816-1820(2000).

RL EMBL: AF226377; AAF42526.1; -

DR SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;

Query Match 9.8%; Score 59; DB 2; Length 526;

Best Local Similarity 100.0%; Pred. No. 6 6e-50; Mismatches 0; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDVNNGDALNVNQLNSGNMLDSKAVAGSSGKIVISGNVSPSKGMDETVINAGNNIEI 442

DB 307 YDVNNGDALNVNQLNSGNMLDSKAVAGSSGKIVISGNVSPSKGMDETVINAGNNIEI 365

RESULT 2  
Q9JPS1 PRELIMINARY; PRT; 530 AA.  
AC Q9JPS1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGF26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226380; AAF42529.1; -;  
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;

Query Match 9.8%; Score 59; DB 2; Length 530;  
Best Local Similarity 100.0%; Pred. No. 6.6e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 442  
Db 311 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 369

RESULT 3  
Q9JPS1 PRELIMINARY; PRT; 589 AA.  
AC Q9JPS1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGP165; PubMed=10710308;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226384; AAF42533.1; -;  
DR EMBL: AF226362; AAF42511.1; -;  
DR EMBL: AF226363; AAF42512.1; -;  
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95DA486856A6 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 7.2e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 384 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 442  
Db 369 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 427

RESULT 4  
Q93QY1 PRELIMINARY; PRT; 589 AA.  
AC Q93QY1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P20;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157610; AAK68871.1; -;  
SQ SEQUENCE 589 AA; 61448 MW; 1F1A80C610CB230 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 7.2e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 442  
Db 369 YDVAWGALNVNOJLNGSGWNLDSKAVAGSSGKVTSGNVSPSKGMDEVTNINAGNIEI 427

RESULT 5  
Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -;  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 590;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Oy 384 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 442  
|||||  
Db 370 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 428

RESULT 6  
ID 09JPS7 PRELIMINARY; PRT: 591 AA.  
AC 09JPS7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-B2147;  
RX MEDLINE=20175756; PubMed-10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing."  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226366; AAF42515.1;  
SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91EIF CRC64;

Query Match 9.8%; Score 59; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 384 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 442  
|||||  
Db 372 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 430

RESULT 7  
ID 0930Y3 PRELIMINARY; PRT: 591 AA.  
AC 0930Y3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-EG329;  
RT Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157606; AAK68867.1;  
SQ SEQUENCE 591 AA: 62048 MW: CDDC600798859C65 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 384 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 442  
|||||  
Db 372 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 430

Db 372 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 430

RESULT 8  
ID 09JRI8 PRELIMINARY; PRT: 591 AA.  
AC 09JRI8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE  
DE PROTEIN).  
GN GNA992 OR NMB0992 OR NHHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
RX MEDLINE=20175756; PubMed-10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing."  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed-10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,  
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanthoeven J.,  
RA Gill J., Scariato V., Maignani V., Pizze M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
RT MC58."  
RL Science 287:1809-1815(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-N.meningitidis; STRAIN-PMC21;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226375; AAF42524.1;  
DR EMBL: AE002450; AAF41395.1;  
DR EMBL: AF226367; AAF42516.1;  
DR EMBL: AF226370; AAF42519.1;  
DR EMBL: AF226374; AAF42523.1;  
DR EMBL: AF157611; AAK68872.1;  
DR TIGR: NMB0992;  
KW Complete proteome.  
SQ SEQUENCE 591 AA: 62112 MW: 7C22F3CAEF73BC6 CRC64;

Query Match 9.8%; Score 59; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 384 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 442  
|||||  
Db 372 YDVNVDALNVNQLNSGNLDSKAVAGSSGKIVISGNVSPSKGKMDETVINAGNNIEI 430

RESULT 9  
 ID 09AOF0 PRELIMINARY; PRT; 592 AA.  
 AC 09AOF0;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN.  
 GN NHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 RX NCBI\_TaxID=487;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF125375; AAK09243.1; -  
 SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 442  
 DB 373 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 431

RESULT 10  
 ID 09JPS9 PRELIMINARY; PRT; 592 AA.  
 AC 09JPS9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 RX NCBI\_TaxID=487;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=860800;  
 RX MEDLINE=20175756; Pubmed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226361; AAF42510.1; -  
 SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 442  
 DB 372 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 430

RESULT 11  
 093QY2

ID 093QY2 PRELIMINARY; PRT; 592 AA.  
 AC 093QY2;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE NHA OUTER MEMBRANE PROTEIN.  
 GN NHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 RX NCBI\_TaxID=487;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H41;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157609; AAK68870.1; -  
 SQ SEQUENCE 592 AA; 61869 MW; F9403A0B4A18EEA7 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 442  
 DB 372 YDVAVGALNVNQLNSGWNIDSKAVAGSSGKVISGNVSPSKGMDETWINAGNNIEI 430

RESULT 12  
 ID 09JOW4 PRELIMINARY; PRT; 592 AA.  
 AC 09JOW4;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PUTATIVE SURFACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).  
 GN NNA1200 OR GNA992.  
 OS Neisseria meningitidis (serogroup A), and  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 RX NCBI\_TaxID=65699, 487;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / SEROTYPE 4A;  
 RX MEDLINE=20222556; Pubmed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,  
 RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,  
 RA Raftery M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 meningitidis 22491."  
 RL Nature 404:502-506(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=205900, B2133, F6124, AND 22491;  
 RX MEDLINE=20175756; Pubmed=10710308;  
 RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AL162755; CAB84461.1; -  
 DR EMBL: AF226357; AAF42506.1; -  
 DR EMBL: AF226365; AAF42514.1; -

DR EMBL: AF226373; AAF42522.1; -  
DR EMBL: AF226386; AAF42535.1; -  
KW Complete proteome.  
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 9.8%; Score 59; DB 16; Length 592;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 372 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 430

## RESULT 13

OJUP13 PRELIMINARY; PRT; 594 AA.  
AC OJUP13;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND B2232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -  
DR EMBL: AF226369; AAF42518.1; -  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 374 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 432

## RESULT 14

OJUP52 PRELIMINARY; PRT; 594 AA.  
AC OJUP52;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -  
DR EMBL: AF157604; AAK68865.1; -  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 9.8%; Score 59; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 374 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 432

## RESULT 15

OJUPH7 PRELIMINARY; PRT; 594 AA.  
AC OJUPH7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198, AND 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=B2198;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF226368; AAF42517.1; -  
DR EMBL: AF226358; AAF42507.1; -  
DR EMBL: AF157604; AAK68865.1; -  
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 9.8%; Score 59; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 7.3e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 442  
DB 374 YDVNVGDALNVQNLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDFTVINAGNNIEI 432

Search completed: July 3, 2002, 08:34:10  
Job time: 221 sec





DT 26-FEB-2001 (first entry)  
XX  
XX Neisserial conserved peptide #13.  
DE  
XX Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;  
KM gene therapy; conserved sequence.  
XX  
XX Neisseria sp.  
OS  
XX  
PN (#WO200066741-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000MO-IB00642.  
XX  
PR 30-APR-1999; 99GB-0010168.  
PR 09-MAR-2000; 2000GB-0005728.  
XX  
XX (CHIR-) CHIRON SPA.  
PA  
XX  
PI Rappuoli R;  
XX  
XX WPI; 2000-687543/67.  
DR  
XX  
XX Novel Neisserial protein fragments and their corresponding nucleic  
PT acids, useful in the manufacture of medicines for the prevention of  
PT Neisserial infection, and in the manufacture of diagnostic reagents -  
XX  
XX Claim 15; Page 57; 157pp; English.  
XX  
XX The present peptide is a conserved region of a Neisserial protein.  
CC Neisserial proteins containing this sequence, and the nucleic acids  
CC that encode such proteins, are useful in the manufacture of medicines  
CC for the prevention of Neisserial infection, and in the manufacture of  
CC multi-specific diagnostic reagents.  
XX  
SQ Sequence 72 AA:  
  
Query Match 9.8%; Score 59; DB 21; Length 72;  
Best Local Similarity 100.0%; Pred. No. 2.6e-50;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 384 YDYNVGDALNVNOLNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEI 442  
DB 1 ydvnvgdalinvglnqnsynldskavagssgkvisgnvpskxgkmdetvniagnniei 59  
  
RESULT 3  
AAU06184  
ID AAU06184 standard; Protein; 407 AA.  
XX  
AC AAU06184;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
XX N. meningitidis PMC21 Nhha deletion mutant #2.  
DE  
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KM mutant; mutein.  
XX  
XX Neisseria meningitidis strain PMC21.  
OS Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Protein 52..407  
FT /label= Mature\_Nhha\_deletion\_mutant\_#2  
FT /note= "Predicted mature protein, specifically  
claimed in claim 12"  
XX  
XX  
PN WO20015182-A1.

XX  
XX 02-AUG-2001.  
PD  
XX  
XX 25-JAN-2001; 2001WO-AU00069.  
PF  
XX  
XX 25-JAN-2000; 2000US-0177917.  
PR  
XX  
XX (UYOU ) UNIV QUEENSLAND.  
PA  
XX  
XX Peak IRA, Jennings MP;  
PI  
XX  
XX WPI; 2001-48774/53.  
DR  
XX  
XX N-PSDB; AAS09174.  
DR  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 12; Fig 7; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis strain PMC21 surface  
CC antigen Nhha deletion mutant #2.  
XX  
XX  
SQ Sequence 407 AA:  
  
Query Match 9.8%; Score 59; DB 22; Length 407;  
Best Local Similarity 100.0%; Pred. No. 1.2e-49;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 384 YDYNVGDALNVNOLNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEI 442  
DB 188 ydvnvgdalinvglnqnsynldskavagssgkvisgnvpskxgkmdetvniagnniei 246  
  
RESULT 4  
AAU06185  
ID AAU06185 standard; Protein; 433 AA.  
XX  
AC AAU06185;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
XX N. meningitidis PMC21 Nhha deletion mutant #3.  
DE  
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;  
KM mutant; mutein.  
XX  
XX Neisseria meningitidis strain PMC21.  
OS Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..51  
FT /label= Signal\_peptide  
FT Protein 52..433  
FT /label= Mature\_Nhha\_deletion\_mutant\_#3  
FT /note= "Predicted mature protein, specifically  
claimed in claim 12"  
XX  
XX  
PN WO20015182-A1.  
XX  
XX 02-AUG-2001.  
XX

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:39 ; Search time 34.02 Seconds

(without alignments)  
1972.033 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 604  
Sequence: 1 MNXIRITMNSALNMAVXVS.....TASGNSRGHFQASASVGYOM 604

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq.032802.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	77.6	604	22	AAU06181
2	59	9.8	72	21	AAU06181
3	59	9.8	407	22	AAU06184
4	59	9.8	433	22	AAU06185
5	59	9.8	502	22	AAU06186
6	59	9.8	512	22	AAU06182
7	59	9.8	513	22	AAU06183
8	59	9.8	589	20	AAU06173
9	59	9.8	589	22	AAU06173
10	59	9.8	591	20	AAU06173
11	59	9.8	591	20	AAU06173

#### ALIGNMENTS

12	59	9.8	591	20	AAU06173	A surface protein
13	59	9.8	591	21	AAU06173	BA5B029 amino acid
14	59	9.8	591	22	AAU06171	N. meningitidis PM
15	59	9.8	591	22	AAU06175	N. meningitidis EG
16	59	9.8	592	20	AAU06173	Amino acid sequenc
17	59	9.8	592	20	AAU06173	A surface protein
18	59	9.8	592	20	AAU06173	A surface protein
19	59	9.8	592	22	AAU06172	N. meningitidis H4
20	59	9.8	592	22	AAU06180	N. meningitidis Z2
21	59	9.8	594	20	AAU06173	A surface protein
22	59	9.8	594	20	AAU06173	A surface protein
23	59	9.8	594	21	AAU06174	BA5B029 amino acid
24	59	9.8	594	22	AAU06174	N. meningitidis EG
25	59	9.8	594	22	AAU06179	N. meningitidis BZ
26	59	9.8	598	20	AAU06173	A surface protein
27	59	9.8	598	20	AAU06173	A surface protein
28	59	9.8	598	22	AAU06177	N. meningitidis H1
29	59	9.8	598	22	AAU06178	N. meningitidis BZ
30	59	9.8	599	20	AAU06173	A surface protein
31	59	9.8	599	22	AAU06176	N. meningitidis H3
32	59	9.8	599	22	AAU06176	Neisserial conserv
33	59	9.8	599	22	AAU06176	Neisserial conserv
34	59	9.8	599	22	AAU06176	Neisserial conserv
35	59	9.8	599	22	AAU06176	Neisserial conserv
36	59	9.8	599	22	AAU06176	Neisserial conserv
37	59	9.8	599	22	AAU06176	Neisserial conserv
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39	59	9.8	599	22	AAU06176	Neisserial conserv
40	59	9.8	599	22	AAU06176	Neisserial conserv
41	59	9.8	599	22	AAU06176	Neisserial conserv
42	59	9.8	599	22	AAU06176	Neisserial conserv
43	59	9.8	599	22	AAU06176	Neisserial conserv
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45	59	9.8	599	22	AAU06176	Neisserial conserv

#### RESULT 1

AAU06181	Standard; Protein: 604 AA.
ID	AAU06181
AC	AAU06181
XX	24-0CT-2001 (first entry)
DT	24-0CT-2001 (first entry)
XX	N. meningitidis surface antigen Nhma consensus polypeptide sequence.
XX	Surface antigen Nhma: meningococcal disease: meningitis vaccine.
XX	Neisseria meningitidis.
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XX	/note= "Encoded by AGN"
XX	/note= "Encoded by NTG"
XX	51..108
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XX	109..120
XX	/label= C2
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XX	/note= "Variable region 2"
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FT /label= C3  
FT /note= "Conserved region 3"  
FT Misc-difference 174  
FT /note= "Encoded by TTN"  
FT Misc-difference 192  
FT /note= "Encoded by ATN"  
FT Region 199..220  
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FT /note= "Variable region 3"  
FT Region 221..239  
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FT /note= "Conserved region 4"  
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FT /note= "Encoded by AGN"  
FT Misc-difference 226..227  
FT /note= "Encoded by AANCAN"  
FT Misc-difference 229..230  
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FT /note= "Encoded by AAN"  
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FT /note= "Variable region 4"  
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FT /label= Unknown  
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FT Region 249..604  
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FT Misc-difference 249  
FT /note= "Encoded by AAN"  
FT Misc-difference 293  
FT /note= "Encoded by ATN"  
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FT /note= "Encoded by CAN"  
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XX  
PN W0200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001MO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
(UY00 ) UNIV QUEENSLAND.  
XX  
PA  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR MPI; 2001-486774/53.  
XX  
N-PSDB; AAS09171.  
XX  
PT New Nhma surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 10; Fig 1; 91pp; English.  
XX

CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhma  
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence represents N. meningitidis surface antigen Nhma  
CC consensus polypeptide sequence. The wild type Nhma polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains are  
CC also given in the present invention.  
XX  
SQ Sequence 604 AA;  
  
Query Match 77.6%; Score 469; DB 22; Length 604;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNXIXRIINWSALNAMYVSELTFRNHRKRASATVYXTAVLATLXATYQAXXXXXXXXXX 60  
DB 1 mxixriinwsalnawxyveltrnhktrasatvxtavlatlilxatvaxxxxxxxxxx 60  
  
QY XLXVXRXVXXXXXXXXXXEGXEXEXXXXXXXXXXXXXXXXXXXXXXTLKAGDLKIKQ 120  
DB 61 xlxvrxrvxxxxxxxxxxegexexxxxxxxxxxxxxxxxxxxxxxllkagdnllkq 120  
  
QY 121 XXXXXXXXXXXXXFTYSLKRLXLLXVYTEKLSFYANXXKVINISDTKGLNPAKXTAX 180  
DB 121 xxxxxxxxxxxxxxxffyslkkxllxlvxteklsfxanxxknixsdtkglnfakxtax 180  
  
QY 181 TNGDXYTHLNGISGTLFDLXAXXAXXXXXXXXXXXXTXAXXKXDVLAAGNRIKVKX 240  
DB 181 tngdxythlngisgtdldlaxxaxxxxxxxxxxxxtxaxxkxdvlagwnlikvxx 240  
  
QY 241 GXTXXXXXNDFVXTYDTVEFLSADTKTTVNVESKDNKGXTEVKIGAKTSVIEKDKGL 300  
DB 241 gtxcxxxxnndfvxttydtveflsadtktttvnnveskdnkgxtxevkigaktsviekdkgl 300  
  
QY 301 VTGKXXKXENSSIDXGELVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSQTXV 360  
DB 301 vtgkxxkxenssidxgeglvtakevidavnkagwrmttlangtqgdkfeytvsqtxv 360  
  
QY 361 TFPASGXTTATVSKDDGNTVYXDVVNGDALNNOQNSGMNLDKRAVAGSSGKXVSGN 420  
DB 361 tfpasyxttatvskddgntlvxydvngdalinvgdlqnsqwnldskavagssgkvysgn 420  
  
QY 421 VSPSKGKMEETVINAGNNIEIXKNGKNIDATSMXPOFSSVSLGAGADPTLSVDXXA 480  
DB 421 vpskgykmedetvinagnnieixrngknidatasmxpfssvslgagadpplsvdxxa 480  
  
QY 481 LNVGSXXXXNRPVRIITNVAPGVKEGDTVTVNAQLKGVAQNLNNXIDNVXGNRAGIAQAIAT 540  
DB 481 lnvgskxxnkrpvriltvnapgvkegdvtnvaqlkgyvaqnlmxiidnvxgnragiaqaiat 540  
  
QY 541 AGLXQATLPKSMMAIGGXTYXGAGYAIGYSSTISXXGNMXIKGTASGNRGRHGXASV 600  
DB 541 aglxqaylpgksmmaigyxtyxgagyaigyssisxxgnwxikgtasgnrghfxasv 600  
  
QY 601 GYOW 604  
DB 601 gyow 604  
  
QY 601 GYOW 604  
DB 601 gyow 604  
  
RESULT 2  
AAB37830  
ID AAB37830 standard; peptide; 72 AA.  
XX  
AC AAB37830;  
XX



CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 XX Sequence 591 AA;

Query Match 9.8%; Score 59; DB 22; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-49;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 YDYNVGDALNVNQI NSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVNNAGNNIEI 442  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 372 ydvnvgdalinvnq lqnsqwnldskavagssgkvisgnvpskxmdetvlnaagniel 430

## RESULT 15

AAU06175  
 ID AAU06175 standard; Protein; 591 AA.

AC AAU06175;

DT 24-OCT-2001 (first entry)

XX N. meningitidis EG329 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain EG329.

XX Location/Qualifiers

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FT 51..108  
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FT 121..124  
 /label= V2  
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FT 125..188  
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FT 189..210  
 /label= V3  
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FT 211..229  
 /label= C4  
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FT 230..236  
 /label= V4  
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FT 237..591  
 /label= C5  
 /note= "Conserved region 5"

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

PF 25-JAN-2001; 2001WO-AU00069.

PR 25-JAN-2000; 2000US-0177917.

PA (UYQU ) UNIV QUEENSLAND.

PI Peak IRA, Jennings MP;

DR WPI: 2001-488774/53.

DR N-PSDB; AAS09165.

PT New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria

XX meningitidis mutant polypeptides of the surface antigen Nhha

XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

XX characterised by deletions of non-conserved amino acids, particularly

XX the deletion of variable regions. The deletion mutants are useful in

XX diagnostics, therapeutic and prophylactic vaccines against a broader

XX spectrum of N. meningitidis, and in designing and/or screening of

XX medicaments. The mutant proteins when used as a vaccine can effectively

XX immunise against a broader spectrum of N. meningitidis strains than

XX would be expected from a corresponding wild-type surface antigen.

XX The present sequence representing the wild type surface antigen Nhha

XX from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences

XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

XX the present invention.

XX Sequence 591 AA;

XX Query Match 9.8%; Score 59; DB 22; Length 591;

XX Best Local Similarity 100.0%; Pred. No. 1,7e-49;

XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 YDYNVGDALNVNQI NSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVNNAGNNIEI 442

||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 372 ydvnvgdalinvnq lqnsqwnldskavagssgkvisgnvpskxmdetvlnaagniel 430

Search completed: July 3, 2002, 08:30:12

Job time: 1053 sec

WO200155182-A1.

02-AUG-2001.

XX

XX



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:30:39; Search time 13.48 Seconds

(without alignments)  
1734.912 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 604  
Sequence: 1 MNXIXRIIMNSALNAMYXS.....TASGNSRGHFGXSASVGYQW 604

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	8	1.3	400	1	PUR2_THEMA
5	7	1.2	87	1	SODC_ACTAC
6	7	1.2	127	1	FUR_SYN7
7	7	1.2	164	1	YOR2_AZOVI
8	7	1.2	187	1	SODC_HAEPN
9	7	1.2	187	1	SODC_HAEPN
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15	7	1.2	292	1	YAD0_SCHPO
16	7	1.2	294	1	YAD0_SCHPO
17	7	1.2	301	1	YAD0_SCHPO
18	7	1.2	315	1	YAD0_SCHPO
19	7	1.2	360	1	YAD0_SCHPO
20	7	1.2	407	1	YAD0_SCHPO
21	7	1.2	409	1	YAD0_SCHPO
22	7	1.2	429	1	YAD0_SCHPO
23	7	1.2	439	1	YAD0_SCHPO
24	7	1.2	466	1	YAD0_SCHPO
25	7	1.2	473	1	YAD0_SCHPO
26	7	1.2	496	1	YAD0_SCHPO
27	7	1.2	527	1	YAD0_SCHPO
28	7	1.2	555	1	YAD0_SCHPO
29	7	1.2	573	1	YAD0_SCHPO
30	7	1.2	653	1	YAD0_SCHPO
31	7	1.2	700	1	YAD0_SCHPO
32	7	1.2	714	1	YAD0_SCHPO
33	7	1.2	739	1	YAD0_SCHPO

34	7	1.2	739	1	PURL_LACCA	Q92b06 lactococcus
35	7	1.2	740	1	PURL_LACCA	P35852 lactobacill
36	7	1.2	796	1	YPC3_YEAST	P43573 saccharomyc
37	7	1.2	835	1	GLND_STRCO	O69873 streptomyc
38	7	1.2	1103	1	VG37_BPARI	O990b5 bacterioph
39	7	1.2	1108	1	EMBA_MYCAV	P71485 mycobacteri
40	7	1.2	1714	1	SYEP_DROME	P28668 drosophila
41	7	1.2	3092	1	IRAI_YEAST	P18963 saccharomyc
42	6	1.0	48	1	YK82_ARCFU	O28197 archaeglob
43	6	1.0	51	1	R27A_METTH	O26368 methanobact
44	6	1.0	55	1	YHFL_ECOLI	P43538 escherichia
45	6	1.0	56	1	RL33_RICPR	Q92c89 rickettsia

## ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
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5	SODC_PASMU	7	1.2	87	1	SODC_ACTAC
6	SODC_PASMU	7	1.2	127	1	FUR_SYN7
7	SODC_PASMU	7	1.2	164	1	YOR2_AZOVI
8	SODC_PASMU	7	1.2	187	1	SODC_HAEPN
9	SODC_PASMU	7	1.2	187	1	SODC_HAEPN
10	SODC_PASMU	7	1.2	222	1	YAD0_SCHPO
11	SODC_PASMU	7	1.2	237	1	YAD0_SCHPO
12	SODC_PASMU	7	1.2	246	1	YAD0_SCHPO
13	SODC_PASMU	7	1.2	259	1	YAD0_SCHPO
14	SODC_PASMU	7	1.2	292	1	YAD0_SCHPO
15	SODC_PASMU	7	1.2	292	1	YAD0_SCHPO
16	SODC_PASMU	7	1.2	294	1	YAD0_SCHPO
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22	SODC_PASMU	7	1.2	429	1	YAD0_SCHPO
23	SODC_PASMU	7	1.2	439	1	YAD0_SCHPO
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25	SODC_PASMU	7	1.2	473	1	YAD0_SCHPO
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FT METAL 113 113 ZINC (BY SIMILARITY).  
FT METAL 122 122 ZINC (BY SIMILARITY).  
FT METAL 125 125 ZINC (BY SIMILARITY).  
FT METAL 160 160 COPPER (BY SIMILARITY).  
FT DISULFID 86 182 BY SIMILARITY.  
FT CONFLICT 130 130 A -> V (IN REF. 2).  
SQ SEQUENCE 186 AA; 19718 MW; 34D702070EE0DDC CRC64;

Query Match 1.3%; Score 8; DB 1; Length 186;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKDGLV 301  
DB 89 KKDGLV 96

RESULT 2  
SODC\_ACTPL STANDARD; PRT; 190 AA.  
ID SODC\_ACTPL  
AC P24702; 059135; Created  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).  
GN SODC.  
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Actinobacillus.  
OX NCBI\_Taxid=715;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE III / ISOLATE 1421 (NIELSEN);  
RX MEDLINE=97101016; PubMed=8945543;  
RA Langford P.R., Loynds B.M., Kroll J.S.;  
RT Cloning and molecular characterization of Cu,Zn superoxide dismutase  
from Actinobacillus pleuropneumoniae.";  
RL Infect. Immun. 64:5035-5041(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S 4074 / SEROTYPE 1;  
RA Helie M.C., Sirols M., Ouellet C., Boissinot M.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 180-190 FROM N.A.  
RC STRAIN-SEROTYPE III / ISOLATE 1421 (NIELSEN);  
RX MEDLINE=92158680; PubMed=1741300;  
RA Loynds B.M., Langford P.R., Kroll J.S.;  
RT "recf in Actinobacillus pleuropneumoniae.";  
RL Nucleic Acids Res. 20:615-615(1992).  
RN [4]  
RP SEQUENCE OF 91-177 FROM N.A.  
RC STRAIN-SEROTYPE III / ISOLATE 1421 (NIELSEN);  
RX MEDLINE=96118708; PubMed=7496539;  
RA Kroll J.S., Langford P.R., Wilks K.E., Keil A.D.;  
RT "bacterial [Cu,Zn]-superoxide dismutase: phylogenetically distinct  
from the eukaryotic enzyme, and not so rare after all!";  
RL Microbiology 141:2271-2279(1995).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=20124004; PubMed=10656823;  
RA Forest K.T., Langford P.R., Kroll J.S., Getzoff E.D.;  
RT "Cu,Zn superoxide dismutase structure from a microbial pathogen  
establishes a class with a conserved dimer interface.";  
RL J. Mol. Biol. 296:145-153(2000).  
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE  
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.  
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC -1- COFACTOR: Copper and zinc.  
CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; X99396; CA67771.1; -;  
DR EMBL; U51440; AAB02816.1; -;  
DR EMBL; X63626; CAA45174.1; -;  
DR EMBL; X83123; CAA58204.1; -;  
DR PIR; S22161; S22161.  
DR PIR; S22815; S22815.  
DR PDB; 2AP5; 25-FEB-99.  
DR InterPro; IPR001424; SOD\_CU\_ZN.  
DR Pfam; PF00080; sodcu; 1.  
DR ProDom; PD000469; SOD\_CU\_ZN; 1.  
DR PROSITE; PS00087; SOD\_CU\_ZN.1; 1.  
DR PROSITE; PS00332; SOD\_CU\_ZN.2; 1.  
KW Oxidoreductase; Copper; Zinc; Periplasmic; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 190 SUPEROXIDE DISMUTASE [CU-ZN].  
FT METAL 83 83 COPPER.  
FT METAL 85 85 COPPER.  
FT METAL 108 108 COPPER AND ZINC.  
FT METAL 117 117 ZINC.  
FT METAL 126 126 ZINC.  
FT METAL 129 129 ZINC.  
FT METAL 164 164 COPPER.  
FT DISULFID 90 186  
FT CONFLICT 113 113 E -> D (IN REF. 2).  
FT CONFLICT 124 124 N -> D (IN REF. 2).  
FT CONFLICT 134 136 FVE -> TTA (IN REF. 2).  
SQ SEQUENCE 190 AA; 20207 MW; 5FC1F3148972DC83 CRC64;

Query Match 1.3%; Score 8; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKDGLV 301  
DB 93 KKDGLV 100

RESULT 3  
SODC\_HAEDU STANDARD; PRT; 199 AA.  
ID SODC\_HAEDU  
AC 059452; 059449; 059453;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).  
GN SODC.  
OS Haemophilus ducreyi.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_Taxid=730;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=35000;  
RX MEDLINE=97286949; PubMed=9143881;  
RA Langford P.R., Kroll J.S.;  
RT "Distribution, cloning, characterisation and mutagenesis of sodC, the  
gene encoding copper/zinc superoxide dismutase, a potential  
determinant of virulence, in Haemophilus ducreyi.";  
RL FEMS Immunol. Med. Microbiol. 17:235-242(1997).  
RN [2]  
RP SEQUENCE FROM N.A.

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RC STRAIN=35000;
RA MEDLINE=97149276; PubMed=8996084;
RA Stevens M.K., Hassett D.J., Radolf J.D., Hansen E.J.;
RT "Cloning and sequencing of the gene encoding the Cu,Zn-superoxide
RL dismutase of Haemophilus ducreyi."
RN Gene 183:35-40(1996).
RM [3]
RP SEQUENCE OF 100-186 FROM N.A.
RC STRAIN=35000;
RA MEDLINE=96118708; PubMed=7496539;
RA Kioll J.S., Langford P.R., Wilks K.E., Keil A.D.;
RT "Bacterial [Cu,Zn]-superoxide dismutase: phylogenetically distinct
RL from the eukaryotic enzyme, and not so rare after all!"
RM Microbiology 141:2271-2279(1995).
RC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS. MAY PLAY A ROLE IN THE
CC INTERACTIVE BIOLOGY OF ORGANISMS WITH THEIR HOSTS AND SO
CC CONTRIBUTE TO THEIR CAPACITY TO CAUSE DISEASE.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Copper and zinc.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
CC -----
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CC -----
DR EMBL: X98737; CA67289.1; -
DR EMBL: U47664; AAB41293.1; -
DR EMBL: X83125; CA58206.1; -
DR HSSP: P24702; 2APS.
DR InterPro: IPR001424; SOD_CU_ZN.
DR Pfam: PF00080; sdcu; 1.
DR PROSITE: PS00087; SOD_CU_ZN_1; 1.
DR PROSITE: PS00332; SOD_CU_ZN_2; 1.
KW Oxidoreductase; Copper; Zinc; Periplasmic; Signal.
FT SIGNAL 1 22
FT CHAIN 1 199
FT METAL 92 92 COPPER (BY SIMILARITY).
FT METAL 94 94 COPPER (BY SIMILARITY).
FT METAL 117 117 COPPER AND ZINC (BY SIMILARITY).
FT METAL 126 126 ZINC (BY SIMILARITY).
FT METAL 135 135 ZINC (BY SIMILARITY).
FT METAL 138 138 ZINC (BY SIMILARITY).
FT METAL 173 173 COPPER (BY SIMILARITY).
FT DISULFID 99 195 BY SIMILARITY.
SQ SEQUENCE 199 AA; 21402 MW; 841D3210AB2BC06C CRC64;

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Query Match 1.3%; Score 8; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 294 KKKDKLV 301
DB 102 KKKDKLV 109

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RESULT 4
ID PUR2_THEME STANDARD; PRT: 400 AA.
AC 09XOX7:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide
ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase).

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GN PURD OR TM1250.
OS Bacterioga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=3336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RA MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL genome sequence of Thermotoga maritima."
CC Nature 399:323-329(1999).
CC -1- CATALYTIC ACTIVITY: ATP + 5-phosphoribosylamine + glycine = ADP +
CC phosphate + 5'-phosphoribosylglycinamide.
CC -1- PATHWAY: SECOND STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE GARS FAMILY.
CC -----
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CC -----
DR EMBL: AE001780; AAD36325.1; -
DR HSSP: P15640; IGSO.
DR TIGR: TM1250; -
DR InterPro: IPR000115; GARS.
DR Pfam: PF01071; GARS; 2.
DR Pfam: PF02842; GARS_B; 1.
DR Pfam: PF02843; GARS_C; 1.
DR Pfam: PF02844; GARS_N; 1.
DR PROSITE: PS00184; GARS; 1.
KW Purine biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 400 AA; 44326 MW; 411CE014DD7DE90F CRC64;

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Query Match 1.3%; Score 8; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 295 EKKDKLV 302
DB 351 EKKDKLV 358

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RESULT 5
ID SODC_ACTAC STANDARD; PRT: 87 AA.
AC 059081:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Fragment).
GN SODC.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74;
RA MEDLINE=96118708; PubMed=7496539;
RA Kioll J.S., Langford P.R., Wilks K.E., Keil A.D.;
RT "Bacterial [Cu,Zn]-superoxide dismutase: phylogenetically distinct
RL from the eukaryotic enzyme, and not so rare after all!"

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RL Microbiology 141:2271-2279(1995).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) -> O(2) + H(2)O(2).
CC -1- COFACTOR: Copper and zinc.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
CC -----
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CC -----
DR EMBL: X8122; CA58203.1; -.
DR HSSP: P24702; 2APS.
DR InterPro: IPR001424; SOD_CU_ZN.
DR Pfam: PF00080; sodcu. 1.
DR ProDom: PD000469; SOD_CU_ZN. 1.
DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE: PS00332; SOD_CU_ZN_2; PARTIAL.
DR Oxidoreductase; Copper; Zinc; Periplasmic.
FT NON_TER 1 1
FT METAL 18 18 COPPER AND ZINC (BY SIMILARITY).
FT METAL 27 27 ZINC (BY SIMILARITY).
FT METAL 36 36 ZINC (BY SIMILARITY).
FT METAL 39 39 ZINC (BY SIMILARITY).
FT METAL 74 74 COPPER (BY SIMILARITY).
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 9287 MW; 6704173D25976550 CRC64;

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Query Match 1.28; Score 7; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 294 KENKDKL 300
    |||||
Db 3 KENKDKL 9

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RESULT 6
FUR_SINYP7 STANDARD; PRT; 127 AA.
AC Q55244;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ferric uptake regulation protein (Ferric uptake regulator).
GN FUR.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96262718; PubMed=8704986;
RA Chasseman M., Straus N.A.;
RT "Fur regulates the expression of iron-stress genes in the
RT cyanobacterium Synechococcus sp. strain PCC 7942.";
RL Microbiology 142:1469-1476(1996).
CC -1- FUNCTION: ACTS AS A GLOBAL, NEGATIVE CONTROLLING ELEMENT. EMPLOYING
CC FE(2+) AS A COFACTOR TO BIND THE OPERATOR OF THE RERESSED GENES
CC REGULATES GENES INVOLVED IN IRON SCAVENGING OR PHOTOSYNTHETIC
CC ELECTRON TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FUR FAMILY.
CC -----
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CC -----
DR EMBL: L41065; AAB41546.1; -.
DR InterPro: IPR002481; FUR.
DR Pfam: PF01475; FUR. 1.
DR ProDom: PD002003; FUR. 1.
KW Transcription regulation; Repressor; DNA-binding; Iron.
FT DOMAIN 73 76 HIS-RICH.
SQ SEQUENCE 127 AA; 14451 MW; 71586B10BCA69426 CRC64;

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Query Match 1.28; Score 7; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 285 KIGAKTS 291
    |||||
Db 95 KIGAKTS 101

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RESULT 7
YOR2_AZOVI STANDARD; PRT; 164 AA.
ID YOR2_AZOVI
AC Q69219;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical 17.8 kDa protein (ORF2).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98250785; PubMed=9582371;
RA Zheng L., Gash V.L., Flint D.H., Dean D.R.;
RT "Assembly of iron-sulfur clusters. Identification of an iscSUA-hscBA-
RT id gene cluster from Azotobacter vinelandii.";
RL J. Biol. Chem. 273:13264-13272(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0074 (REF2) FAMILY.
CC -----
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CC -----
DR EMBL: AF010139; AAC24480.1; -.
DR InterPro: IPR000944; UPF0074.
DR Pfam: PF02082; UPF0074. 1.
DR ProDom: PD003632; UPF0074. 1.
DR PROSITE: PS01332; UPF0074. 1.
KW Hypothetical protein.
SQ SEQUENCE 164 AA; 17831 MW; B03C777BF30654CE CRC64;

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Query Match 1.28; Score 7; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 324 EVIDAVN 330
    |||||
Db 78 EVIDAVN 84

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RESULT 8
SODC_HAEIN

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ID SODC\_HAEIN STANDARD: PRT: 187 AA.  
AC P25841;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Superoxide dismutase [Cu-Zn] like precursor.  
GN SODC.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-NCIC 8468 / SEROTYPE B;  
RX MEDLINE=92041655; PubMed=1938942;  
RA Kroll J.S., Langford P.R., Loynds B.M.;  
RT "Copper-zinc superoxide dismutase of Haemophilus influenzae and H. parainfluenzae."  
RT J. Bacteriol. 173:7449-7457(1991).  
CC - FUNCTION: THIS PROTEIN LACKS ENZYMATIC ACTIVITY (PROBABLY BECAUSE OF THE PRESENCE OF A TYROSINE INSTEAD OF AN HISTIDINE AT RESIDUE 82).  
CC - COFACTOR: Copper and zinc.  
CC - SUBUNIT: HOMODIMER.  
CC - SUBCELLULAR LOCATION: Periplasmic (Potential).  
CC - SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: M84012; AAA24953.1;  
DR PIR: A41654; A41654.  
DR HSSP: P24702; 2APS.  
DR InterPro: IPR001424; SOD\_CU\_ZN.  
DR Pfam: PF00080; sodcu.1.  
DR ProDom: PD000469; SOD\_CU\_ZN.1.  
DR PROSITE: PS00087; SOD\_CU\_ZN.1; FALSE\_NEG.  
DR PROSITE: PS00332; SOD\_CU\_ZN.2; 1.  
KW Copper; zinc; Periplasmic; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 187  
FT METAL 80 80  
FT SITE 82 82  
FT METAL 105 105  
FT METAL 114 114  
FT METAL 123 123  
FT METAL 126 126  
FT METAL 161 161  
FT DISULFID 87 183  
SQ SEQUENCE 187 AA; 19536 MW; 3EE95EFPD52425B3 CRC64;

Query Match 1.2%; Score 7; DB 1; Length 187;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKDGL 300  
DB 90 KKDGL 96

RESULT 9  
SODC\_HAEPA STANDARD: PRT: 187 AA.  
AC P25842;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).  
GN SODC.  
OS Haemophilus parainfluenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1391;  
RX MEDLINE=92041655; PubMed=1938942;  
RA Kroll J.S., Langford P.R., Loynds B.M.;  
RT "Copper-zinc superoxide dismutase of Haemophilus influenzae and H. parainfluenzae."  
RT J. Bacteriol. 173:7449-7457(1991).  
CC - FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.  
CC - DISMUTATION: MAY CONFER SURVIVAL ADVANTAGE BY ACCELERATING PEROXIDE, DISRUPTIVE TO THE NORMAL MUCCOCILIARY CLEARANCE PROCESS IN THE HOST.  
CC - CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC - COFACTOR: Copper and zinc.  
CC - SUBUNIT: HOMODIMER.  
CC - SUBCELLULAR LOCATION: Periplasmic (Potential).  
CC - SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: M84013; AAA24954.1;  
DR PIR: B41654; B41654.  
DR HSSP: P24702; 2APS.  
DR InterPro: IPR001424; SOD\_CU\_ZN.  
DR Pfam: PF00080; sodcu.1.  
DR ProDom: PD000469; SOD\_CU\_ZN.1.  
DR PROSITE: PS00087; SOD\_CU\_ZN.1; 1.  
DR PROSITE: PS00332; SOD\_CU\_ZN.2; 1.  
KW Oxidoreductase; Copper; zinc; Periplasmic; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 187  
FT METAL 80 80  
FT METAL 82 82  
FT METAL 105 105  
FT METAL 114 114  
FT METAL 123 123  
FT METAL 126 126  
FT METAL 161 161  
FT DISULFID 87 183  
SQ SEQUENCE 187 AA; 19510 MW; AOC3A61EFAF201D5 CRC64;

Query Match 1.2%; Score 7; DB 1; Length 187;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKDGL 300  
DB 90 KKDGL 96

RESULT 10  
YACD\_SCHPO STANDARD: PRT: 222 AA.  
AC Q10092;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Hypothetical 24.2 kDa protein C11D3.13 in chromosome I.

GN SPAC11D3.13.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 NC NCB1\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE YMR322C/YOR391C/YPL280W (YEAST),  
 SPAC11F.06/SPAC3H10.02C/SPAC11D3.13 (S.POMBE FAMILY).  
 CC -----  
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 CC -----  
 DR EMBL: Z68166; CAA92314.1; -  
 DR InterPro: IPR002818; TH1J.  
 DR Pfam: PF01965; TH1J; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 222 AA; 24225 MW; 9AA66B806AF17AD6 CRC64;

Query Match 1.2%; Score 7; DB 1; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 DGKLVWG 303  
 |||||  
 DB 197 DGKLVWG 203

RESULT 11  
 YMG9\_YEAST  
 ID YMG9\_YEAST STANDARD; PRT; 237 AA.  
 AC 004902;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 26.0 kDa protein in FET4-ERR1 intergenic region.  
 GN YMR322C OR YMG924.14C  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 NC NCB1\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / AB972;  
 RA Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE YMR322C/YOR391C/YPL280W (YEAST),  
 SPAC11F.06/SPAC3H10.02C/SPAC11D3.13 (S.POMBE FAMILY).  
 CC -----  
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 CC -----  
 DR EMBL: Z54141; CAA90840.1; -  
 DR SGD: S0004941; YMR322C.  
 DR InterPro: IPR002818; TH1J.  
 DR Pfam: PF01965; TH1J; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 237 AA; 26039 MW; 004EA3E702332905 CRC64;

Query Match 1.2%; Score 7; DB 1; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 DGKLVWG 303  
 |||||  
 DB 212 DGKLVWG 218

RESULT 12  
 VMTV\_LAMB  
 ID VMTV\_LAMB STANDARD; PRT; 246 AA.  
 AC P03733;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-NOV-1988 (Rel. 09, Last annotation update)  
 DE Major tail protein V.  
 GN V.  
 OS Bacteriophage lambda.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 CC Lambda phage group.  
 NC NCB1\_TaxID=10710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83189071; PubMed=6221115;  
 RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;  
 "Nucleotide sequence of bacteriophage lambda DNA."  
 J. Mol. Biol. 162:729-773(1982).  
 CC -1- FUNCTION: GENE V PROTEIN IS THE MAJOR COMPONENT OF THE TAIL. IT  
 CC MAKES UP THE TUBULAR PORTION OF THE TAIL, WHICH IS COMPOSED OF  
 CC ABOUT 32 HEXAMERIC DISCS. THERE ARE 135-212 COPIES OF GENE V  
 CC PROTEIN PER MATURE PHAGE.  
 CC -----  
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 CC -----  
 DR EMBL: J02459; AAA96545.1; -  
 DR PIR: A04359; TUBPV.  
 DR InterPro: IPR003343; Big\_2.  
 DR Pfam: PF02368; Big\_2; 1.  
 KW SEQUENCE 246 AA; 25810 MW; 3E9B2124F2E80CB CRC64;

Query Match 1.2%; Score 7; DB 1; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 VTAKVVI 326  
 |||||  
 DB 131 VTAKVVI 137

RESULT 13  
 PPH\_MYCPN  
 ID PPH\_MYCPN STANDARD; PRT; 259 AA.  
 AC P75525;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative protein phosphatase (EC 3.1.3.16).  
 GN MPN247 OR MP585.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollitutes;  
 CC Mycoplasmataceae; Mycoplasma.  
 NC NCB1\_TaxID=2104;  
 RN [1]



RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 29342 / M129;  
RX MEDLINE=97105885; PubMed=8948633;  
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,  
RT Herrmann R.;  
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
pneumoniae.";  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -I- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2O) -> A PROTEIN +  
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).  
CC -I- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.  
CC -----  
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CC -----  
DR EMBL; AE000057; AAB96233.1;  
DR InterPro; IPR001932; PP2C\_domain.  
DR InterPro; IPR003643; Putat\_PPase.  
DR Pfam; PF00481; PP2C; 2.  
DR PRODOM; PD006823; Putat\_PPase; 1.  
DR SMART; SM00332; PP2C; 1.  
DR SMART; SM00332; PP2C; 1.  
KW Hypothetical protein; Hydrolase; Complete proteome.  
KW DOMAIN 19 259 PP2C-LIKE.  
FT SEQUENCE 259 AA; 29689 MW; 4EE599CD210A66D8 CRC64;  
SQ

Query Match 1.2%; Score 7; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 TATVSKD 375  
|||||||  
DB 176 TATVSKD 182

RESULT 14  
NPM\_MOUSE STANDARD: PRT: 292 AA.  
AC Q61937;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin)  
DE (Nucleolar protein NO38).  
GN NPM1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89120362; PubMed=3219912;  
RA Schmidt-Zachmann M.S., Franke W.W.;  
RT "DNA cloning and amino acid sequence determination of a major  
RT constituent protein of mammalian nucleoli. Correspondence of the  
RT nucleoplasmic-related protein NO38 to mammalian protein B23.";  
RL Chromosoma 96:417-426(1988).  
CC -I- FUNCTION: ASSOCIATED WITH NUCLEOLAR RIBONUCLEOPROTEIN STRUCTURES  
CC AND BIND SINGLE-STRANDED NUCLEIC ACIDS. IT MAY FUNCTION IN THE  
CC ASSEMBLY AND/OR TRANSPORT OF RIBOSOME.  
CC -I- SUBCELLULAR LOCATION: NUCLEAR. GENERALLY NUCLEOLAR, BUT IS  
CC TRANSLOCATED TO THE NUCLEOLAR PLASM IN CASE OF SERUM STARVATION OR  
CC TREATMENT WITH ANTICANCER DRUGS.  
CC -I- PTM: PHOSPHORYLATED.  
CC -I- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; M33212; AAA39801.1;  
DR MGD; MGI:106184; Npm1.  
DR InterPro; IPR004301; Nucleoplasmn.  
DR Pfam; PF03066; Nucleoplasmn; 1.  
KW Nuclear protein; Phosphorylation; RNA-binding.  
FT DOMAIN 1 9  
FT DOMAIN 120 132 MET-RICH.  
FT DOMAIN 152 157 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 158 187 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 190 196 ASP/GLU-RICH (HIGHLY ACIDIC).  
FT MOD\_RES 125 125 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 125 125 PHOSPHORYLATION (BY SIMILARITY).  
FT MOD\_RES 185 185 PHOSPHORYLATION (BY CK2) (POTENTIAL).  
FT MOD\_RES 198 198 PHOSPHORYLATION (BY SIMILARITY).  
FT SEQUENCE 292 AA; 32560 MW; E68750C549ED25E6 CRC64;  
SQ

Query Match 1.2%; Score 7; DB 1; Length 292;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 462 VSLGAGA 468  
|||||||  
DB 47 VSLGAGA 53

RESULT 15  
NPM\_RAT STANDARD: PRT: 292 AA.  
AC P13084; Q64269; O63698;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin)  
DE (Nucleolar protein NO38).  
GN NPM1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (B23.1).  
RX MEDLINE=88330763; PubMed=3417636;  
RA Chang J.-H., Dumbat T.S., Olson M.O.J.;  
RT "cDNA and deduced primary structure of rat protein B23, a nucleolar  
RT protein containing highly conserved sequences.";  
RL J. Biol. Chem. 263:12824-12827(1988).  
RN [2]  
RP SEQUENCE FROM N.A. (B23.2).  
RX MEDLINE=89308567; PubMed=2745414;  
RA Chang J.-H., Olson M.O.J.;  
RT "A single gene codes for two forms of rat nucleolar protein B23  
RT mRNA.";  
RL J. Biol. Chem. 264:11732-11737(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91009311; PubMed=2211699;  
RA Chang J.-H., Olson M.O.J.;  
RT "Structure of the gene for rat nucleolar protein B23.";  
RL J. Biol. Chem. 265:18227-18233(1990).  
CC -I- FUNCTION: ASSOCIATED WITH NUCLEOLAR RIBONUCLEOPROTEIN STRUCTURES  
CC AND BIND SINGLE-STRANDED NUCLEIC ACIDS. IT MAY FUNCTION IN THE  
CC ASSEMBLY AND/OR TRANSPORT OF RIBOSOME.  
CC -I- SUBUNIT: DISULFIDE-LINKED DIMERS UNDER CERTAIN CONDITIONS.  
CC -I- SUBCELLULAR LOCATION: NUCLEAR. GENERALLY NUCLEOLAR, BUT IS  
CC TRANSLOCATED TO THE NUCLEOLAR PLASM IN CASE OF SERUM STARVATION OR  
CC TREATMENT WITH ANTICANCER DRUGS.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: B23.1 (SHOWN HERE) AND B23.2;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- PTM: PHOSPHORYLATED.  
CC -1- PTM: THE N-TERMINUS IS BLOCKED.  
CC -1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.  
CC -----  
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CC -----  
DR EMBL: J03969: AAA40796.1: -;  
DR EMBL: M37039: AAA41730.1: -;  
DR EMBL: M37035: AAA41730.1: JOINED.  
DR EMBL: M37036: AAA41730.1: JOINED.  
DR EMBL: M37037: AAA41730.1: JOINED.  
DR EMBL: M37038: AAA41730.1: JOINED.  
DR EMBL: M37041: AAA41731.1: -;  
DR EMBL: M37035: AAA41731.1: JOINED.  
DR EMBL: M37036: AAA41731.1: JOINED.  
DR EMBL: M37037: AAA41731.1: JOINED.  
DR EMBL: M37038: AAA41731.1: JOINED.  
DR EMBL: M37040: AAA41731.1: JOINED.  
DR EMBL: M25062: AAA40795.1: -;  
DR EMBL: J04943: AAA40794.1: -;  
DR EMBL: J04944: AAA40793.1: -;  
DR PIR: A28939: A28939.  
DR InterPro: IPR004301: Nucleoplasmin.  
DR Pfam: PF03066: Nucleoplasmin: 1.  
KW Nuclear protein; Phosphorylation; RNA-binding; Alternative splicing.  
FT DOMAIN 1 9 MET-RICH  
FT DOMAIN 120 132 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 152 157 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 158 187 ASP/GLU-RICH (HIGHLY ACIDIC).  
FT DOMAIN 190 196 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 125 125 PHOSPHORYLATION.  
FT MOD\_RES 185 185 PHOSPHORYLATION (BY CK2) (POTENTIAL).  
FT MOD\_RES 198 198 PHOSPHORYLATION.  
FT VARSPPLIC 256 292 GGSLLPKVEAKFTINVKNCFRMTDDEAIQIDLMQWRKSL ->  
AH (IN ISOFORM B23.2).  
SQ SEQUENCE 292 AA; 32560 MW; 1372A474F9ED2457 CRC64;

QY 462 VSIGAGA 468  
|||||  
Db 47 VSIGAGA 53

Search completed: July 3, 2002, 08:34:30  
Job time: 231 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:26:29 ; Search time 20.95 Seconds  
(without alignments)  
2770.308 Million cell updates/sec

Title: US-09-771-382-11

Perfect score: 604

Sequence: 1 MNXIXRIINNSALNANVXVS.....TASGNSRGHFGXSASVGYQM 604

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	9.8	591	2	G81133
2	59	9.8	592	2	A81888
3	12	2.0	298	2	I64138
4	8	1.3	98	2	I39650
5	8	1.3	199	2	JC5718
6	8	1.3	400	2	D72277
7	8	1.3	438	2	B83295
8	8	1.3	498	2	B95998
9	8	1.3	574	2	A69196
10	8	1.3	1797	2	F69195
11	7	1.2	87	2	I39485
12	7	1.2	110	2	AD0902
13	7	1.2	111	2	AD0425
14	7	1.2	120	2	B69456
15	7	1.2	157	2	A75398
16	7	1.2	164	2	T44280
17	7	1.2	171	2	A11962
18	7	1.2	173	2	C83839
19	7	1.2	180	2	T34110
20	7	1.2	183	2	S73086
21	7	1.2	187	1	A41654
22	7	1.2	187	1	B41654
23	7	1.2	201	2	A98970
24	7	1.2	201	2	G90767
25	7	1.2	209	2	G85717
26	7	1.2	220	2	H85742
27	7	1.2	222	2	T37522
28	7	1.2	237	2	S65313
29	7	1.2	246	1	TLBPVL

30	7	1.2	246	2	H90833	major tail protein
31	7	1.2	250	2	A90900	hypothetical prote
32	7	1.2	250	2	A90997	hypothetical prote
33	7	1.2	250	2	G85817	hypothetical prote
34	7	1.2	253	2	H83238	probable peptidyl-
35	7	1.2	256	2	B85691	probable tail comp
36	7	1.2	257	2	A34168	nucleolar phosphop
37	7	1.2	259	2	S73911	protein phosphatase
38	7	1.2	264	2	D97344	amino acid (probab
39	7	1.2	292	2	A28939	nucleophosmin - ra
40	7	1.2	292	2	A36089	nucleolar phosphop
41	7	1.2	292	2	I52858	nucleolar protein
42	7	1.2	292	2	JC4741	mosquitoicidal toxi
43	7	1.2	294	1	A32915	nucleophosmin - hu
44	7	1.2	301	2	B35694	cut2 protein - fis
45	7	1.2	315	2	T06944	DNA-directed RNA p

#### ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: G81133

R:Rettein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Piazza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <TER>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AA41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 9.8%; Score 59; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.8e-51;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YVNVNGDALNVNOLNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDEYNNAGNNIEI 442  
Db 372 YVNVNGDALNVNOLNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDEYNNAGNNIEI 430

RESULT 2

A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

roldroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: A81775; MUID:20222556

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1200

Query Match 9.8%; Score 59; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.8e-51;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDYNVGDALNVNOLNOLNSGMWLDKRAVAGSSGKYISGNVSPSKRMPTVINANNIEI 442  
|||||  
DB 372 YDYNVGDALNVNOLNOLNSGMWLDKRAVAGSSGKYISGNVSPSKRMPTVINANNIEI 430

## RESULT 3

164138

adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997

C:Accession: 164138

R:Reischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kjerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Meldman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; M0ID:95350630

A:Accession: 164138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 &lt;TIGR&gt;

A:Cross-references: GB:U32846; GB:I42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 2.0%; Score 12; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 KDVLNAGWNIGK 237  
|||||

DB 200 KDVLNAGWNIGK 211

## RESULT 4

139650

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Actinobacillus pleuropneumoniae (fragments)

C:Species: Actinobacillus pleuropneumoniae

C:Date: 16-Aug-1996 #sequence\_revision 05-Mar-1999 #text\_change 20-Jun-2000

C:Accession: 139650; S22815; S22161

R:Kroll, J.S.; Langford, P.R.; Wilks, K.E.; Keil, A.D.

Microbiology 141, 2271-2279, 1995

A:Title: Bacterial [Cu Zn]-superoxide dismutase: phylogenetically distinct from the euk

A:Reference number: I39485; M0ID:96118708

A:Accession: 139650

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-87 &lt;KRO&gt;

A:Cross-references: EMBL:X83123; NID:g1019747; PIDN:CAA58204.1; PID:g1019748

R:Lojnds, B.M.; Langford, P.R.; Kroll, J.S.

Nucleic Acids Res. 20, 615, 1992

A:Title: recf in Actinobacillus pleuropneumoniae.

A:Reference number: S22813; M0ID:92158680

A:Accession: S22815

A:Molecule type: DNA

A:Residues: 88-98 &lt;LOY&gt;

A:Cross-references: EMBL:X63626; NID:g38951; PIDN:CAA5174.1; PID:g1333704

A:Note: this sequence was submitted to the EMBL Data Library, December 1991

A:Note: neither the complete nucleic acid sequence nor the complete translation are show

C:Genetics:

A:Gene: sodC

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: superoxide dismutase (Cu-Zn)

C:Keywords: copper; metalloprotein; oxidoreductase; zinc

F:18,27,36,39/Binding site: zinc (His, His, His, Asp) #status predicted

F:91/Active site: Arg #status predicted

Query Match 1.3%; Score 8; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKKDGKLV 301  
|||||

DB 3 KKKDGKLV 10

## RESULT 5

JC5718

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) precursor - Haemophilus ducreyi

C:Species: Haemophilus ducreyi

C:Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 18-Jun-1999

C:Accession: JC5718

R:Stevens, M.K.; Hassett, D.J.; Radolf, J.D.; Hansen, E.J.

Gene 183, 35-40, 1996

A:Title: Cloning and sequencing of the gene encoding the Cu,Zn-superoxide dismutase o

A:Reference number: JC5718; M0ID:97149276

A:Accession: JC5718

A:Molecule type: DNA

A:Residues: 1-199 &lt;STE&gt;

A:Cross-references: GB:U47664; NID:g1305411; PIDN:AB841293.1; PID:g1305412

C:Genetics:

A:Gene: sodC

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxyg

C:Superfamily: superoxide dismutase (Cu-Zn)

C:Keywords: copper; metalloprotein; oxidoreductase; zinc

F:1-22/Domain: signal sequence #status predicted &lt;Sig&gt;

F:23-199/Product: superoxide dismutase (Cu-Zn) #status predicted &lt;MAT&gt;

F:92,94,117,173/Binding site: copper (His) #status predicted

F:99-195/Disulfide bonds: #status predicted

F:192/Active site: Arg #status predicted

Query Match 1.3%; Score 8; DB 2; Length 199;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KKKDGKLV 301  
|||||

DB 102 KKKDGKLV 109

## RESULT 6

D72277

phosphoribosylamine--glycine ligase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: D72277

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; M0ID:99287316

A:Accession: D72277

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 &lt;ARN&gt;

A:Cross-references: GB:AE001780; GB:AE000512; NID:g4981796; PIDN:AAD36325.1; PID:g498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1250

C:Superfamily: phosphoribosylamine--glycine ligase; phosphoribosylamine--glycine liase

Query Match 1.3%; Score 8; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 EKDGLVT 302  
|||||||  
DB 351 EKDGLVT 358

RESULT 7  
B83295  
hypothetical protein PA2794 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: B83295  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; Lim,  
-; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337  
A:Accession: B83295  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-438 <STO>  
A:Cross-references: GB:AE004707; GB:AE004091; NID:g9948876; PIDN:AAG06182.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2794

Query Match 1.3%; Score 8; DB 2; Length 438;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 KAVAGSSG 414  
|||||||  
DB 274 KAVAGSSG 281

RESULT 8  
B95998  
Probable sugar uptake ABC transporter ATP-binding protein SMD21422 [imported] - Sinorhiz  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: B95998  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: B95998  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-498 <KUR>  
A:Cross-references: GB:AL591985; PIDN:CAC49650.1; PID:g15141137; GSPDB:GN00167  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, J.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kallman, S.; Keating, D.H.; Kiss, E.; Kemp, C.; Leilaure,  
heault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMD21422  
A:Genome: plasmid

Query Match 1.3%; Score 8; DB 2; Length 498;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 ADAPPLSV 475  
|||||||  
DB 90 ADAPPLSV 97

RESULT 9  
A69196  
cell surface glycoprotein (s-layer protein) - Methanobacterium thermoautotrophicum (s

C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C:Accession: A69196  
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T  
; Olu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,  
k, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514  
A:Accession: A69196  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-574 <MTH>  
A:Cross-references: GB:AE000851; GB:AE000666; NID:g2621803; PIDN:AAB85224.1; PID:g262  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH719  
A:Start codon: TTG

Query Match 1.3%; Score 8; DB 2; Length 574;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 TVNINAGN 438  
|||||||  
DB 482 TVNINAGN 489

RESULT 10  
F69195  
cell surface glycoprotein (s-layer protein) - Methanobacterium thermoautotrophicum (s  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Dec-1997  
C:Accession: F69195  
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T  
; Olu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,  
k, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu  
A:Reference number: A69000; MUID:98037514  
A:Accession: F69195  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1197 <MTH>  
A:Cross-references: GB:AE000666  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH716

Query Match 1.3%; Score 8; DB 2; Length 1797;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 TVNINAGN 438  
|||||||  
DB 1705 TVNINAGN 1712

RESULT 11  
139485  
superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Actinobacillus actinomycetemcomitans (fr  
C:Species: Actinobacillus actinomycetemcomitans  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 18-Jun-1999  
C:Accession: 139485  
R:Kroll, J.S.; Langford, P.R.; Wilks, K.E.; Kell, A.D.  
Microbiology 141, 2271-2279, 1995

A:Title: Bacterial [Cu,Zn]-superoxide dismutase: phylogenetically distinct from the euk  
A:Reference number: I39485; M0ID:96118708  
A:Accession: I39485  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <RES>  
A:Cross-references: EMBL:X83122; NID:g1019745; PIDN:CA58203.1; PID:g1019746  
C:Genetics:  
A:Gene: sodC  
C:Function:  
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C:Superfamily: superoxide dismutase (Cu-Zn)  
C:Keywords: copper; metalloprotein; oxidoreductase; zinc  
F:18,27,36,39/Binding site: zinc (His, His, His, Asp) #status predicted

Query Match 1.2%; Score 7; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 KEXDGL 300  
|||||  
DB 3 KEXDGL 9

RESULT 12  
AD0902  
protein-export membrane protein [imported] - Salmonella enterica subsp. enterica serovar  
C:Species: Salmonella enterica subsp. enterica serovar Typh  
A:Note: this species has also been called Salmonella typh  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD0902  
R:Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
th, T.; Conerton, P.; Croxin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AD0902  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-110 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD07810.1; PID:g16504358; GSPDB:GN00176  
C:Genetics:  
A:Gene: secG  
C:Superfamily: protein-export protein secG

Query Match 1.2%; Score 7; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TAVIATL 42  
|||||  
DB 56 TAVIATL 62

RESULT 13  
AD0425  
protein-export membrane protein [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AD0425  
R:Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0425  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-111 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92728.1; PID:g15981423; GSPDB:GN00175  
C:Genetics:  
A:Gene: secG  
C:Superfamily: protein-export protein secG

Query Match 1.2%; Score 7; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TAVIATL 42  
|||||  
DB 56 TAVIATL 62

RESULT 14  
B69456  
lungsten formylmethanofuran dehydrogenase, subunit D (fwcd-1) homolog - Archaeoglobus  
C:Species: Archaeoglobus fulgidus  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 21-Jul-2000  
C:Accession: B69456  
R:Kienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,  
Smith, H.O.; Mosee, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
A:Reference number: A69250; MUID:98049343  
A:Accession: B69456  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-120 <KLE>  
A:Cross-references: GB:AE000989; GB:AE000782; NID:g2689312; PIDN:AAB89592.1; PID:g264

Query Match 1.2%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 GYKGDV 506  
|||||  
DB 46 GYKGDV 52

RESULT 15  
A75398  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: A75398  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J  
., Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: A75398  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-157 <WHI>  
A:Cross-references: GB:AE001986; GB:AE000513; NID:g6459162; PIDN:AAF10987.1; PID:g645  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1406  
A:Map position: 1

Query Match 1.2%; Score 7; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	501	VKGDVT	507
Db	51	VKGDVT	57

Search completed: July 3, 2002, 08:31:01  
Job time: 272 sec

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PI	Peak IRA, Jennings MP;
XX	
DR	WPI: 2001-488774/53.
DR	N-PSDB; AAS09172.
XX	
PT	New Nhha surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 12; Fig 5; 91pp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhha
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence represents N. meningitidis strain PMC21 surface
CC	antigen Nhha deletion mutant #1.
XX	
SO	Sequence 512 AA;
	Query Match 9.8%; Score 59; DB 22; Length 512;
	Best Local Similarity 100.0%; Pred. No. 1,5e-49;
	Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	384 YDVNYGDAALNWNQLONSGWNLDKSAVAGSSGKRVISGNAVSPSKGKMDFTVINAGNNIEI 442
Db	293 ydvnygdalnvngqlngsqnwdskavagssgkvisgnvpskgykndevrlnaagniel 351
RESULT 7	
AAU06183	AAU06183 standard; Protein; 513 AA.
XX	AAU06183;
AC	
XX	24-OCF-2001 (first entry)
XX	
DE	N. meningitidis H41 Nhha deletion mutant.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW	mutant; muteln.
OS	Neisseria meningitidis strain H41.
OS	Synthetic.
XX	
FH	Key
FT	Peptide
FT	Protein
FT	Location/Qualifiers
FT	1..51
FT	/label= Signal_peptide
FT	52..513
FT	/label= Mature_Nhha_deletion_mutant
FT	/note= "Predicted mature protein, specifically
FT	claimed in claim 12"
XX	
PN	WO200155182-A1.
PD	
XX	02-AUG-2001.
XX	
PF	25-JAN-2001; 2001WO-AU00069.
XX	
PR	25-JAN-2000; 2000US-0177917.
XX	
PA	(UYOU ) UNIV QUEENSLAND.
XX	
PI	Peak IRA, Jennings MP;
XX	
DR	WPI: 2001-488774/53.

DR	N-PSDB; AAS09173.
XX	New Nhma surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 12; Fig 6; 91pp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhma
CC	(AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	immunoagents. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	could be expected from a corresponding wild-type surface antigen.
CC	The present sequence represents N. meningitidis strain H41 surface
CC	antigen Nhma deletion mutant.
XX	
SQ	Sequence 513 AA;
	Query Match 9.8%; Score 59; DB 22; Length 513;
	Best Local Similarity 100.0%; Pred. No. 1,5e-49;
	Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	364 YDVANNGDALNNVNOLONSGMNLDKRAVGSGGKVISGNVSPSKGMDERIVNAGNNIEI 442 
Db	293 ydvnnvgdalnvnqjngswndskavagsggkvvisgnvspkskgmdervnlnagnmiei 351
RESULT 8	
AAZ23745	
ID	AAZ23745 standard; Protein: 589 AA.
XX	
AC	AAZ23745;
XX	
DT	08-SEP-1999 (first entry)
XX	
DE	A surface protein of Neisseria meningitidis.
XX	
KW	Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
XX	
OS	Neisseria meningitidis.
XX	
PN	W09931132-A1.
XX	
PD	24-JUN-1999.
XX	
PF	14-DEC-1998; 98WO-AU01031.
XX	
PR	12-DEC-1997; 97GB-0026398.
PA	(ISIS-) ISIS INNOVATION LTD. (UYOU ) UNIT V QUEENSLAND.
XX	
PI	Jennings MP, Moxon ER, Peak IRA;
XX	
DR	WPI; 1999-418754/35.
XX	
PT	N-PSDB; AAX85197.
XX	
PT	Neisseria meningitidis surface proteins useful for treating N. meningitidis infections
XX	
PS	Claim 1; Page 122-124; 132pp; English.
XX	
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

SQ Sequence 589 AA;

Query Match 9.8%; Score 59; DB 20; Length 589;

Best Local Similarity 100.0%; Pred. No. 1.7e-49; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGKMDFTVINAGNIEI 442  
|||||  
Db 369 ydvnvgdalnvnnqngswldskavagssgkvisgnvpskgykmdetvlnagndlei 427

RESULT 9

AAU06173 standard; Protein; 589 AA.

XX AAU06173;

AC 24-OCT-2001 (first entry)

DE *N. meningitidis* P20 surface antigen Nhma polypeptide sequence.

XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.

OS *Neisseria meningitidis* strain P20.

XX Key Location/Qualifiers

FT 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT /label= V1

FT /note= "Variable region 1"

FT 106..117

FT /label= C2

FT /note= "Conserved region 2"

FT 118..121

FT /label= V2

FT /note= "Variable region 2"

FT 122..185

FT /label= C3

FT /note= "Conserved region 3"

FT 186..205

FT /label= V3

FT /note= "Variable region 3"

FT 206..224

FT /label= C4

FT /note= "Conserved region 4"

FT 225..233

FT /label= V4

FT /note= "Variable region 4"

FT 234..589

FT /label= C5

FT /note= "Conserved region 5"

WO200155182-A1.

02-AUG-2001.

25-JAN-2001; 2001WO-AU00069.

25-JAN-2000; 2000US-0177917.

(UYQU ) UNIV QUEBENS LAND.

Peak IRA, Jennings MP.

DR WPI; 2001-488774/53.

XX N-PSDB; AAS09163.

PT New Nhma surface antigen polypeptides and polynucleotides from

PT *Neisseria meningitidis*, useful in producing vaccines for treating or

PT preventing broad spectrum of *Neisseria meningitidis* -

PS Claim 9; Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel *Neisseria*

CC meningitidis mutant polypeptides of the surface antigen Nhma

CC (AAU06182-AAU06186). The modified or mutant amino acids, particularly

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of *N. meningitidis*, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of *N. meningitidis* strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhma

CC from *N. meningitidis* strain P20 is 1 of 10 Nhma polypeptide sequences

CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in

CC the present invention.

XX Sequence 589 AA;

SQ

Query Match 9.8%; Score 59; DB 22; Length 589;

Best Local Similarity 100.0%; Pred. No. 1.7e-49; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 YDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGKMDFTVINAGNIEI 442  
|||||  
Db 369 ydvnvgdalnvnnqngswldskavagssgkvisgnvpskgykmdetvlnagndlei 427

RESULT 10

AAAY27202 standard; Protein; 591 AA.

XX AAAY27202;

AC 24-SEP-1999 (first entry)

XX Amino acid sequence of *N. meningitidis* protein CRF40-1.

DE *Neisseria meningitidis* protein; pharmaceutical; vaccine; diagnosis;

XX bacterial infection; treatment.

XX *Neisseria meningitidis*.

OS WO936544-A2.

XX 22-JUL-1999.

PD 14-JAN-1999; 99WO-IB00103.

XX 09-OCT-1998; 98GB-0022143.

PR 14-JAN-1998; 98GB-0000760.

PR 01-SEP-1998; 98GB-0019015.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;

XX WPI; 1999-444400/37.

XX N-PSDB; AAX99124.

XX New protein and its nucleotide sequence, useful in vaccines or

XX diagnostic compositions for treating and/or preventing *Neisseria*

XX meningitidis infections

XX Claim 1; Page 62; 123pp; English.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:04:58 ; Search time 95.27 Seconds  
(without alignments)  
596.083 Million cell updates/sec

Title: US-09-771-382-1

Perfect score: 3003

Sequence: 1 MNKIYRIINMSALNMAWVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3003	100.0	591	2	G81133
2	2464.5	82.1	592	2	A81888
3	609	20.3	298	2	I64138
4	393	13.1	2059	2	D82671
5	378	12.6	1107	2	AC0976
6	371.5	12.4	1190	2	A82615
7	363	12.1	1588	2	A86036
8	363	12.1	1588	2	H91188
9	331.5	11.0	658	2	AH0110
10	244.5	8.1	1004	2	C82672
11	239.5	8.0	1091	2	G64964
12	232.5	7.7	1036	2	A43855
13	221	7.4	2020	2	C46399
14	220	7.3	1477	2	B43855
15	219	7.3	1910	2	AF0394
16	216.5	7.2	1286	2	S28634
17	216	7.2	949	2	D90803
18	216	7.2	1005	2	H85611
19	213.5	7.1	5291	2	F90696
20	213	7.1	4919	2	T31105
21	212.5	7.1	1018	2	H83135
22	212	7.1	1635	2	A10452
23	211.5	7.0	4152	2	T31102
24	210.5	7.0	1109	2	A56143
25	209	7.0	2273	2	T09083
26	208.5	6.9	936	2	A10711
27	207.5	6.9	1577	2	A35140
28	207	6.9	5188	2	B85547
29	206	6.9	1325	2	A64905

30	199	6.6	1461	2	E90696	hypothetical prote
31	198	6.6	3705	2	AD0123	probable autotrans
32	197	6.6	585	2	F90961	flagellin [limpore
33	197	6.6	585	2	F85809	hypothetical prote
34	196.5	6.5	1343	2	D85724	hypothetical prote
35	196.5	6.5	1487	2	AG2560	hypothetical prote
36	195	6.5	1461	2	A85547	hypothetical prote
37	194.5	6.5	1428	2	AC3224	hypothetical prote
38	194.5	6.5	3029	2	S76109	hypothetical prote
39	193.5	6.4	1343	2	E90893	hypothetical prote
40	193.5	6.4	3013	2	AB0480	probable invasin Y
41	193.5	6.4	4936	2	AH2515	hypothetical prote
42	192	6.4	1430	2	AF0351	probable autotrans
43	191.5	6.4	1608	2	A28182	hemolysin A - Serr
44	191	6.4	2249	2	A41477	190k surface anti
45	190.5	6.3	1035	2	AD3203	autotransporter pr

ALIGNMENTS

RESULT 1	
G81133	adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species:	Neisseria meningitidis
C>Date:	31-Mar-2000 #sequence,revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession:	G81133
R:RefSeq:	R.1:tel1, H. J. Saunders, N. J. Heidelberg, J. Jeffries, A. C. Nelson, K. E. Eisen, Hickey, E. K. Haft, D. H. Salzberg, S. L. White, O. Fleischmann, R. D. Dougherty, B. Science 287, 1809-1815, 2000
A:Authors:	Grandt, G.; Sun, L.; Smith, H. O.; Fraser, C. M.; Moxon, E. R.; Rappaport, R. A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; M0ID:20175755
A:Accession:	G81133
A:Molecule type:	DNA
A:Status:	preliminary
A:Residues:	1-591 <TEP>
A:Cross-references:	GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAFA1395.1; PID:g722
A:Experimental source:	serogroup B, strain MC58
C:Genetics:	
A:Gene:	NMB0992
Query Match	100.0%; Score 3003; DB 2; Length 591;
Best local Similarity	100.0%; Pred. No. 7e-141;
Matches 591; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1	MNKIYRIINMSALNMAWVVS...ELTRNHTKRASATVKTAVLATLTFATVQASANNEBOEDL 60
DB 1	MNKIYRIINMSALNMAWVVS...ELTRNHTKRASATVKTAVLATLTFATVQASANNEBOEDL 60
QY 61	YLDPVORTAVLVNSDKESTGKEKEVEENSDDAVFNEKGVLTAREITLKADNLKIKO 120
DB 61	YLDPVORTAVLVNSDKESTGKEKEVEENSDDAVFNEKGVLTAREITLKADNLKIKO 120
QY 121	NGTNYFYSKKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNDTIVHLN 180
DB 121	NGTNYFYSKKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNDTIVHLN 180
QY 181	GIGSTLDTLTLNGATTNTNDVTDDEKRRASVSDVNLNAGNINIGVKGTTASNDVF 240
DB 181	GIGSTLDTLTLNGATTNTNDVTDDEKRRASVSDVNLNAGNINIGVKGTTASNDVF 240
QY 241	VRIYDVEEFLSADTKTTTVNVEESKDKKTEYKIGAKTSYIKKEDKLYTGKDGENGSS 300
DB 241	VRIYDVEEFLSADTKTTTVNVEESKDKKTEYKIGAKTSYIKKEDKLYTGKDGENGSS 300
QY 301	TDEGBELVTAKEVIDAVNKRAGRPKTTTANGOTGADKFTVTSGNVTVPASGKGTATV 360
DB 301	TDEGBELVTAKEVIDAVNKRAGRPKTTTANGOTGADKFTVTSGNVTVPASGKGTATV 360
QY 361	SKDDGNITVIMYVNVGDLNLVNLQNSGWNLDKSKAVAGSGKGVISGNVSPSKGMDTV 420

```

Db 361 SKDDQGNITVWYVNGDALNVQNLQNSGWNLDKSAVAGSSGKVTGSAVSPSKGKDETV 420
      |||
Oy 421 NINAGNNIETTRGNKNDIATSMTPQFSSVSLGAGADAPLTSVDGDLANYSKKDNKPV 480
      |||
Db 421 NINAGNNIETTRGNKNDIATSMTPQFSSVSLGAGADAPLTSVDGDLANYSKKDNKPV 480
Oy 481 ITTVAPGKEDVTNVAQLKGVANLNINRIDVGNARAGIAQAIATAGLVQAVLPKSKM 540
      |||
Db 481 ITTVAPGKEDVTNVAQLKGVANLNINRIDVGNARAGIAQAIATAGLVQAVLPKSKM 540
Oy 541 MAIGGTYRREAGYALGYSSISDGGNMIITKGTASGNRGRHFGASASVGYOM 591
      |||
Db 541 MAIGGTYRREAGYALGYSSISDGGNMIITKGTASGNRGRHFGASASVGYOM 591

```

## RESULT 2

probable surface fibril protein NMA1200 [imported] - *Neisseria meningitidis* (strain Z249)

C:Species: *Neisseria meningitidis*  
 C:Date: 05-May-2000 #sequence\_rev: 1000 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
 ; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutre, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A:Reference number: A81775; MUID:2022556

A:Accession: A81888  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-592 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84461.1; PID:9737968  
 A:Experimental source: serogroup A, strain Z2491  
 A:Genetics:  
 A:Gene: NMA1200

Query Match 82.1%; Score 2464.5; DB 2; Length 592;  
 Best Local Similarity 84.2%; Pred. No. 2,4e-114;  
 Matches 506; Conservative 30; Mismatches 46; Indels 19; Gaps 8;

```

Oy 1 MNKTYRIIWSALNAAVVSSELTNRHNRKASATYKTAVALTLFATVQASANNNEOEEDL 60
      |||
Db 1 MNKTYRIIWSALNAAVVSSELTNRHNRKASATYKTAVALTLFATVQASANNNEOEEDL 59
Oy 61 YLDPVORTVAALIVNSDEKGEKEKVE-ENSDMAVYFNEGVLTAAREITLKAGDNLIK 119
      |||
Db 60 -LESVQKSV-VGSIQASMEGSELETISLSMTNDSKEFVDYIV---VTLKAGDNLIK 113
Oy 120 Q-----NGTNYTSLKDLTDLTSVGTETKLSFANGKNVITSDTKGLNFAKETAGTNG 173
      |||
Db 114 QNTNENTNASSFTYSLKDLTGLINVTETKLSFGANGKKNVITSDTKGLNFAKETAGTNG 173
Oy 174 DTYVHLNGISLTDLTLNLTGATNTVNDNTYDDEKRAASVKNVLANGNMINKGKPEPT 233
      |||
Db 174 DTYVHLNGISLTDLTLNLTGATNTVNDNTYDDEKRAASVKNVLANGNMINKGKPEPT 231
Oy 234 A--SDNVDFVRYDVEFLSADFTKTTVNVESKDNKKTEVKIGAKTSVIREKDKLVTG 291
      |||
Db 232 TGQSENVDVRYDVEFLSADFTKTTVNVESKDNKKTEVKIGAKTSVIREKDKLVTG 291
Oy 292 KDKGENSSSTDEGEGLVTAKEVIDAVNRKGRMKTTTANGQTQADKEFTVTSNTVFA 351
      |||
Db 292 KDKGENSSSTDEGEGLVTAKEVIDAVNRKGRMKTTTANGQTQADKEFTVTSNTVFA 351
Oy 352 SGKGTATVAVSKDDGNTVMDVNVGDLNVLQNSGWNLDKSAVAGSSGKVTGSAVSP 411
      |||
Db 352 SGKGTATVAVSKDDGNTVMDVNVGDLNVLQNSGWNLDKSAVAGSSGKVTGSAVSP 411
Oy 412 SKGKDEVTNINAGNNIETTRGNKNDIATSMTPQFSSVSLGAGADAPLTSVDGDLAN 470
      |||
Db 412 SKGKDEVTNINAGNNIETTRGNKNDIATSMTPQFSSVSLGAGADAPLTSVDGDLAN 471

```

```

Oy 471 GSKDKKPVRIITVAPGVKEDVTNVAQLKGVANLNINRIDVGNARAGIAQAIATAGL 530
      |||
Db 472 GSKDKKPVRIITVAPGVKEDVTNVAQLKGVANLNINRIDVGNARAGIAQAIATAGL 531
Oy 531 VOAVLPKSKMAIGGTYRREAGYALGYSSISDGGNMIITKGTASGNRGRHFGASASVGY 590
      |||
Db 532 VOAVLPKSKMAIGGTYRREAGYALGYSSISDGGNMIITKGTASGNRGRHFGASASVGY 591
Oy 591 W 591
      |||
Db 592 W 592

```

## RESULT 3

adhesin homolog HI1732 - *Haemophilus influenzae* (strain Rd KW20)

C:Species: *Haemophilus influenzae*  
 C:Date: 18-Aug-1995 #sequence\_rev: 1000 18-Aug-1995 #text\_change 24-Oct-1997  
 C:Accession: I64138

R:Rieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman,  
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
 Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.  
 A:Reference number: A64000; MUID:95350630

A:Accession: I64138  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-298 <TIGR>  
 A:Cross-references: GB:U32846; GB:LA2023; NID:91574588; PID:91574589; TIGR:HI1732

Query Match 20.3%; Score 609; DB 2; Length 298;  
 Best Local Similarity 46.2%; Pred. No. 2,7e-23;  
 Matches 146; Conservative 42; Mismatches 92; Indels 36; Gaps 8;

```

Oy 1 MNKTYRIIWSALNAAVVSSELTNRHNRKASATYKTAVALTLFATVQASANNNEOEEDL 60
      |||
Db 1 MNKTYRIIWSALNAAVVSSELTNRHNRKASATYKTAVALTLFATVQASANNNEOEEDL 49
Oy 61 YLDPVORTVAALIVNSDEKGEKEKVE-ENSDMAVYFNEGVLTAAREITLKAGDNLIK 119
      |||
Db 50 -INDAGTFVAVKQSTEDIEDSAK--DDNKNQALKAGD-----TLTKAGDNLIK 99
Oy 120 QNTNENTNASSFTYSLKDLTGLINVTETKLSFGANGKKNVITSDTKGLNFAKETAGTNG 173
      |||
Db 100 DQGGKSVTALAKDLDDVYKAVSDTLTGNTPAAGATPKVSTSTPADGLKLAK---GT 156
Oy 172 NGDTVHLNGISLTDLTLNLTGATNTVNDNTYDDEKRAASVKNVLANGNMINKGKPEPT 231
      |||
Db 157 NGDTVHLNGISLTDLTLNLTGATNTVNDNTYDDEKRAASVKNVLANGNMINKGKPEPT 215
Oy 232 TTASNDVDFVRYDVEFLSADFTKTTVNVESKDNKKTEVKIGAKTSVIREKDKLVTG 291
      |||
Db 216 GGNTEVDVLAQYDVEITTDKNTLDVYLAKEGKTEVKFPKPSVINDNNGKLLTG 275
Oy 292 KD--KGNGSSSTDEGE 305
      |||
Db 276 KQDKDANTGTATNATE 291

```

## RESULT 4

surface protein XE1529 [imported] - *Xylella fastidiosa* (strain 9a5c)

C:Species: *Xylella fastidiosa*  
 C:Date: 18-Aug-2000 #sequence\_rev: 1000 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: D82671

R:anonymous, The *Xylella fastidiosa* Consortium of the Organisation for Nucleotide Seq  
 Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A:Reference number: A82515; MUID:20365717  
 A:Note: for a complete list of authors see reference number A59328 below

Query Match	13.1%	Score 393;	DB 2;	Length 2059;
Best Local Similarity	24.3%	Pred. No. 1.4e-11;		
Matches 173; Conservative	93;	Mismatches 216;	Indels 230;	Gaps 31

QY 540 MMAIGGTYRGEAGYAICYSSISDGGNWI IKGTASGNSRGHFGASASVGYQW 591

Query Match	12.6%	Score 378;	DB 2;	Length 1107;
Best Local Similarity	21.6%;	Pred. No. 3.5e-11;		
Matches 185; Conservative	109;	Mismatches 250;	Indels 312;	Gaps 34;

[illegible]

Db 854 LDRFTNJIENGIGDITVTGTSFKYFKTNTGDADANAOQADSVAIIGSGSIAMENSVALCTN 913

Qy 460 TLTVDGDLANTGSKKDNKPVRTTNAPGVEGDYTNVAOLK----- 500

Db 914 SVADANTVSVGSS7QOOR--RITTNVAGVNMNTDAVNVAAQLAKASGASVRYETTNADGSVNY 971

Qy 501 -----GVAQ-----NLNRRIDNVG 515

Db 972 SVLTNIGDSSGGTTRTCGNVSAAVNDIDAVNVAAQLKRSVEATNTYTTQKKGENSKTKGIEN 1031

Qy 516 NARAGIAQAIATAGLVQAYLPKSKMAIGCGTYRGEAGYAIGYSSISDGCMMIITKGTASG 575

Db 1032 KMSGGIASAMAMAGAPQAYAPGANTMTSIAGGTFFNESAVALGVSMVSESGGVYTKLGTS 1091

Qy 576 NSRGHFSGASASGYQW 591

Db 1092 NSQGDYSAIGAGFOW 1107

RESULT 6

A82615

surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: A82615

R:Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleic Acid Sequencing

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SIM>

A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AA84783.1; GSPDB:GN001

A:Experimental source: Strain 9a5c

R:Stimpson, A.J.G.; Reinhard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
B:Rioses, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, B  
S:Neto, E.; Docena, C.; El-Dorzy, H.; Facincan, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohnh  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miraccea, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1981

```

0Y 179 INGISTLTDLILMTGATNTNTNNVNDDEKKAASVADYLNAG--NMIKGVKPTGTMSD- 236
Db 763 TNGV-----TVSGVYLLSGMLVITDDBGVPSYSSGI-----MAGSQKITVAAGTAPFDA 8311
0Y 237 -----NVDVRYTDPVEEFLSADTKTTTVNESKDNCKKTEVAKIGACTSV 280
Db 832 VNLSQLNTAMAGSGAKSVHYSTYD-----GGTGGGNYNMDGATGTGRSLAVGQITLASA 8855
0Y 281 I KKKGKALVTPAKDKGENC--SSTDGEGGLVTPAKETIDVAVNNAKGMKTKTTANGOFGQADKF 339
Db 886 -----EGATAVSSGGAASCKSGTALIGRNAVVASDQSVALGD--GAKDKARGAEPTTGKISGL 940
0Y 340 ETVTSGTNTVTPASGKGTATVTSKDDQGNITVMDVNYGDAI,NNVQL-----QNSGMNIDSK 395
Db 941 QNNFTGVTSVGDASKGETRTVS-----NVADAKFAT--DAVNLHQDLRVAQDANRYVDNK 9933
0Y 396 AVAGSSGKAVIGSNVSPSKGKDETVYNINAGNNIEITRNGKNIDITAMTPOFSSVSLGAG 4555
Db 994 IESISEGGTF-----VKVNSLNN-----SATP-----IAAG 101
0Y 456 ADAPLTISV-----DGDALNVGSK-----KDNKPV-----RITNV 484
Db 1020 VDATAIGVATASGADSLAMONKASASADNVALIGNHSVADPRANTSVSGASGSRQYTNV 107
0Y 485 APVKEGQVTVNAOLKGYAQNMLNRRIDNVDCNAR---AGTAAQIATAGLVOAYLPEKSM 540
Db 1080 AAGFTADTPAVNVSQLNOGLITAKQYTTDGVVSGLETRDTPDGVAAAIATVANI,POAYIPERGM 113
0Y 541 MAIGGATRGEGAVYALIGSSISDQGNMIIKCTASGNSRGHVGGAASVGYOM 591
Db 1140 TSVGVSTSRGOSALAVGVSSYSESGRNVYFKRSGSANTRSOYIGAGYGYOM 1190

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RESULT      7
A:Gene:      A86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species:   Escherichia coli
C:Date:      16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
  iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
  Nature 409, 529-533, 2001
A:Title:     Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference numbers: A85460; MUID:21074933; PMID:11206551
A:Accession: A86036
A:Status:    preliminary
A:Molecule type: DNA
A:Residues:  1-1588 <SPO>
A:Cross-references: GB:A0005174; NID:G12518349; PIDN:AMG58749.1; GSPDB:GN00145; UMGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene:      Z5029

```

```

Query Match      12.4%  Score 371.5;  DB 2;  Length 1190;
Best Local Similarity 23.5%  Pred. No. 8e-11;
Matches 167;  Conservative 88;  Mismatches 243;  Indels 213;  Gaps

Oy  17  VVSELRNHTTKRASATVKTAVLATLTLPATVQASANNDEEDLYDPVORT-----VAV 71
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  557  VTSSGISAGNCKITINVAGTADTDAVNFSQLQAAVSTASKGNLLASGANSNVPGESV 616
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  72  LIVNSDKRGTEKEKEVEENSMAVYFNFKEGVLTAARELT-----LKAQDLKTKON 121
      | | | | | : : : | | | : : : | | | : : : | | | : : : |
Db  617  DLKNSD -GNLLITKTDSDN--VTFNLTATLAKVDSLTTGTANTTTCGAVTGSNVLGST 672
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  122  GTNFYSLKLDLTJTSVGETEKLSPFSANGKV-NI-----TSDTKGLNFA----- 165
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  673  GLVIT- -DGPSVTSNG-----ISAGNCKITINVAGTADTDAVNFSQLQAAVSTASKG 722
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  166  -----KETAG----- -NGDITVH 178
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  723  WNLASGANSNVAPGESVDLTKNTDGNIVISKESGSDVLEFNLSLKLDTKTYGVIVMT 762
      | : : : : : | : : : : : | : : : : : | : : : : : |

```

Query Match	12.1%	Score 363	DB 2	Length 1588:
Best Local Similarity	24.7%	Pred. No. 3e-10:		
Matches 145; Conservative	78;	Mismatches 228;	Indels 136;	Gaps 22;
OY	121	NCNTFTYSIKKDLDTLTSVGTEKLSFSANGKNV-ITSDTKGLNFAKETAGTNGDPTVYHL	179	
Db	1022	NATNMMEONTQIINQLAGNTDATYIOENGAINVRYRTDDEIAFNDSASQGVGATAGY	1081	
OY	180	NGI-----GSTDLDTLNTGA-TTNTYNDNV-----TDDE	208	
Db	1082	NSVAKGDSVAIGQSSVDPDTGIALGSSSVRYIAKSRPDSITENGVGTYGPTDDE	1141	
OY	209	KKRASVVD-----VLNAGWIKAKKPGTSDVDVFPRTDYVEPLSADTKTTVANE	262	
Db	1142	LLGALISIGDGGKRYRIIN-----VAQSEAHDAVT-VROLQNLGAVATTPTKYFPHN	1193	
OY	263	SKDNCK-----KTEVKGAKTSYIAKE-----DGKLYTGKDKGE-----	296	

Db 1194 STEEDSLAVGTDLSLMAKATYVNGDKIGIGYGAAYVDANALNGIAIGSNAQYIHVNSIAI 1253  
QY 297 -NGSSSTDEGEGLVTAKKEYIDAVNKAQMRKTTTANGQ-----TGQADKEFTVTSCTNV 348  
Db 1254 GMSSTTRKCAQNTYATAYNADAPQNSGEPFVSAGDQROITVVAAGSAD-----TDVAVV 1308  
QY 349 TFSAGKGTATVSKDDQGNITVM-----YDVNVGDAL-----NVNQL 385  
Db 1309 --GOLKVTDAQVSOQNTQ--SITMLDNRVTNLDSRVTNIEGIDITYTSGTKFKFKNTDQV 1365  
QY 366 QNSGNNLDSKAVAGSSGKAVISGNSPSKGM--DETVINAGNNEIETRN--GKN--- 436  
Db 1366 DASAGCKDSVAIGSGSIAAADNSVALGTGSVATEENTISVSGSTNORRTITNVAAGKNATD 1425  
QY 437 -IDIAFSMTPOFSSVSLGADAPLTVSDGDLNVGSKDKNPVRTYNAAPVKEGDVYN 495  
Db 1426 AVNVAKLSSESGVRYDTKADG---SIDYSNITLGG--GNGGTTTRISNVSAGVNNNDVYN 1481  
QY 496 VQOLKGVAQ-----NLNRRIDNVGNARAGIAQAIATAGIYQAYLPKSKMAIG 544  
Db 1482 YQOLKQSVQETKQYTDQRMVENDNKLSTKESLGSIGIASAMMTGLPQAYTTPGASMASIG 1541  
QY 545 GGTYGEAGYATIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591  
Db 1542 GGTYNGESAVALGVSMVSNANGRMVYKLOGSTNSGGEYSALGAGIQW 1588

RESULT 8  
H91188  
probable adhesin Ecs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R1MD)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
R:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.  
Nucleotide Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156331, PMID:11258796  
A:Accession: H91188  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:G13363955; GSPDB:GN00154  
C:Experimental source: strain O157:H7, substrain R1MD 05095952  
C:Genetics:  
A:Gene: Ecs4480

Query Match 12.1%; Score 363; DB 2; Length 1588;  
Best Local Similarity 24.7%; Pred. No. 3e-10; Mismatches 228; Indels 136; Gaps 22;  
Matches 145; Conservative 78;

QY 121 NGNTFTYSLKDKLDTLTSVTEKLSFSANGKNVN-ITSDPTKGLNFAKTAGTNGDTTVHL 179  
Db 1022 NATNMIMIQNOIINQLAGNIDPATYIOENGAGINVTNRDDELATNDASQGVGATICY 1081  
QY 180 NCI-----GSTLTDTLLTGA-TTNTVNDNV-----TDE 208  
Db 1082 NSVAGDSSVAIGQSYSDVDTGIALGSSSVSRVIAKSRDTSITENGVIGYDTTDE 1141  
QY 209 KRAASVMD-----VIANGMNKGKVPCTASDVNDPVRTDYEFLSADTKTTTVAE 262  
Db 1142 LIGALISIGDGGKYYROIIN-----VADGSEAHDAVT-VROLQNAIGAVATTPTYEFHAN 1193  
QY 263 SKDNCK-----KTEVIGAKTSYIKER-----DGLVTYDKGE----- 296  
Db 1194 STEEDSLAVGTSLAMGAKTIYNGDKIGIGYGAAYVDANALNGIAIGSNAQYIHVNSIAI 1253  
QY 297 -NGSSSTDEGEGLVTAKKEYIDAVNKAQMRKTTTANGQ-----TGQADKEFTVTSCTNV 348  
Db 1254 GMSSTTRKCAQNTYATAYNADAPQNSGEPFVSAGDQROITVVAAGSAD-----TDVAVV 1308  
QY 349 TFSAGKGTATVSKDDQGNITVM-----YDVNVGDAL-----NVNQL 385

Db 1309 --GOLKVTDAQVSOQNTQ--SITMLDNRVTNLDSRVTNIEGIDITYTSGTKFKFKNTDQV 1365  
QY 386 QNSGNNLDSKAVAGSSGKAVISGNSPSKGM--DETVINAGNNEIETRN--GKN--- 436  
Db 1366 DASAGCKDSVAIGSGSIAAADNSVALGTGSVATEENTISVSGSTNORRTITNVAAGKNATD 1425  
QY 437 -IDIAFSMTPOFSSVSLGADAPLTVSDGDLNVGSKDKNPVRTYNAAPVKEGDVYN 495  
Db 1426 AVNVAKLSSESGVRYDTKADG---SIDYSNITLGG--GNGGTTTRISNVSAGVNNNDVYN 1481  
QY 496 VQOLKGVAQ-----NLNRRIDNVGNARAGIAQAIATAGIYQAYLPKSKMAIG 544  
Db 1482 YQOLKQSVQETKQYTDQRMVENDNKLSTKESLGSIGIASAMMTGLPQAYTTPGASMASIG 1541  
QY 545 GGTYGEAGYATIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591  
Db 1542 GGTYNGESAVALGVSMVSNANGRMVYKLOGSTNSGGEYSALGAGIQW 1588

RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
R:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:G15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.0%; Score 331.5; DB 2; Length 658;  
Best Local Similarity 25.2%; Pred. No. 3.5e-09; Mismatches 204; Indels 113; Gaps 22;  
Matches 132; Conservative 74;

QY 101 GVLTRREITLAKADNLKIKONGTNTFTYSLKDKLDTLTSVTEKLSFSANGKNVNTSDTK 160  
Db 217 GAVTSQANSIALG-AASINTVGAQSSYSAVALTAPQASVGEIGIG-TALGNR-KITGVAA 273  
QY 161 GLNFAKETAGTNGDTTVHLNGISITLDTLLTNGATTNTN--DNVTDEKRAASVKYV 218  
Db 274 G-----SASSDAVNVVAQLTAVGDQVQN-----TANTISLGGRTTLE-----GSMASI 317  
QY 219 LNAGNMNKGKVPCTASDVNDPVRTDYEFLSADTKTTTVAESKDNGKKT-----EV 272  
Db 318 ANG-GVAKTFHANSTOPEV-----ASGNSVAITPASILASNAALASAGAV 364  
QY 273 KIGAKTSYIKERDGLKLVTKGKNGSSSTDEGEGLTAKREVDAVNAKQMRKTTTANGQ 332  
Db 365 AIG--DGAASADGSVALIGQSGDNGREYENIG-----KYSNANSTS 405  
QY 333 TGQADKEFTVTSCTNVTFASGKGTATYVSKDDQGNITWYDVNVGDALNVNQLQNSGNL 392  
Db 406 SG-----TVSVGNAT-----GETRTYSNVADG-----LQARDVAVNLRLDQ----- 442  
QY 393 DSKAVAGSSGKAVISGNSPSKGMDETVINAGNNT-ETTRNGKNNDI--ATSMPOFSS 449  
Db 443 -----IASTVYVENNVSLQNGTDMFOYNNSSGLAKSAGANSATGAGASVAGNS 497  
QY 450 VSLGAGADAP-----TLSDGDLNVGSKDKNPVRTYNAAPVKEGDVYNVQAL 499  
Db 498 TAFSGAKRTAANSAALGANSVAADRANSVSGSVGNER--QITNVAAPAQGDVAVNFDDL 555



OY 500 KGAQN-----LNNRDNVDGNAR-----AGIAQAIATAGLVOAYLPGKSMALGGCTY 548  
 Db 556 KSISSNOTNATNORSEYSELKODLRKRONSVLSAGIASAMSMSLTPYTSGSSMTTIGASY 615  
 OY 549 RGEAGYAIYSSYSDGNNIITKTAAGNSRCHFPASASVGYOW 591  
 Db 616 RGOSALSLGVSSISDSGRWWSKLOASSNTGODFGIGVGYOW 658

RESULT 10  
 C82672  
 Surface-exposed outer membrane protein Xf1516 [imported] - Xylella fastidiosa (strain 9a)

C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: C82672

Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
 Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82672

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <SIM>

A:Cross-references: GB:AE003981; GB:AE003849; NID:99106543; PIDN:AAF84325.1; GSPDB:GN001

A:Experimental source: strain 9a5c

A:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorty, H.; Facincani, A.F.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

Rodrigues, V.; Rosa, A.O. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshakko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf1516

Query Match 8.1%; Score 244.5; DB 2; Length 1004;  
 Best Local Similarity 22.3%; Pred. No. 0.00012;  
 Matches 162; Conservative 96; Mismatches 277; Indels 193; Gaps 34;

OY 2 NKIYRIIWSALNAAVYVSELTNRH-----TKRASATVKTAVIATLTFATVOASANNEE 55  
 Db 4 NOIYRKFWNLISLGSMSVASHMTNDGCSDVYLRHSGVNRSLVLAIGLALTSVTHAQSVK 63  
 OY 56 QEEDLYIDPVGRTVA-VLIYNSDKE-----GTGEKKVYENSGMNV----- 95  
 Db 64 -----SPANVASKVAWVAHVDSQVNRKTADRIPTGDSSELTMTMALDWMKFFPGNNSIA 116  
 OY 96 --YENEGVLTAREITLKAGDNLIKONGTFTYSLKKDLTDLTSVGEKESFSGANGKV 153  
 Db 117 IGYRSKAFAPRA-----IALGNSSVTOSANN-GVALGSNSI-VSGVSVVALGASMSASEL 170  
 OY 154 NITSDFGLNFAKETAGTNGDTVHLNGISSTLDTLLNTGATTNVTNDVYTDDEKRAA 213  
 Db 171 NVISVGG-----DGVTPAVRRIYVNG-----DGIGNDVAVKSQLDGVATASVNDVAA 219  
 OY 214 SYVDYL-----MAGMNIKGVKPGTTA-SDNVDFRTDYEF----- 249  
 Db 220 SVKTIALTNOVTGSSVASGKESSTAIGSGAQAADN-----TVAFGRAIANAVGA 271  
 OY 250 --LSADT-----KTTYNVESKDNKRTKTEYKIGAKTSV-----IKERDGLTYTKD 293  
 Db 272 SALGDFDHAGKINSTYTGTSVSLG-OGGVSLGYNISFVGBESFNGLALGNSLVLLIGVD 330  
 OY 294 KGENGS-----STDEGEGL-VTAKEVI-----DAVNKAGWBMKTTTANGQ 332

Db 331 SVALLSGSMASEPNNVSVSGDGLRGPAVRRIYVNGDIGNNPAVNSQDGYTASVNDV 390  
 OY 333 TGQADRKEVY--TSGTIVTFASGKGTAT-VSKDDOGNITVMTDVNVDALANVQLONSG 389  
 Db 391 VASYKNITAGAIQITGSSVAVSGODSTAGASQAQADSSIA-----LGARSRAAISSA 446  
 OY 390 WNLID-----SKAVAGSSGRKVISGNVPSKGMDETVMNAGNMLEITFRGNIDTATS 442  
 Db 447 LGVDGHALGANSTALGQGTALISGGLTSLG-----YNSFVGSATNGALGNSN-----A 495  
 OY 443 MTPQFSSVSLGACADAPTLVY-----DGDALNVSCKKRNKRYRTITNAPVKEGDTVVAQ 498  
 Db 496 IVSGVNSVALGAGSVASELNVISVGGDGYTGPAVR-----RIYVNGDIGNNDVAVKRSQ 550  
 OY 499 LKGAQNALNN-----RIDVDDGNAR---AGIQAQI---ATAGLVOAYLPGKSMALIG----- 544  
 Db 551 LDGYTASVNDVAAVSKKIYVITQITGSGVASALGKDSATAGASQAQAVGDSVALGTRATA 610  
 OY 545 -----GGTYRGEAGYAIYSSISDGNMILK-----GTASGNSRCHFG 582  
 Db 611 NATGSSVLYGDSRRARGINSTALRGQSNALIGDGSVSLGFNSFVRQSGEHRGVALGTDAVSG 670  
 OY 583 A-SASVGY 589  
 Db 671 KDSIALGY 678

RESULT 11  
 G64964  
 hypothetical protein b2000 - Escherichia coli  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
 C:Accession: G64964  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A.: Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617  
 A:Accession: G64964  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1091 <BLAT>  
 A:Cross-references: GB:AE000291; GB:U00096; NID:q1788298; PIDN:AACT5061.1; PID:q17883  
 A:Experimental source: strain K-12, substrain MG1655  
 A:Keywords: nucleotide binding; P-loop  
 F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 8.0%; Score 239.5; DB 2; Length 1091;  
 Best Local Similarity 23.3%; Pred. No. 0.00023;  
 Matches 145; Conservative 71; Mismatches 202; Indels 205; Gaps 35;

OY 1 MKIYRIIWSALNAAVYVSELTNRH-----TKRASATVKTAVIATLTFATVOASANNEE 60  
 Db 57 LNTCYRLVNMNHMGAFVASELARARCKRGVAVALSLAVTSLSPLVAA-----DI 107  
 OY 61 YLDPVGRTAVLIYNSDKE-----GTGEKKVYENSGMNV----- 117  
 Db 108 VHPGEFVNGCTLANHNOIVFGT----- 131  
 OY 118 IKONGTFTYSLKKDLTDLTSVGEKLSFSGANGKVNITSDFGLNFAKETAGTNGDTTV 177  
 Db 132 --TGMGNTISGLEYGPNNEANTGQWQDGTANKTIVTS6--GLQ-RVMPGGSVSDTVI 186  
 OY 178 HLNGISSTL---TDILLNTG-----ATTNVTNDVNTDDEKKAASVQVYLANAGN 224  
 Db 187 SAGG-GOSLOGRAVNTTLNNGEOMMHGAIATATGVINDK----- 227  
 OY 225 IKGVKPGTASDNDVDFRT-----YDYVEFLSADTKTTTYNVESKDNKRTKTEYK 274  
 Db 228 V--VKPGTAVTDIV--VNTGAEQGPDAENGDGTGQFVAGDAVRTIIN---KNGQIVRAE 279





```
Db 303 EGGSTTTNGCTGTOINDDATANNNGKTYVDGKDSCTGTEINGNNGKYIOD-----GDL 356
Oy 218 VLAMGNRIKVRKGTASDNVDFVRYDYVEF--LSADTKTTTVNESK-----265
Db 357 VSGGGHCF-DITGDSATVDKGTMTVTIDPESIGIOYDGDQAVVNBESAITNGICTOI 415
Oy 266 NGKTEVIGAKTSVIREKDKLVTKGD-KENG-----SSTD 302
Db 416 NGDDATANNNGKTTV-----DGKDSGTGEIAGNNGKVIOGDDLDVSGGGHGDITGDSATV 471
Oy 303 EGGGLYTAKE-----VIDA-----YKAGWRMKTITANAGTQADKREYTSCTNVTAS 352
Db 472 DNKGTMVTIDPESIGIOIDDDQAVNNEG---ESTTNGGTG-----TQINGDAD-AN 521
Oy 353 GKGTATVSKD-----QGNTVWYDVYDGDALNV-----NOLSGMN--LDSK-----A 396
Db 522 NSGKTYVDGKDSGTGKTAGNIGT---VNLGSLITVYGAGHVERIGDNGTVNNKGDIVS 578
Oy 397 VAGSSGKVISGNVSPSKKMDFTVINAGNNIETRNKNIADITSN-TPQFS-----448
Db 579 DTGSGVLINGEGATVSNMGDVANS-NEATGFSITTSKGVSLAGSMQVDFSTGVDLNG 637
Oy 449 ---SVSLGA-----GADAPTLVSDGDLNV--GSKKDKPVRITVA-----PGV---488
Db 638 NNNSVTLAAKDLKVYCGKACGINVSGDANTVITGNVLVDKTDADAAEFEDPSVGIN 697
Oy 489 ---KEGDTVNAQLKGAQN-LNNRIDNV-DGNARAGIAQAIATAGIV-----531
Db 698 VYSGDNNTVLTDGKLTIVSDSEVTSKOSNLPDGSAE-----KTSGLVITGDNVTMMNG 750
Oy 532 -QAVLPCKSMATGCTGYRGEAGYAI-----GYSSISDGMNIMG 571
Db 751 GLELIGKKNALADSGYTSLRTGYSTSVIVSGESSVYVINGDPTTISG 798
```

```
RESULT 14
B43855
high-molecular-weight surface-exposed protein - Haemophilus influenzae
C:Species: Haemophilus influenzae
C>Date: 10-Mar-1993 #sequence-revision 18-Nov-1994 #text-change 18-Nov-1994
C:Accession: B43855
R:Barenkamp, S.J.; Jerninger, E.
Infect. Immun. 60, 1302-1313, 1992
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus pertussis.
A:Reference number: A43855; MID:92192797
A:Accession: B43855
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1477 <BAR>
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBI:P:89240)
```

```
Query Match 7.3%; Score 220; DB 2; Length 1477;
Best Local Similarity 22.6%; Pred. No. 0.0031;
Matches 139; Conservative 92; Mismatches 231; Indels 152; Gaps 30;
```

```
Oy 11 SALNAVYVSELTNRNHT---KRASATVKTAVLATLFAVQASANNBQEDLDLYPQR 67
Db 821 NAINSTNISTIGGNVTLGGONSSSI-TGNITTEKAAVTLNANPNQONI-RDRYIK 878
Oy 68 TVAAVLIVNSDEKGEKEKEVENSMDWAVFNEKGVLTAREITL---KAGDLKTIKONGT 124
Db 879 -LGSLLVNGSISLTGENADI-----KGNLTITSESATKGTTRDTLNTGFTN 925
Oy 125 FTVSLKDLTDLTSVTEKLSFSANGKNVITSDTK-----GLNFAKET 168
Db 926 -NGTAEIINIQ---GVYKLGIVNTDGLDINTTHAKRQRISIIIGDIINKKSLINI---976
Oy 169 AGTNGDTTHVHLNGISLTTLTTLNTGATTVNT-----NDNVTDDE 208
```

```
Db 977 TDSNDAEIOIGCNISOKBECNLTITSSDKINITKOITIKKIDCEBSSSATSANLT-IK 1035
Oy 209 KKRASVYKDVLANAGWNIVKGYKPGTASDNVDFVRYDYVEFLSADTKTTTVNESKDNK 268
Db 1036 TKELKLTLEDLSISGFN---KAEITAKDGRDLITGNSNDGSAEAKTTFN-----NVK 1086
Oy 269 KTEVKIGAKTSVIREKDKLVTKGDKGNSSTDEBGL-VTAKEYIDAVNKAQWRMKT 327
Db 1087 DSKISADGHVTL---NSKVKITSSNMGRESNDNDGLITAKN--EVNKOITISLKV 1141
Oy 328 TANGQGTQADKFEYVTSVTGTFASGKTATVSKDQGNITVWYDVYDGDALNVOLQN 387
Db 1142 NIT-----ASEKVTYTAGSTINATNGKASTITTGDISGITS-----GNTYSVA---1186
Oy 388 SGWNLDSKAAVAGSSGKVISG--NVSPSKGMDFTVINAGNNIETRNKNIADITSNTP 445
Db 1187 ---TVDLTTSKSGKIEAKSEANVTSATGTIGT1---SCNTVNTVANAGDLTVG-----1235
Oy 446 QFSSVSLGACADAPTLVSDGDL--NVGSKDKNPVRITVAAGVKEGDTVNTAQLKVA 503
Db 1236 --NGAEINATEGAATVLTATNTLTTEAGSS-----ITST-----KGVDLLAONGSIA 1281
Oy 504 QNLNRRIDNVDCNARAGIAQAIATAGIVQAVLPCKSMATGCTGYRGEAGYAGISSISD 563
Db 1282 GSIN--AAVNTLN-----TTG-----TLTVAGSDIKATSC-----TLVIN 1315
Oy 564 GGNWIIKGTASGNS 577
Db 1316 AKDAKLNGDASGDS 1329
```

```
RESULT 15
AF0394
probable adhesin hmwA (imported) - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence-revision 02-Nov-2001 #text-change 02-Nov-2001
C:Accession: AF0394
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
demo-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MID:21470413; PMID:11586360
A:Accession: AF0394
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
C:Genetics:
A:Gene: hmwA
```

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Query Match 7.3%; Score 219; DB 2; Length 1910;
Best Local Similarity 20.5%; Pred. No. 0.0048;
Matches 148; Conservative 92; Mismatches 255; Indels 228; Gaps 28;
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Oy 14 NAWVYVSELTNRNHTKRASATVKTAVLATLFAVQ-----ASA 51
Db 898 NATITANNISMN---GNITANDAVLMTNFTLAKGDIKIDTLPKGLWFRNGGWTAA 953
Oy 52 NNEQBEDLDYDPQRFVAVVIVNSDKGEKGEKEVENSMDWAVFNEKGVLTAREITL 111
Db 954 NN-----ILLVANS--TSGETVKINASS---NKMNTTACKDITSI 990
Oy 112 AG-----DNLKIKONGTNTFYSLKDLTDLTSVTEKLSFSANGKNVITSDT 159
Db 991 AGNSKTIATGPNINIEVNIETNNGFT-----TNGITSTVLSGVNVSANG--VDITSNS 1042
Oy 160 KGLNFAKETAGTNGDTVHLNGISLTTLTTLNTGATTVNTNDVDEKRAASVVDV- 218
Db 1043 TG-----TGGIYLDNNTNLTFTVGD-----IN-IVTNSGKGIWIKSNSTLNSKNDIT 1089
Oy 219 ---LMAGNINIKGV--KPGTTASDNVDFVRYDYVEFLSADTKTTTVNESKDNKKTIEVK 273
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```

Db 1090 LNVGSAGON-EGYIIQSSSPASHRN-----NISAQNTTLIGKMGNGSGQSHLIN 1137
QY 274 IG--AKTSYIKKEDGKLVGKDGKENGSSSTDEEGLVTAKEVIDAYNKAQRKTKTTA-- 329
Db 1138 LGNVSLTS-----SGRNIDINGSSAGTGDVYFTNVEIENATAGNVSIYAETKTALS 1187
QY 330 -----NGOTGOADKFEFTVSGTNVTFASGKGTATVSKDQGNITV----- 370
Db 1188 TSLNAVLSLGGNNSIKAONGWLIGKAFNTTQAGIGFRANSSLSVDGNITLKGTEGVGA 1247
QY 371 -----MYDVNVGDALNVQNLQNSGNLDSKAVAG----- 399
Db 1248 TRKGIDFYGANTLNIKGSQLSLIGENKGAODTACGNGISYTSIAKLTVNNNGSLKMEGR 1307
QY 400 -----SSGVIGSNVSPSKGMD----- 417
Db 1308 STSGTGINFPPSSNNLTVPNGDGTLLIKSSVACTGAISGVVNNSTGPMTEIGISTDGAG 1367
QY 418 -----ETVNNINAGN-----NIEITRNKNIDIA-TSMTPQSSVSLGA--GADAPT 460
Db 1368 VHLFSAEHRIDRINTVSGSTHAEGLRISGMAALVDITLTKSINGSGVKIDSLPGSSVYT 1427
QY 461 LSVDDGDLNVGSKKDNKPVRTINVAPGVKEGDTNVAQLKGAQNLNRRIDNVGNAKAG 520
Db 1428 RSVLDNATLNGSSSGKGEITSIDINGIHSSINGTTGTGCGIDIGEN-SNVTGTSEAD 1486
QY 521 --IAQAIATAGL-VQAYLPQKSMMAIGGTYRREAGYAIGYSS-ISDGGNMIITKGTASGN 576
Db 1487 LLILOGVAATGTGTGIKILGNNDLNTSLNSSAVDGIALDITGIPLANOGVLIINGTASGS 1546
QY 577 SRG 579
Db 1547 GIG 1549

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Search completed: July 3, 2002, 08:11:59  
Job time: 421 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:29 ; Search time 48.34 Seconds

(without alignments)  
473.381 Million cell updates/sec

Title: US-09-771-382-1

Perfect score: 3003  
Sequence: 1 MNKIVRIINMSALNANVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	239.5	8.0	1039	1 AG43_ECOLI	P39180 escherichia
2	221	7.4	2003	1 YDBA_ECOLI	P33666 escherichia
3	216.5	7.2	1286	1 AIDA_ECOLI	Q03155 escherichia
4	207.5	6.9	1577	1 HLYA_PROMI	P16466 proteus mir
5	206	6.9	1325	1 YDEK_ECOLI	P33051 escherichia
6	201	6.7	1654	1 OMPB_RICRI	Q35047 r outer mem
7	191.5	6.4	1608	1 HLYA_SERNA	P15320 serratia ma
8	191	6.4	2249	1 OMPA_RICRI	P15921 rickettsia
9	189.5	6.3	1953	1 BIGA_SALTU	P25927 salmonella
10	186.5	6.2	1655	1 OMPB_RICCN	Q9Kk3 r outer mem
11	185	6.2	1645	1 OMPB_RICRY	P66989 r outer mem
12	183	6.1	1007	1 Y741_CHLMU	Q9jfe chlamydia m
13	182	6.1	917	1 HXA3_HAETN	P43355 haemophilus
14	181.5	6.0	933	1 SLAP_CAMEE	P35827 campylobact
15	181	6.0	1656	1 OMPB_RICJA	Q06653 r outer mem
16	180.5	6.0	928	1 HXA2_HAETN	P43354 haemophilus
17	180.5	6.0	1569	1 VPJA_ECOLI	P53143 escherichia
18	180	6.0	1861	1 APU_THETU	P38536 t amylopull
19	180	6.0	2334	1 WAPA_BACSU	Q07833 bacillus su
20	175.5	5.8	1567	1 ICEN_XANCT	P18127 xanthomonas
21	174	5.8	918	1 YAJB_CAEEL	P34487 caenorhabdi
22	172.5	5.7	2021	1 OMPA_RICCN	Q52657 rickettsia
23	167	5.6	1643	1 OMPB_RICPR	O53020 r outer mem
24	166.5	5.5	1148	1 ICEK_PSEEX	O30611 pseudomonas
25	166	5.5	1025	1 SLAP_CAUCR	P38528 shigella fla
26	163	5.4	550	1 FLIC_SHIFL	Q08860 campylobact
27	161.5	5.4	1300	1 12OK_RICRI	P19194 rickettsia
28	161.5	5.3	642	1 MRSP_STAUV	P80544 stephylococ
29	160.5	5.3	444	1 FLID_LACAC	P35829 lactobacilli
30	159.5	5.3	642	1 FLID_CAMEE	Q9phw6 campylobact
31	159	5.3	671	1 ALYS_ENTRA	P37710 enterococcu
32	159	5.3	928	1 PM10_CHLPN	Q9db65 chlamydia p
33	158	5.3	497	1 FLIC_ECOLI	P04949 escherichia

34	158	5.3	1694	1 IGA0_HAETN	P44969 haemophilus
35	158	5.2	1702	1 IGA2_HAETN	P45384 haemophilus
36	157.5	5.2	1153	1 PVDB_PLAKN	P50493 plasmodium
37	157	5.2	1196	1 ICEV_PSEEX	O33479 pseudomonas
38	156.5	5.2	817	1 YGAL_YEAST	P46949 saccharomyc
39	156	5.2	1200	1 ICEN_PSEEX	P06620 pseudomonas
40	155.5	5.2	1076	1 NUP1_YEAST	P20676 saccharomyc
41	154.5	5.1	507	1 FLIC_SALON	Q06974 salmonella
42	154.5	5.1	948	1 HPIL_DEIRA	P56867 deinococcus
43	154.5	5.1	954	1 FLEY_CAUCR	P15345 calobacter
44	154.5	5.1	1250	1 YFAL_ECOLI	P45508 escherichia
45	154	5.1	1288	1 VACA_HELPJ	Q92kws helicobacte

## ALIGNMENTS

RESULT 1  
AG43\_ECOLI STANDARD: PRT: 1039 AA.  
AC P39180: P76360: P75614: P97241: Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (Ag43) (fluffing protein).  
GN FLU OR B2000.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blactner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
[2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=9725158; PubMed=9097040;  
RA Iton T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
[3]  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ML 308-225;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Henderson I.R., Owen P.;  
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
[4]  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN-ML 308-225;  
RX MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
[5]  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN-K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded

RT in the genome of *Escherichia coli* K-12." ;  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [6].  
 RP GENE NAME.  
 RX MEDLINE=97257509; Pubmed=9103983;  
 RA Henderson I.R., Meehan M., Owen P.;  
 RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
 RT determines colony morphology and autoaggregation in *Escherichia coli*  
 RT K-12." ;  
 RL FEMS Microbiol. Lett. 149:115-120(1997).  
 CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY  
 CC FUNCTION AS AN ADHESIN.  
 CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
 CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
 CC CHAIN).  
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.  
 CC -1- SIMILARITY: TO ADHESIN AIDI-1 AND TO BORDETTELLA PERTACTIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; AE000291; AAC75061.1; ALT\_INIT.  
 DR EMBL; D90838; BAI15825.1; ALT\_INIT.  
 DR EMBL; D90839; BAI15832.1; ALT\_INIT.  
 DR EMBL; U24429; AAB47869.1; -.  
 DR EcoGene; EGI2686; flu.  
 DR Outer membrane: Signal: Complete proteome.  
 KW SIGNAL.  
 FT 1 52  
 FT CHAIN  
 FT 53 551  
 FT CHAIN 552 1039  
 FT VARIANT 2  
 FT 41 42  
 FT VARIANT 46 46  
 FT 157 157  
 FT VARIANT 188 188  
 FT 303 305  
 FT VARIANT 320 320  
 FT 372 372  
 FT VARIANT 493 493  
 FT 497 497  
 FT VARIANT 585 585  
 FT 709 709  
 FT VARIANT 721 721  
 FT 751 753  
 FT VARIANT 803 803  
 FT 815 815  
 FT VARIANT 824 824  
 FT 829 835  
 FT VARIANT 845 847  
 FT 855 855  
 FT VARIANT 888 888  
 FT 1025 1025  
 FT VARIANT 61 63  
 FT CONFILCT  
 FT 1039 AA; 106841 MW; 5170D647CDBEEB50 CRC64;  
 SEQUENCE  
 ANTIGEN 43 ALPHA CHAIN.  
 K -> N (IN STRAIN ML 308-225).  
 SL -> FF (IN STRAIN ML 308-225).  
 T -> K (IN STRAIN ML 308-225).  
 W -> L (IN STRAIN ML 308-225).  
 V -> F (IN STRAIN ML 308-225).  
 ATN -> STI (IN STRAIN ML 308-225).  
 N -> Q (IN STRAIN ML 308-225).  
 N -> Q (IN STRAIN ML 308-225).  
 E -> V (IN STRAIN ML 308-225).  
 S -> N (IN STRAIN ML 308-225).  
 H -> Y (IN STRAIN ML 308-225).  
 E -> K (IN STRAIN ML 308-225).  
 M -> T (IN STRAIN ML 308-225).  
 GHL -> SHF (IN STRAIN ML 308-225).  
 S -> P (IN STRAIN ML 308-225).  
 A -> V (IN STRAIN ML 308-225).  
 C -> S (IN STRAIN ML 308-225).  
 LNWHTS -> MNLTYNA (IN STRAIN ML 308-225).  
 QGT -> LGA (IN STRAIN ML 308-225).  
 S -> T (IN STRAIN ML 308-225).  
 O -> L (IN STRAIN ML 308-225).  
 S -> I (IN STRAIN ML 308-225).  
 ETV -> TTT (IN REF. 5).  
 5170D647CDBEEB50 CRC64;

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Query Match 8.0%; Score 239.5; DB 1; length 1039;
Best Local Similarity 23.3%; Pred. No. 9,1e-05;
Matches 145; Conservative 71; Mismatches 202; Indels 205; Gaps 35;

Qy 1 MKKIRIINSLNNMAYVSELTNRHTKASFTVTAVALTITLLEATYQASANNEDCDL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 LMFICRLVNNHTGFAVVASSELARARGKGVAVALISLAATVSLPYLA-----DI 55
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 YLDPQVQRTAVLIVNSDKE--GTGKEKEVEENSDMAVYENEGVLTAREITLKAGDNLK 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 VVHPGTVNGGTLAHNDNOIVEGT----- 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Oy	118	IKGNTNYSLLKKDLINDLINSVGRKESLFSANGKKNVITSDTLGNPAKFEAGNSPTV	177
Db	80	-TNGMTISTGLEEGPDNEATGCGWVODGSTANKTIVTSG--GLO-RVNPGGSVSPVI	134
Oy	178	HLNIGISGTL---DDTLINTG-----ATTNVTNDNVTDDEKKRAASVDYVLNAGWN	224
Db	135	SAGG-CGSLQRAVNTLTNLNGEGQMMHGGALATGTVINDK-----GMQ	175
Oy	225	IKGKPPGTASDNVDFKRT-----YDYVEFLSADIKTTTVNVEESDNCKKTEVKI	274
Db	176	V--VKPQVATDTV--VNTGAEGGPDANENGDPTGQFVGDVAVRTIN---KNGQIVRAE	227
Oy	275	G-AKTSVTKKEDKGLVYNGKDGKENGSSSTDE-----GEGJLV---TAKEVIDAVKAKGRM-	324
Db	228	GTANTTV-----YAGGDPTVGHALDITLNLNGIYQYVHNGGASPTV--VNSDCMQIV	278
Oy	325	-----KITTANGQGTQADKEFEVTSCTNVPFASG---KGTATVSKDDOG-NITVMYD	373
Db	279	KNGGAGVATTVN-QKGR-LQVDAGGTATNVTNLKGALVYSTATV----GIKRLGAFS	332
Oy	374	VNVGDALVNLQNSGHWLDSKAAGSSGKVIISGVNPSKCKMDYVNNANNNIETRN	433
Db	333	VVEGKADNV-VLENGG-RLD-----VLTSHTATN-----TRVDDGGTLVD-RN	372
Oy	434	GKNIDIASMTPFORSVSLGAGADAPTLSDVDALNLNGSKDKNPVRITVNAPEKKEGDV	493
Db	373	G-----GTAIT-----VSMNGG---VLLADSGAASVSTRDCK-----APSIGGQA	412
Oy	494	TNVNQLKGAONLNNRINDNVNAGRAGIAQAIAVLAVQAVLPKSMALIGGTYRKEAG	553
Db	413	DALMEKSSSEFTLN-----AGDTATDTT-----VNGGLTFARG	446
Oy	554	YAIYSSISDGGNNIIRKTAGSN	576
Db	447	TLAGTTTLNNGAIIITLGSQTVNN	469
RESULT 2			
YBBA_ECOLI			
ID	YBBA_ECOLI	STANDARD:	PRF: 2003 AA.
AC	P33666; P76087; P76088; P76856; P76857; P76859;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hypothetical protein ybba.		
GN	YBBA OR B1401/B1405.		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC	Escherichia.		
OX	NCBI_TaxID=562;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-K12 / MG1655.		
RX	MEDLINE=97426617; PubMed=9278503;		
RA	Baltner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,		
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,		
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
RA	Mau B., Shao Y.;		
RT	"The complete genome sequence of Escherichia coli K-12.";		
RL	Science 277:1453-1474(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-K12;		
RX	MEDLINE=97251357; PubMed=9097039;		
RA	Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,		
RA	Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,		
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,		
RA	Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,		
RA	Samei G., Seki Y., Sivasubdaram S., Tagami H., Takeda J.,		
RA	Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horichi T.;		
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome		
RT	corresponding to the 28.0-40.1 min region on the linkage map.";		

RL	DNA Res. 3:363-377(1996).
RN	[3]
RP	SEQUENCE OF 464-2003 FROM N.A.
RC	STRAIN-K12;
RX	MEDLINE-92190338; PubMed-1665988;
RA	Moszer I., Glaser P., Danchin A.;
RT	"Multiple IS insertion sequences near the replication terminus in
RL	<i>Escherichia coli</i> K-12.";
CC	Biochimie 73:1361-1374(1991).
CC	-I- SIMILARITY: TO S. TYPHIMURUM ORF NEAR CYS3 (AC P25928).
CC	-I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC	THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC	BETWEEN AMINO ACIDS 839 AND 840.
CC	-----
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).
CC	-----
DR	EMBL: AE000237; AACT4483.1; ALT_SEQ.
DR	EMBL: AE000237; AACT4487.1; ALT_SEQ.
DR	EMBL: D90778; BAA15009.1; ALT_SEQ.
DR	EMBL: D90778; BAA18880.1; ALT_SEQ.
DR	EMBL: D90779; BAA18881.1; ALT_SEQ.
DR	EMBL: X62680; -; NOT_ANNOTATED_CDS.
DR	EcoGene; EG11307; ydba.
DR	Hypothetical protein; Complete proteome.
FT	CONFIRM 489 489 I -> V (IN REF. 2).
FT	CONFLICT 495 495 I -> V (IN REF. 2).
SQ	SEQUENCE 2003 AA: 205949 MW: B83A12C8B53220EE CRC64;

Query Match	7.4%	Score 221;	DB 1;	Length 2003;
Best Local Similarity	23.6%	Pred. No. 0.0016;		
Matches 167;	Conservative 75;	Mismatches 230;	Indels 236;	Gaps 40;

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QY 50 SANNEQEDEDJLJLPVQCTV-----AVLLVNSRKEST-----GEKEKV-----EEND 92
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 141 SPNN-----DYLDKTEKTLTIRDSVFYTYEADDTISLQDSNGKRKATINLQJDEANNT 195
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 93 WAV-----YNEKGVLTAREITLKAGDNLIKONGTNYTSLKKDLTDLTSVGT 141
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 196 VALLEGVSADGATKMQYHNHNGELVI-----TGDNATVNNNG-----KTVYDGKDSGT 242
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 142 E-----KLSFSANGKVAITSDT-----KG-----LNF 164
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 243 EINGNNGKVIODGGDLDVSGGGHGIDITDSDATVBNKGTMTVTPDPSMGIOIDGKRAIVNN 302
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 165 AKETAGTNGDTFTVHLNG-----IGSTLTPDLTLNGATTNTNPNVTDEDEKKAASVND 217
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 303 EGESITITNGGCTGTQINGDDATATANNNGKTTYDGKDSGTGLEIKNNNGKVIOD-----GDL 356
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 218 VLMAGWNIKGVKPGCTTASDNVDFVRYTYDVE-LSADTKTTYVNESKD----- 265
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 357 VSGGGHGI-DITGDSATVDNKGKMTMTVTPDPSIGIQVDGQAVAVNNEGEATINGGTGQT 415
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 266 NGKTEYVATIGAKTSYITREKDGKLVTKGD-KGENG-----SSTD 302
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 416 NGDDATATANNNGKTVY-----DGRDSTGTETELAGNNGKVIODGDLVSGGGHGIDITGDSAV 471
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 303 EGEGLVTAKE-----VIDA-----VNKAGWKRUKTTTANGTQGAQDKFETVTSQWTVFAS 352
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 472 DNKGMTMTVTPDPSIGIQIDGQAIYVNNNGS-----ESTITNGCTG-----TQJNGDNAT-AN 521
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 353 GKGTATFVSKD-----OGNITVMTDVVNGVALNY-----NOLONGWN--LDSK-----A 396
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 522 NSGKTTVYDGKDSGTGKRIANGIGI-----VNLGDSLVTYGAHGVENIGDNQNTVANNKGDIYVS 578
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 397 VAGSSGKVIISGVNVSCKGKMDETVIMANNNIETIRNGKNIDIAISM-TPOFS----- 448
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

```

[illegible]

RESULT	3
AIDA_ECOLI	
ID	AIDA_ECOLI
AC	003155;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	01-JUN-1994 (Rel. 29, Last annotation update)
DE	Adhesin aida-I precursor.
GN	AIDA-I.
OS	Escherichia coli.
OC	plasmid PIB6.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Escherichia.
OX	NCBI_Taxid=562;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
CC	003155..003157

```

RT "AIDA-1: the adhesin involved in diffuse adherence of the
RL diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546 (1992).
CC -1- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X65022; CAA46156.1; -.
DR PIR: S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-1.
FT PROPEP ? 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

```

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Cc      121 SGGIQRVSSGGVASATNLSGGAONITNMGHASNVIYFSGGNOTIFSGITDSTNISSGGQ 180
Cc      142 EKLSFSGNKNVITSDTKGLNFAKTAGTNGDTYHLN-----GIGSTLPTLTLNT 194
Cc      181 ORV--SSGVAASNTTINS--AONILSEGAISTHSSGNOYISAGANATETIYNSG 235
Cc      195 APTNVTNDNTDDEKRAASVYDLNAGWNIGVYKPGTASDNVDVFTYDVEFLSADT 254
Cc      236 GFGVNSG-----AVATGTVLSG--TQNVSSGSAISTSVYNSGQTV--FAGATV 283
Cc      255 KTTIVNNEKSN-----GKTEVKGATSVYKEDGKLYTKDGENSSSTDEGEGLVTA 310
Cc      284 TDTTVNSGNGONISSGGIVSETVNVSGTONIYSGSALSANIKGS-----329
Cc      311 KEVIDAVKAKGRMKTTFANG-----QTQADKEFTVSTGNTVFASG-----KGT 356
Cc      330 ----QIVNSEBTAINTLVSDGCGHIRNGGIAAGTIYNOGYVNISSGVAESTITINS 385
Cc      357 TATVSKDDQGNITMYD--VNVGD-ALNVQNLQNSGWNL-----DSKAVAGSSG--K 403
Cc      386 TLRYLSDGYARGTILNNSGRENVSNGGVSYNAMITGNGOYISDGEATAIIVTSGFOR 445
Cc      404 VISGNVSKKMDJETVINAGN---NIETRNKN-----IDIASMPQF 447
Cc      446 INSGTAVQVSVVYVTRVSSAKPFDAEYVSGKQYVYLRGTYMSNFLTAVWSPMPC 505
Cc      448 SS---VSLGAGADAPTLSDVDALN-----VGSKKDNKPYRITNVAPGV 488
Cc      506 ASGANVNLSGLNMFAGNVVGTILNQBGRQYVYGATATSTVNGEGEYV-----LSGI 561
Cc      489 KEGDTYVAQLKGYAQNLRIDVNDGNARA-----GIAQAIATAGVQAVLPCKSMAT 543
Cc      562 TDTGTVNLSCGLOAVSSG-----GRASATVINEGAGQFVYDGGVY---TGTNIK-- 606
Cc      544 GGGTYRGGAGYALGYSSISDGSN 566
Cc      607 NGGTRVDSGASALNIALSSGN 629

Db      607 NGGTRVDSGASALNIALSSGN 629

RESULT 4
HLTA_PROMT ID HLTA_PROMT STANDARD; PRT: 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_Taxid=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hmba and hmbb) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shla and shlb).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
CC REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
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Cc      Cc      use by non-profit institutions as long as its content is in no way
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Cc      Cc      entities requires a license agreement (See http://www.isb.ch/announce/
Cc      Cc      or send an email to license@isb.ch).
Cc      Cc      -----
Cc      DR EMBL; M30186; AAA25657.1; -.
Cc      DR PIR; A35140; A35140.
Cc      KM Hemolysis; Toxin; Outer membrane; signal.
Cc      FT SIGNAL 1
Cc      FT CHAIN 30 1577
Cc      FT SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match
Best Local Similarity 22.3%; Score 207.5; DB 1; Length 1577;
Matches 154; Conservative 86; Mismatches 258; Indels 193; Gaps 32;

Cc      QY      22 LTRNHTKRSATVAVATLLEFATVQASANNEOEEDLYDPQRTVAVLYNSDK--- 78
Cc      Db      306 ITVNSSSSQTLTKTELKKNI--TLVASSHQIKASDMLMDDDITLQAGDLTIDGKQLQ 363
Cc      QY      79 -----EGGKEKYE-----ENDMAVYERKGVLTARETTLKAGNLK 117
Cc      Db      364 KETDIDNRMFYSMKYDVYKREKQIQIGSQIDAKNNATLTATKGDVTLDAKINAGNLLA 423
Cc      QY      118 IKONGTETYSLKRDITLTSVG--TEKLSFSGANGKNVITS-----DYKGLNFA 165
Cc      Db      424 INAN-----KDIHNGLEVKESEKREKNNHRSRLSSGMSNSHOTETLKAS 471
Cc      QY      166 KETAG-----TNGDTYVHLN---GIGSTLDTLL---NT 193
Cc      Db      472 ELTAGKDLGDAQSITAQAKLANEVLVNAKDINILANQKTNNDKTVYDNNHVMGCI 531
Cc      QY      194 GATTNVNDN-----VTDEKTRASVYKDLNMGWNIKG-----YKGTASDNVD 239
Cc      Db      532 GGGONKNNNOQVSHATQLPADGQLLADNANNITGSOYKQAGAFV--TTGGDVYI 589
Cc      QY      240 FVRTYDVEFLSAD-----TKTTVNESKDNKTEVYIGAKTSYKED-----GKL 288
Cc      Db      590 DNALSETISKIDERTGTAFTNTKSSHKNETKOTSTGSELISDQLYVSGNDVNVGSL 649
Cc      QY      289 VTGRDK-----GE-NGSST-----DEGEGLVT--AKEVIDAVNKAGRMKTTPANG 331
Cc      Db      650 IKSADKLIHSLGIDINVASAQOVTKIDKETSIAITGHAKEVEDKQYSAGFHITHTTKN 709
Cc      QY      332 QTQADKFEYVTSNTVYFASGKGTATVS--KDDGNTVNVYDNGDALNVQNLQNSG 389
Cc      Db      710 TSTTEQANSTISGANVDLQNKDVYTFAGSDLKTYYAGNASTIGD--NVAEYSTERKKQTD- 767
Cc      QY      390 WNLDSKAVAGSSGKVIYSGNVSPSKGMDJETVINAGNIEITRN--GNKIDIASMTPOFS 448
Cc      Db      768 -NTDTTISGFS---YTCGVYKVSADFOYD--KQHTQETVTKNRSGQTEVAGGLITAN 822
Cc      QY      449 SVSLGAGA-----DAPTLSDVDALNVGSKKD-----NKPV 479
Cc      Db      823 KDLHLEGASHHVEGRYQESGENIOHLAVNDSETSKT--DSLNVGIDVGVNIDYSGVTKPV 880
Cc      QY      480 R-----ITNAPGVKEDVDVNVQNLKGVANLNNRIDVNDGNARAGIAQAIATAGLVQA 533
Cc      Db      881 KKAIEDGVNTKPG--NNTDLTKRYTARALANLNL--LSNLE--TPNVGEVGIK----- 930
Cc      QY      534 YLPCKSMAIGGTYRGGAGYALGYSSISDG 564
Cc      Db      931 -----GGGSQSQSDSOAVSTINAG 951

RESULT 5
YDEK_ECOLI ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051; P76140; P77168;
```



DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical lipidprotein ydek precursor (ORF1).  
 GN YDEK OR ORF1 OR B1510.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12.  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Samped G., Seki Y., Sivasubram S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horinchi T.,  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL DNA Res. 3:363-377(1996).  
 RN [3]  
 RP SEQUENCE OF 585-1325 FROM N.A.  
 RX MEDLINE=94100243; PubMed=8274505;  
 RA Cartwright P.J., Tims M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;  
 RT "An Escherichia coli gene showing a potential ancestral relationship  
 to the genes for the mitochondrial import site proteins ISP42 and  
 MOM38.";  
 RL Blochim. Biophys. Acta 1153:345-347(1993).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 (Potential).  
 CC -1- SIMILARITY: TO E.COLI YEAL.  
 CC -1- SIMILARITY: SOME TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
 CC ISP42 AND MOM38.  
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
 FRAMESHIFT IN POSITION 653.  
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 CC -----  
 DR EMBL: AE000248; AAC74583.1;  
 DR EMBL: D90793; BAA15190.1; ALT\_INIT.  
 DR EMBL: D90794; BAA15197.1; ALT\_INIT.  
 DR EMBL: X73295; CAA51730.1; ALT\_FRAME.  
 DR PIR: S34315; S34315.  
 DR Ecogene: EG11780; ydek.  
 DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
 FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT CONFLICT 884 884 N -> K (IN REF. 3).  
 FT CONFLICT 1317 1317 M -> S (IN REF. 3).  
 FT SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 6.9%; Score 206; DB 1; Length 1325;  
 Best Local Similarity 22.8%; Pred. No. 0.0052;  
 Matches 147; Conservative 72; Mismatches 267; Indels 160; Gaps 27;  
 QY 1 MKKIYRIINNSALNANVVVSELTNRHTKRASATVKTAVLATLLEFATVQASANNEDEEDL 60  
 DB 1 MKRIYRVINNCVQLQVQACSELTFRAGKSTVNLRRKSSGLTKFRSL----- 47  
 QY 61 YLDPQRTVAVLIVNSDKGTGKEKEVEENSDMAVFNEKGVLTAREITLKKAGDNLIKQ 120  
 DB 48 -----TLGVLLALS-----GSASGASLEVDNDI----- 71  
 QY 121 NCTNFTYSKKDLDLTLSVTEKLSFANGKNVITSDTKGLFAKETAGTNGDTVHLN 180  
 DB 72 --TNIDTVAIYALVGVGTGLNLAGN-ASLTITTSV-----IGANDSGLYV 122  
 QY 181 GIGST--LTFD-----LNTG-----ATVNTDNDVTDEKKRAVSKVYLNAGNIRKYK 229  
 DB 123 VLGGTWRLYDSGNBAPLNVAGSGTGLNIKQKGVHDG-----GYLRIGSSYGVV- 172  
 QY 230 PGTTASDNDVFRVTVTFEFLSADTKTTVNVNSKNGKTE-----VKIGAKTSYIK 282  
 DB 173 -GTVNVGEBDSVLTTLFELISYGTSLNIT---DKGVYTSIVAILGYQAGSNGQVYV 227  
 QY 283 EKDGK-LVTGKDKG-----ENGSTDEGELVTAKEYIDAVNKAWRMKTTTANQGT 333  
 DB 228 EKGEWLNKNDSSIFQIGNGTGATIREGLVTAENTIIIGNATG---IGTLNVO- 282  
 QY 334 GQADKEFTVYSGTNTVPASGKTATVSKDDGNITVMDVNVGALN--VNOJLQNSGN 391  
 DB 283 -DDSVITVRLYNGYENG--TVNISNGLINNKREYSLVGVQDSHGIVNTDGRHWN 338  
 QY 392 L-----DSKAVAGSSGKYISGVNSKSKMDT-----VNI 423  
 DB 339 FLCTGAFPRYIYIGADGDELNVSSSEKVDGSGITIG--MKETGNTITVKDKNSVITN 395  
 QY 424 AGNNIEITRNGKNIDATVMTPOFSSVLCAGADAPLTVSDGALVNSKDK-NKPVRI 482  
 DB 396 LGNLGIDGHEMNISNOGLVNSGSSILGY---ETGVGNVSIITGGGWMEVKNKYVTT 451  
 QY 483 NVAPEGEDVTNVAQLKVAQNLNRRIDVNDGNARAGIAQALATVAGLVQAVLP--GKSM 540  
 DB 452 IGAVAGVNLINISDGG--KFVSQNTIFLGDKASGIGTLNLMDATSSPDVGINVNGSGSI 509  
 QY 541 MAIGGTYRGEAGYAL-----GYSSISDGNMIIKGTASGNSR 578  
 DB 510 VNVSNCATLNSICGYFIGNASGKGIYVISTSLMNLK-TSSYNAQ 554  
 RESULT 6  
 OMPB\_RICRI STANDARD; PRT; 1654 AA.  
 AC 053047;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)  
 DE (rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein  
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).  
 GN OMPB.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=92167802; PubMed=1724278;  
 RA Gilmore R.D. Jr., Cleplak W. Jr., Pollicastro P.F., Hackstadt T.;  
 RT "The 120 kDa outer membrane protein (rOmp B) of Rickettsia  
 rickettsii is encoded by an unusually long open reading frame:  
 evidence for protein processing from a large precursor.";

RL M01. Microbiol. 5:2361-2370(1991).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN-R;  
 RX MEDLINE=90136087; Pubmed=2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RL M01. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X16353; CA34403.1; -  
 DR InterPro: IPR003858; COMPACTOMP.  
 DR Pfam: PF02708; COMPACTOMP; 1.  
 KW Antigen; S-layer; Cell wall.  
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT DOMAIN 1334 1654 32 KDA BETA PEPTIDE.  
 FT DOMAIN 1181 1188 POLY-PHR.  
 SO SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.7%; Score 201; DB 1; Length 1654;  
 Best Local Similarity 22.6%; Pred. No. 0.012;  
 Matches 164; Conservative 83; Mismatches 282; Indels 196; Gaps 33;

QY 7 TIMSALNAMYVSELR-----NHTKASATVKTAVLATLTFATVQASAN 52  
 DB LLLMTANLAVTSBDTIGFTVNVNHAHSFNLTNG--KTLTIGQGVTAQAAT 148  
 QY 53 NEBOEDILYLPVQRTAVLVNSDEKTEGEKEVEENSDMAVFNNEGVLARTITKA 112  
 DB KNAQNV-----VVOFNNGCAIDNNDLKGVG--RIDFGAPSTLVFNLANPTTQAPLIL 200  
 QY 113 GDNLIKONGNFTYSLKKDLTDLT--SVGTEKLSFSANGKVNTPSTGKLNFAKETAG 170  
 DB 201 GDNNAV-ANGVNGTLVNGFIQVSNKSFATYKAINIDGGIITNTANNANTLNLQA- 258  
 QY 171 TNGDTVHLANGISGTLTNTLTGATTVNTDNTVDEKKRAASVADVLANGMNIGVAP 230  
 DB 259 --GGTTINFTGIDGTGRVLVLSKHA--ATNPNTIG-----SLGGLNGVIE 301  
 QY 231 GTTASDNVDFRYDYVFEVLSNOKTTTVN-----VESKDNCKTEV--KICAKSV 280  
 DB 302 FNTVA-----VDGQLTANAGANNAVITGNGAGRAAGFVSVDNKAVATIIGQVYAKDMV 356  
 QY 281 IKERKGLVTK-----DKGENS-----STDEGEGVTAKEVI 314  
 DB 357 IQSAN--ATQOVNFRHIVDVGDTTAKTPASKVTTITQDSNFGCNTPG-NLAQIKVP 412  
 QY 315 DAV-----NKAGWRMKTATTANG--QTGADKEFVYSGTNVTFASGKT-- 356  
 DB 413 NAITLTGTFGDASNPWTAG--VITPDANGTLESASADANAVAVTNNTITALEASAGVYQ 470  
 QY 357 -----TATVSDDOGNITVTMDVNGDALN--VNOLONSGMNLSKAVAGSGKATISGNV 409  
 DB 471 LSGTHAAELRLGNAGSIFKLAD--GTIVNGVNOFTALVGALAGTITLDSATITEDI 527  
 QY 410 SPKSGKM-----DETVININ--GNIEITRNKNI-----D 438  
 DB 528 GNAAGAAALORITLNDAAKKTITLTGAGANIGAGGSTITDQANGTITKLSTONNIVDPD 587

QY 439 IANSMPQESSVSLGADAPTLSVDG-----DALVNGSK--DNKPVARTN 483  
 DB 588 LATA-TDQTVVDASSLTNQOTLTINCKITGANNKTLGOFNPGSKVTLSSNGVAINE 646  
 QY 484 VAPVKEGDV-----TNVAQLKGAQNLNRIIDVGNARAGIAQATATAGVQAY 534  
 DB 647 LVIG-NDGAVQPAHDYTLITRTTNAAGQKIIFPVVNNGTTLAAGTNGSATNPPLAEIN 705  
 QY 535 LPGR-----SMAIGGCTYRGEAGYA-----IGYSSIDGGMNIIKGTASGNSRGH 580  
 DB 706 FGSGAVVDVILVNGSEVNL-----YATNITTDANVGSFVFNAGGTIVSGTVGGQGNK 761  
 QY 581 FGASA 585  
 DB 762 FNTVA 766

RESULT 7  
 HLVA\_SERMA STANDARD; PRT; 1608 AA.  
 AC P15320;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN SHLA.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 OX NCBI\_Taxid=615;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
 RC STRAIN=SN8;  
 RA MEDLINE=88257037; Pubmed=3290200;  
 RX Poole K., Schiebel E., Braun V.;  
 RT "Molecular characterization of the hemolysin determinant of Serratia  
 RT marcescens.";  
 RL J. Bacteriol. 170:3177-3188(1988).  
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
 CC DEFINED.  
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
 CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
 CC REQUIRES SHLB FUNCTION.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane.  
 CC -1- SIMILARITY: TO P. MIRABILIS HEMOLYSIN (HPMA).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M22618; AAA50323.1; -  
 DR PIR: A28182; A28182.  
 KW Hemolysis; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 1608 HEMOLYSIN.  
 SO SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.4%; Score 191.5; DB 1; Length 1608;  
 Best Local Similarity 21.8%; Pred. No. 0.033;  
 Matches 151; Conservative 87; Mismatches 239; Indels 217; Gaps 34;

QY 24 RNHTR-----ASATVKTAVLATLTFATVQASANNEEQ-----EDLYLP--- 64  
 DB 460 RNHTSLRTGRMSNDESESLKASRLRSEGETLTAKGRNVSTOGAKVHAQDLITIDADNQ 519  
 QY 65 -----VQRTVAVLIVNSDEKTEGEKEVEENSDMAVFNNEGVLARTITLAKGNLKI 120

```
DB 520 IQGVQKTAANAKAVHDDKTSWG-----GIGGGDN-----K 549
QY 121 NCTNFTYSKLKUL---TDLTSVTEKLSFANGNK-VNIT-SDTYGLNPAKTAGTNGDT 175
DB 550 NNSN-----RREISHASELTSGLTURL---NGOOGVITTSKARGOKGGEVTA-THGGL 599
QY 176 TVHLNGIGSTLDTLLNCGATNTVNDVNTDDEKKRAASVKVYLAAGWIKRKKGTAS 235
DB 600 RID-NALSTTVDKIDARTGTAFNITSSSHKADNYSOSTASL-----KSD 644
QY 236 DANVDFRYDYEF-----LSADTKTTVNVE----- 262
DB 645 TNLTLVSHKADAVISQVASSGELSVESTGTGNINKAERQONIDEOKALTAVNGYAKKA 704
QY 263 -----SKONGKTEVRIKGAITSVIERKDKLVTKDKGNGSS--TDEGGL 307
DB 705 GDKQYRAGLRIEHTDSEKTTTENSAS--SSLGSGSVKLKAEDVTFSGSKLVADKGDAS 762
QY 308 VTAKEV--IDAVNKAAGWIKTTTANG---QTGQADKFEVYTGSTVNTFASGCTATVSK 362
DB 763 VSGNVSFLAADKTAASTEQTKIGGGEYTGIDK--LGSVGEAGYEENK--TOAQSSK 818
QY 363 -----DDQNTTVYDVVGDALNVNOLONGMNLDSKAVAGSSGKVISGVNPSKGM 416
DB 819 AITSGSDVKGNLT-----INARKLTOGQAGHVGAGAYQENAGVHDLAADTASTTTT 874
QY 417 DETVINAGNNIETRNKNIDIASMTPOFSSVSLGA-----GADAPLTVD 464
DB 875 DVGWNI-----GANVDYSATVRPERAVGKAAKLDTAGVINDIGIGAPNVGID 923
QY 465 GQALVWGSKK--DNKPVRTNVAAGV---KEGDV---TNAQLKGVANQLN----- 507
DB 924 IGAQGGSSSKSSSSQAVVSVQASIDINAKGEVRDOCTQYQASG-AVNLTADSHRSE 982
QY 508 ---NRIDNVGNARAGIAQAIATAGLVQAVLPKGSMAIG---GGTYGEGAGYAGISS 560
DB 983 AANANQDEGSRPTR-----GSAG-VRYTTTGSDLPTVDAGEGTQHSNSASQAVTG 1034
QY 561 ISDGGW-----IIKGTASGNSRGHFAGASA 585
DB 1035 SIDAANGINNVNKKDAIYOGTALNGRGKTAVNA 1068

RESULT 8
OMPA_RICRI STANDARD: PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).
DE OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxId=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M31227; AAA26380.1; -.
DR PIR, A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 2249
FT DOMAIN 212 1180
FT REPEAT 212 286
FT REPEAT 287 358
FT REPEAT 359 430
FT REPEAT 431 505
FT REPEAT 506 577
FT REPEAT 578 652
FT REPEAT 653 724
FT REPEAT 725 799
FT REPEAT 800 874
FT REPEAT 875 949
FT REPEAT 950 1021
FT REPEAT 1022 1093
FT REPEAT 1094 1165
FT REPEAT 1166 1180
FT SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.4%; Score 191; DB 1; Length 2249;
Best Local Similarity 24.4%; Pred. No. 0.052;
Matches 142; Conservative 56; Mismatches 212; Indels 172; Gaps 30;

QY 98 NEKVLTAREITLTKAGDNLKIKONGTNPYSLKK--DLTDLTSVTEKLSFSA--G 150
DB 766 NANAVALTGAIIDMTTGGDNV---LNLGALSQVYTGIDIGNSLAT--ISVAGATATG 819
QY 151 NKVNITSDTKLNFKAETAGT-----GDT--TVHLNGIGSTLDTLLNT- 193
DB 820 GAVIKATTTKLTNAAASVLTLTANNAVLTGAVDNTTGGDNVGLNLGALSQVYTGIDIGN 879
QY 194 -----GATTNVTNDVNTDDEKKRAASVKVYLAAGWIKRKKGTASDNV 238
DB 880 SLATISVGAGTATLGAVIKATTTKLTN---AASVLTLTANNAVLTGAIIDMTTGGDNV 934
QY 239 DVPRTYDVEPIADPTKTTTVNVEKNGKTEVKIGAKTSVIERKDKLVTKDKGNG 298
DB 935 GVLNLGALSQVYTGIDIGNT-----NSLAT-ISVAGATATL----- 968
QY 299 SSTDEGGLVTAKEVIDAVNKAAGWIKTTTANGQGTQADKFEVYTGSTVNTFASGCTTA 358
DB 969 -----GGAVIKATTTKLTDAASAVKFTNPVYVGTGAIIDNTGNANGI-VFTFGNSVTYG 1020
QY 359 TVSKDDQGNITVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVISGVNPSKGMDE 418
DB 1021 NV-----GFTNALATVNVAGL--LQVGGVYKANTINTLDNAAVTFNTPVYVGTGAI 1073
QY 419 TVNINAG-----NNEITRNKNIDIASMTPOFSSVSGAGADAPTLTVDGAL--NVG 471
DB 1074 TGNANNGIYFTFGNSTVTVNGN-----TNALATVNVAG-----LLOVGGGVYKANT 1122
QY 472 SKKDN-KPVRIITNVAPEKGEVDVTVNQLKGVAONLNRIIDNVGNARA---GIAQATA 526
DB 1123 NLTDNAAVATFTFN--PVVYVGTGAIIDNTG-----NANNGIYFTFGNSTVYTGIDIGN 1173
QY 527 T-----AGL-VQAVLPKGSMA-----IGGTYRGAGATG--SSIS 562
DB 1174 TVNVGAGITLQA---GGSILAANNIDGARSTLEFNGPLDGG-----GAIPYEFKAIA 1224
QY 563 DQGNMIIK-----GTASGNSRGH--FGASASVG 588
```

DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta neptidel]

GN OMPB OR RC1085.  
 OS Rickettsia conorii.  
 OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales:  
 OC Rickettsiaceae: Rickettsiidae: Rickettsia.  
 OX NCBI\_TaxId=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Malish 7;  
 RX MEDLINE-21442074; PubMed-11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Bahe V.,  
 RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";   
 RL Science 293:2093-2098(2001).  
 RN [2]  
 RP SEQUENCE OF 33-1649 FROM N.A.  
 RC STRAIN-Indian tick typhus, and Malish 7;  
 RX MEDLINE-20393643; PubMed-10939649;  
 RA Roux V., Raoult D.;  
 RT "Phylogenetic analysis of members of the genus Rickettsia using the  
 RT gene coding the outer-membrane protein ompB (ompB).";  
 RL Int. J. Syst. Evol. Microbiol. 50:1445-1455(2000).  
 RN [3]  
 RP SEQUENCE OF 353-1655 FROM N.A.  
 RC STRAIN-Malish 7;  
 RA Stenos J., Walker D.;  
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
 RT australis, the most divergent rickettsia of the spotted fever group.";   
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
 CC SIMILARITY).  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: AE008659; AL003623.1; -;  
 DR EMBL: AF123721; AAF34124.1; -;  
 DR EMBL: AF123726; AAF34129.1; -;  
 DR EMBL: AF149110; AAD39533.1; -;  
 DR InterPro: IPR003858; COMPACTOMP.B.  
 DR Pfam: PF02708; COMPACTOMP.B.  
 DR Antigen: S-layer; Cell wall; Complete proteome.  
 KW CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.  
 FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 78 78 G -> N (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 413 413 I -> D (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 988 988 R -> T (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
 FT VARIANT 353 353 K D -> G H (IN REF. 3).  
 FT CONFLICT 776 776 F -> S (IN REF. 3).  
 FT CONFLICT 1159 1159 E -> D (IN REF. 3).  
 FT CONFLICT 1177 1177 G -> S (IN REF. 3).  
 FT CONFLICT 1492 1492 H -> R (IN REF. 3).  
 SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCB37 CRC64;

Query Match

6.2%; Score 186.5; DB 1; Length 1655;

Best Local Similarity 21.6%; Pred. No. 0.06;  
 Matches 161; Conservative 77; Mismatches 266; Indels 241; Gaps 36;  
 OY 10 NSALNANVVSSELT-----RNHTRKASATYKTAVALATLLPATOASANNEQEE 58  
 DB 95 NTAANNLDVTVREDDTLGFTTVNNANHNLMNAGTKTLITGCGITTVQAAATKKNANNV 154  
 OY 59 DLYLDVQRFVAVLVIVSDKEGTGEKEVEENSDMAVYFNEKGVLPARETLKAGDLKI 118  
 DB 155 -----VAQVNNGAIDNNDLQGVGRIDCGAAS--TLVFNLAND--TIQKAPLIGDNAV 206  
 OY 119 KONGTFEYSLKRDLDLTLSVTEKLSFSANGKNVNTSDPKLNFAKETAGTN----- 172  
 DB 207 -VNGANGTLNVTNGEFIKVSS-----KSF-ATVAVINI-GGGQGMFTDADNVNTLMLQA 258  
 OY 173 GDTTVHLNGISLTITLTLTGATNTNDNTVDDEKKRAASKVDVLANAGNNTKGVKPGT 232  
 DB 259 NGATITFNGTGTGRVLTLKRNAA--ATDENVTG-----SLGGLNKGI----- 299  
 OY 233 TASDNVDVFTVTVFVLEADLTFTTVNVEKNGKTEYKIGAKTSVIEKDGKLVTK 292  
 DB 300 -----IEF-----NTVAVNGOLKANA-----GANAIVIGTNG--AGR 330  
 OY 293 DKG-----ENGSS-STDEGE-----GLYTAKEVIDAVNKAQRMTT----- 327  
 DB 331 AAGFVSVSDGKAVATIDGOYVAKDMVIGSANAVGOVNFRIIVDVGTCGTAFAFTAASKVA 390  
 OY 328 -TANGOTGQADK-----EYVSGTNVT-FASGKGTVA-TVSKDQGN-IVMYD 373  
 DB 391 ITONSNEGTVD-FGNLAQIIVPNTMTLNGFTGDASNPNFTAGVITFDANGTLASASAD 449  
 OY 374 VNYGDALNVNQDLSNGNNDLSKA-----VAQS-----SGKVSIGVSPSK----- 413  
 DB 450 ANVAVTNNITALESGAGVQVLSGTHAAELRLGNAGSVFRLADGVTVNGVNDALVGA 509  
 OY 414 -----GKDETVNINA-424  
 DB 510 LAAGTITLDSATITDIGNAGGAALQGITTLANDATKTLTGAGNITIGANGTINQAN 569  
 OY 425 GNNIEITRGNKI---DIATSMTPQESSVSLGADAPPLVSDGALNVGSKKDKPVR 480  
 DB 570 GGTIKTLSTONNVIVVDFDLAIA-TDQGVVDASSLTFAAQITLTKNGKGTGGA--NNKTLG 626  
 OY 481 ITNVAAG--VKRGDV-----TVAQLKGAQMLNRRIDVDC 515  
 DB 627 QFNIGSKTYVLSGDVAINELVIGNNGAVOPAHNTYLTITTNAGGKTLTFNPNVNNNT 686  
 OY 516 NARAGIAQAIATAGLVQAVYLPK-----SMAIIGGTYGEGAGYA-----IGYSS 560  
 DB 687 TLATGTNLGSATNPPLAINEGSKGANVDTVLVNWG-----KGVMLYXANTNITTDANVGSFI 742  
 OY 561 ISDGGNIIKIGTASGNSRGHFGASA 585  
 DB 743 FNAGGTIVYSGTVGGQGNKFNFTVA 767  
 RESULT 11  
 OMPB\_RICTY STANDARD; PRT; 1645 AA.  
 AC P96989;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
 DE (rOmp B) [contains 120 kDa surface-exposed protein (Surface protein  
 DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB OR SLP.  
 OS Rickettsia typhi.  
 OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales:  
 OC Rickettsiaceae: Rickettsiidae: Rickettsia.  
 OX NCBI\_TaxId=785;  
 RN [1]



[illegible]







CC -1 SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1 SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
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CC -----  
CC EMBL: AB003681; BAA20138.1; -  
DR InterPro: IPR003858; rompa\_ompb.  
DR Pfam: PF02708; rompa\_ompb: 1.  
KW Antigen; S-layer; Cell wall.  
FT CHAIN 1 1338 120 KDA SURFACE-EXPOSED PROTEIN.  
FT DOMAIN 1339 1656 32 KDA BETA PEPTIDE.  
FT DOMAIN 528 533 POLY-GLY.  
SQ SEQUENCE 1656 AA; 168097 MW; 3132A69C9D5999F CRC64;

Query Match 6.0%; Score 181; DB 1; Length 1656;

Best Local Similarity 21.9%; Pred. No. 0.11;

Matches 159; Conservative 80; Mismatches 284; Indels 202; Gaps 35;

OY 10 NSALNMMVYVSELT-----RNHKKRASATY--KTAVLATLFAIVQASANNEDQEE 58  
DB 95 SNANNILAVYSEDTYIGFINNANNANRNFLTLDAGKTLITGQGITNWQSAATHN--- 150  
OY 59 DLYLDPVQRTVA-----VLIVNSDKEGTEGEKEVEENSDDAVYFNEKGVLTAREITLKAG 113  
DB 151 -----AQNIIVAKFENGGAALANNDSLGLG---TIDGAAASTIVFDLANPTQKAPLILA 201  
OY 114 DNLIKQNGTNTFTYSLKQDLTLTSVTEKLSFANGKNVITSPTKGLNFAKETAGTN- 172  
DB 202 DNALI-VNANGTLNVTNGFIQVSD-----KSF-ATVKAINI-GDGQGFMENTNATNAN 253  
OY 173 -----GDTTVHLNGIGSTLEDTILN-TGATTNVTNDVTDDEKKRAASVKDVNLACGNIK 226  
DB 254 LNLQAGTTINENGTDGTRGLVLSKNGATDF--NVTG-----SLAGNLIK 297  
OY 227 GVPKTTASDNVDFVRYTVEFLSADTKTTVY-----VESKONGKTEV--KIGA 276  
DB 298 GIIELTVAINGOLIANAG-----PANAVIGTNGAGRAAGFYVSDNGKAATIDQVYA 352  
OY 277 KTSVIKE-----KDGKLVYTKDKGENGSTDEGE--GLVFAK 311  
DB 353 KDMVIGSANNAGOVNFRHIVDVGIDGTTAFKTAASIVAITQNSNFGTTDFGNLAQVTP 412  
OY 312 EYIDAV-----NKAGRMKTTTANG--QTGQADKFEFTVYSGTNVTFASGKT-- 356  
DB 413 DMTLNGNFTGDANNPQNFAG--VITFAANGTLASASADANAVATNNITAIEASGVVVO 470  
OY 357 -----TATVSKDDQGNITWYDVNVDALN--VNOLNSGMNLDKAVAGSSSGKVISGV 409  
DB 471 LSTHTHAELRLGNAGSVFKLAD--GTVINGKYNQTVLVGVLAAAGATILDSGATITGDI 527  
OY 410 SPKSG-----KMDETVINA--GNNIETTRNGKNI---D 438  
DB 528 GNGGGAALQSTILANDATKTLTGLGANIISANGTINFGANGTITKLSTQNNIYVDCD 587  
OY 439 IATSMTPQSSSVSLGAGAPITLSVDG-----DALNVGSK--DNKPYRITN 483  
DB 588 LAIA-TDQTVGVVDASSLTNAQTLTISGTIGIIGANNPTLQGFNIGSSKTTLNGCNVAINE 646  
OY 484 VAPVKEGYV-----TNVAQLKVAQNLNRRIDVNDGNARAGIAQAIAATAGLVOAY 534  
DB 647 LVYIG-NGGSVQFAHNTYLLITRTNAGCGKIIFNPVYNNNTTLAAGTNLGSANPLALEIN 705  
OY 535 LPCK-----SMAAIGGTYRGEGYA-----IGYSSISDGMWIIKGTASGNSRGH 580  
DB 706 FGSKGARADTVLVNVEGVNL-----YATNITTTDANVGSFVFNAGKNIIVSGTVGGQGNK 761

OY 581 FGASA 585  
DB 762 FNTVA 766

Search completed: July 3, 2002, 08:29:38  
Job time: 1149 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:19 ; Search time 168.02 seconds  
(without alignments)  
608.499 Million cell updates/sec

Title: US-09-771-382-1  
Perfect score: 3003  
Sequence: 1 MNKRYRIMNSALNAMYVS.....TASGNSRGHGASASVGYQM 591

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3003	100.0	591	16 Q9JR18	Q9JR18 neisseria m
2	2999	99.9	591	2 Q9JPS7	Q9JPS7 neisseria m
3	2984	99.4	591	2 Q9JQY3	Q9JQY3 neisseria m
4	2971.5	99.0	592	2 Q9AQFO	Q9AQFO neisseria m
5	2885.5	96.1	590	2 Q9JPS3	Q9JPS3 neisseria m
6	2761.5	92.0	600	2 Q9JPS6	Q9JPS6 neisseria m
7	2758.5	91.9	594	2 Q9JQY4	Q9JQY4 neisseria m
8	2751.5	91.6	594	2 Q9JPS2	Q9JPS2 neisseria m
9	2747.5	91.5	594	2 Q9JPS13	Q9JPS13 neisseria m
10	2740.5	91.3	594	2 Q9JPS7	Q9JPS7 neisseria m
11	2738.5	91.2	598	2 Q9JPS8	Q9JPS8 neisseria m
12	2725.5	90.8	598	2 Q9JPS10	Q9JPS10 neisseria m
13	2725.5	90.8	598	2 Q9JPS0	Q9JPS0 neisseria m
14	2716.5	90.5	598	2 Q9JQY5	Q9JQY5 neisseria m
15	2685	89.4	599	2 Q9JPS8	Q9JPS8 neisseria m
16	2616.5	87.1	592	2 Q9JPS9	Q9JPS9 neisseria m

17	2611	86.9	599	2 Q9JPS8	Q9JPS8 neisseria m
18	2574.5	85.7	598	2 Q9JPS7	Q9JPS7 neisseria m
19	2573.5	85.7	592	2 Q9JQY2	Q9JQY2 neisseria m
20	2532	84.3	595	2 Q9JPS0	Q9JPS0 neisseria m
21	2528.5	84.2	599	2 Q9JPS5	Q9JPS5 neisseria m
22	2490	82.9	600	2 Q9JPS10	Q9JPS10 neisseria m
23	2479	82.1	589	2 Q9JQY1	Q9JQY1 neisseria m
24	2464.5	82.6	592	16 Q9JQW4	Q9JQW4 neisseria m
25	2449.5	81.6	526	2 Q9JPS4	Q9JPS4 neisseria m
26	2447.5	81.5	530	2 Q9JPS1	Q9JPS1 neisseria m
27	1247	41.5	2353	2 P71401	P71401 haemophilus
28	1061.5	35.3	1098	2 Q48152	Q48152 haemophilus
29	435.5	14.5	1299	16 Q9F3X6	Q9F3X6 pasteurella
30	393	13.1	2059	16 Q9PD50	Q9PD50 xyella fas
31	378	12.6	1107	2 Q9F2D8	Q9F2D8 salmonella
32	371.5	12.4	1190	16 Q9PC04	Q9PC04 xyella fas
33	368.5	12.3	2712	16 Q9F3X5	Q9F3X5 pasteurella
34	249.5	8.3	1291	16 Q92KQ7	Q92KQ7 rhizobium m
35	244.5	8.1	1004	16 Q9PD63	Q9PD63 xyella fas
36	243	8.1	1953	16 Q98HJ2	Q98HJ2 rhizobium l
37	240	8.0	1265	2 Q9FDA0	Q9FDA0 xanthomonas
38	239.5	8.0	1039	2 Q9L6T7	Q9L6T7 escherichia
39	239.5	8.0	1040	2 Q9AL50	Q9AL50 shigella fl
40	233.5	7.8	2276	2 Q93TY6	Q93TY6 staphylococ
41	233.5	7.8	3930	16 Q98E20	Q98E20 rhizobium l
42	232.5	7.7	1536	2 Q48031	Q48031 haemophilus
43	230.5	7.7	1039	2 Q9L6T8	Q9L6T8 escherichia
44	229	7.6	989	2 Q9XD84	Q9XD84 escherichia
45	227	7.6	832	2 Q54356	Q54356 moraxella c

## ALIGNMENTS

RESULT 1  
Q9JR18 PRELIMINARY: PRT: 591 AA.  
AC Q9JR18:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NMB0992 OR NHHA.  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria: Proteobacteria: beta subdivision: Neisseriaceae: Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masiagnani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B., Ratti G., Santini L., Savino S., Scarselli R., Marchetti E., Mora P., Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.M., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.;  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.M., Peden J.F., Dodson R.J., Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B., Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scariato V., Masiagnani V., Pizza M., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.:  
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
MC58.";  
RL Science 287:1809-1815(2000).  
RN (1)  
RP SEQUENCE FROM N.A.  
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF26375; AAF42524.1; -  
DR EMBL; AF26375; AAF41395.1; -  
DR EMBL; AF26367; AAF42516.1; -  
DR EMBL; AF26370; AAF42519.1; -  
DR EMBL; AF26374; AAF42523.1; -  
DR EMBL; AF157611; AAK68872.1; -  
DR TIGR; NMB0992; -  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F3EC6 CRC64;

Query Match 100.0%; Score 3003; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1e-118; Indels 0; Gaps 0;  
Matches 591; Conservative 0; Mismatches 0;

QY 1 MNKYYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
DB 1 MNKYYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
QY 61 YLDPVQRTAVAVLIYNSDKEGTGEKEKEVENSMAVYNEKGVLTAREITLKAGDNLIKQ 120  
DB 61 YLDPVQRTAVAVLIYNSDKEGTGEKEKEVENSMAVYNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGTFEYSLKLDLDTLSVGTGKLSFSANGKNVITSDTGKLNFAKTAGNGDTYHLN 180  
DB 121 NGTFEYSLKLDLDTLSVGTGKLSFSANGKNVITSDTGKLNFAKTAGNGDTYHLN 180  
QY 181 GIGSTLDTLLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKPGTASDNVDF 240  
DB 181 GIGSTLDTLLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKPGTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVTKDKGENSS 300  
DB 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVTKDKGENSS 300  
QY 301 TDEEGGLTAAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360  
DB 301 TDEEGGLTAAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360  
QY 361 SKDOGNITVAVDVNVDGALNVNOLONGSNWLDKAAVAGSSGKYISGNVSPSKKMDTV 420  
DB 361 SKDOGNITVAVDVNVDGALNVNOLONGSNWLDKAAVAGSSGKYISGNVSPSKKMDTV 420  
QY 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKNKPVR 480  
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKNKPVR 480  
QY 481 ITNVAPEGKEDDVNVAOLKQVAVNLRINDVGNARAGIAOLAATAGLQVAVLPKSKM 540  
DB 481 ITNVAPEGKEDDVNVAOLKQVAVNLRINDVGNARAGIAOLAATAGLQVAVLPKSKM 540  
QY 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 591  
DB 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 591

RESULT 2  
09JPS7 PRELIMINARY; PRT: 591 AA.  
AC 09JPS7;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuli S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF26366; AAF42515.1; -  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 99.9%; Score 2999; DB 2; Length 591;  
Best Local Similarity 99.8%; Pred. No. 1.5e-118; Indels 0; Gaps 0;  
Matches 590; Conservative 1; Mismatches 0;

QY 1 MNKYYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
DB 1 MNKYYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60  
QY 61 YLDPVQRTAVAVLIYNSDKEGTGEKEKEVENSMAVYNEKGVLTAREITLKAGDNLIKQ 120  
DB 61 YLDPVQRTAVAVLIYNSDKEGTGEKEKEVENSMAVYNEKGVLTAREITLKAGDNLIKQ 120  
QY 121 NGTFEYSLKLDLDTLSVGTGKLSFSANGKNVITSDTGKLNFAKTAGNGDTYHLN 180  
DB 121 NGTFEYSLKLDLDTLSVGTGKLSFSANGKNVITSDTGKLNFAKTAGNGDTYHLN 180  
QY 181 GIGSTLDTLLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKPGTASDNVDF 240  
DB 181 GIGSTLDTLLNTGATTNVTNDNTYDDEKKRAASVKDVLNAGNMIKGVKPGTASDNVDF 240  
QY 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVTKDKGENSS 300  
DB 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVTKDKGENSS 300  
QY 301 TDEEGGLTAAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360  
DB 301 TDEEGGLTAAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360  
QY 361 SKDOGNITVAVDVNVDGALNVNOLONGSNWLDKAAVAGSSGKYISGNVSPSKKMDTV 420  
DB 361 SKDOGNITVAVDVNVDGALNVNOLONGSNWLDKAAVAGSSGKYISGNVSPSKKMDTV 420  
QY 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKNKPVR 480  
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKNKPVR 480  
QY 481 ITNVAPEGKEDDVNVAOLKQVAVNLRINDVGNARAGIAOLAATAGLQVAVLPKSKM 540  
DB 481 ITNVAPEGKEDDVNVAOLKQVAVNLRINDVGNARAGIAOLAATAGLQVAVLPKSKM 540  
QY 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 591  
DB 541 MAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 591

RESULT 3  
093QY3 PRELIMINARY; PRT: 591 AA.  
AC 093QY3;  
DT 093QY3

DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF157606; AAK68867.1; -  
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;

Query Match 99.4%; Score 2984; DB 2; Length 591;  
Best Local Similarity 99.5%; Pred. No. 6.2e-118;  
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNKIRIINSLNLMVWVSELTNRHNRKASATVTAVALATLTFATVOASANNEDQEDL 60  
DB 1 MNEILRIINSLNLMVWVSELTNRHNRKASATVTAVALATLTFATVOASANNEDQEDL 60  
OY 61 YLDPVQRTVAVLIVNSDKEGEGEKEVEENSDMAVYFNEKGVLTAREITTLKAGDNLKIK 120  
DB 61 YLDPVQRTVAVLIVNSDKEGEGEKEVEENSDMAVYFNEKGVLTAREITTLKAGDNLKIK 120  
OY 121 NGNTFTYSLKDLTLDSVTEKLSFSSANGKNVITSDTKLNFPAKETAGTNGDTVHLN 180  
DB 121 NGNTFTYSLKDLTLDSVTEKLSFSSANGKNVITSDTKLNFPAKETAGTNGDTVHLN 180  
OY 181 GIGSTLTDLTLNLTGATNTVNDNTDDEKRAASVADVNLNGMNIKGVPPTTASDNDV 240  
DB 181 GIGSTLTDLTLNLTGATNTVNDNTDDEKRAASVADVNLNGMNIKGVPPTTASDNDV 240  
OY 241 VRTYTVFEFLSADPTKTTVNYESKDNKTEKTEKIGAKTSVIEKEDGKLVTKDNGENSS 300  
DB 241 VRTYTVFEFLSADPTKTTVNYESKDNKTEKTEKIGAKTSVIEKEDGKLVTKDNGENSS 300  
OY 301 TDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEYVTSNTVTFASGKGTATV 360  
DB 301 TDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEYVTSNTVTFASGKGTATV 360  
OY 361 SKDDGNTITVMDVAVNGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPSKGMDET 420  
DB 361 SKDDGNTITVMDVAVNGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPSKGMDET 420  
OY 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKDNKPY 480  
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKDNKPY 480  
OY 481 ITNVAPEGVEGVDVNVQALNKAQONLNRRIDVNGNARAGIAQAIATAGLVQATLPKSM 540  
DB 481 ITNVAPEGVEGVDVNVQALNKAQONLNRRIDVNGNARAGIAQAIATAGLVQATLPKSM 540  
OY 541 MAIGGTYRGEAGYALIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591  
DB 541 MAIGGTYRGEAGYALIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

RESULT 4  
ID 09AOF0 PRELIMINARY; PRT: 592 AA.  
AC 09AOF0:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE OUTER MEMBRANE PROTEIN.  
GN NHHA.  
RP SEQUENCE FROM N.A.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;  
RT "Identification and characterisation of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF15375; AAK09243.1; -  
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 99.0%; Score 2971.5; DB 2; Length 592;  
Best Local Similarity 99.0%; Pred. No. 2.1e-117;  
Matches 586; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 1 MNKIRIINSLNLMVWVSELTNRHNRKASATVTAVALATLTFATVOASANNEDQED 59  
DB 1 MNKIRIINSLNLMVWVSELTNRHNRKASATVTAVALATLTFATVOASANNEDPRKDD 60  
OY 60 YLDPVQRTVAVLIVNSDKEGEGEKEVEENSDMAVYFNEKGVLTAREITTLKAGDNLKIK 119  
DB 61 YLDPVQRTVAVLIVNSDKEGEGEKEVEENSDMAVYFNEKGVLTAREITTLKAGDNLKIK 120  
OY 120 NGNTFTYSLKDLTLDSVTEKLSFSSANGKNVITSDTKLNFPAKETAGTNGDTVHLN 179  
DB 121 NGNTFTYSLKDLTLDSVTEKLSFSSANGKNVITSDTKLNFPAKETAGTNGDTVHLN 180  
OY 180 NGISTLTDLTLNLTGATNTVNDNTDDEKRAASVADVNLNGMNIKGVPPTTASDNDV 239  
DB 181 NGISTLTDLTLNLTGATNTVNDNTDDEKRAASVADVNLNGMNIKGVPPTTASDNDV 240  
OY 240 FVRTYTVFEFLSADPTKTTVNYESKDNKTEKTEKIGAKTSVIEKEDGKLVTKDNGENSS 299  
DB 241 FVRTYTVFEFLSADPTKTTVNYESKDNKTEKTEKIGAKTSVIEKEDGKLVTKDNGENSS 300  
OY 300 STDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEYVTSNTVTFASGKGTAT 359  
DB 301 STDEGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEYVTSNTVTFASGKGTAT 360  
OY 360 VSKDDGNTITVMDVAVNGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPSKGMDET 419  
DB 361 VSKDDGNTITVMDVAVNGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPSKGMDET 420  
OY 420 VINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKDNKPY 479  
DB 421 VINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSKKDNKPY 480  
OY 480 RITNVAPEGVEGVDVNVQALNKAQONLNRRIDVNGNARAGIAQAIATAGLVQATLPKSM 539  
DB 481 RITNVAPEGVEGVDVNVQALNKAQONLNRRIDVNGNARAGIAQAIATAGLVQATLPKSM 540  
OY 540 MAIGGTYRGEAGYALIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591  
DB 541 MAIGGTYRGEAGYALIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592

RESULT 5  
ID 09JPS3 PRELIMINARY; PRT: 590 AA.  
AC 09JPS3:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-NGE28;  
RA MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 96.1%; Score 2885.5; DB 2; Length 590;  
Best Local Similarity 97.0%; Pred. No. 8.4e-114;  
Matches 574; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 MNKRYRIMNSALNAAWVSELTFRNHTKRASATYKTAVALTLFPATYQASANNDEEEDL 60  
DB 1 MNKRYRIMNSALNAAWVSELTFRNHTKRASATYKTAVALTLFPATYQASANNDEEED- 59  
QY 61 YLDPVQRTAVLIVNSDKEGTEKEKEVENSMDAAVYFNEKGVLTAETILKAGDNLKIKQ 120  
DB 60 -LDPVQRTAVLIVNSDKEGTEKEKEVENSMDAAVYFNEKGVLTAETILKAGDNLKIKQ 118  
QY 121 NGNFYTSLSKDLDTLTSVGTETKLSFSANGKNVITSDTGLNFAKTAGNGDTYHLN 180  
DB 119 NGNFYTSLSKDLDTLTSVGTETKLSFSANGKNVITSDTGLNFAKTAGNGDTYHLN 178  
QY 181 GIGSTLDTLNTGATNTVNDNTDDEKRAASVKNVLAAGNINIKVPCGTASDNVDF 240  
DB 179 GIGSTLDTLNTGATNTVNDNTDDEKRAASVKNVLAAGNINIKVPCGTASDNVDF 238  
QY 241 VRYDVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIEKDKGLVTKDKGNGSS 300  
DB 239 VRYDVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIEKDKGLVTKDKGNGSS 298  
QY 301 TDDEEGVLTAKVEIDAVNKGWRKTTTANGCGOAKFEFVTSGTWTFPSGKGTATV 360  
DB 299 TDDEEGVLTAKVEIDAVNKGWRKTTTANGCGOAKFEFVTSGTWTFPSGKGTATV 358  
QY 361 SKDOGNITWYDVNVGDALNVNOLQNSGNMLDSKAAVAGSSGKVISGNVSPSKMDETV 420  
DB 359 SKDOGNITWYDVNVGDALNVNOLQNSGNMLDSKAAVAGSSGKVISGNVSPSKMDETV 418  
QY 421 NINAGNIEITRNKNIDTATSMTPPSSVSLGAGADAPTLVDGD-ALNVGSKDKKPV 479  
DB 419 NINAGNIEITRNKNIDTATSMTPPSSVSLGAGADAPTLVDDEGALNVGSKDKANKPV 478  
QY 480 RITVAVAGVREGDVTNVAOLKGVAQNLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKS 539  
DB 479 RITVAVAGVREGDVTNVAOLKGVAQNLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKS 538  
QY 540 MMAIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGYQW 591  
DB 539 MMAIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGYQW 590

RESULT 6  
Q9JPS6 PRELIMINARY; PRT; 600 AA.  
AC Q9JPS6;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA92.  
GN GNA92.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;

RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-E26;  
RA MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; -  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 92.0%; Score 2761.5; DB 2; Length 600;  
Best Local Similarity 91.7%; Pred. No. 1.3e-108;  
Matches 551; Conservative 14; Mismatches 25; Indels 11; Gaps 3;

QY 1 MNKRYRIMNSALNAAWVSELTFRNHTKRASATYKTAVALTLFPATYQASANNDEEEDL 56  
DB 1 MNKRYRIMNSALNAAWVSELTFRNHTKRASATYKTAVALTLFPATYQASADNVQASADN 60  
QY 57 EEDLYLDPVQRTAVLIVNSDKEGTEKEKEVENSMDAAVYFNEKGVLTAETILKAGDNL 116  
DB 61 EEEYLELPVQRTAVLIVNSDKEGTEKEKEVENSMDAAVYFNEKGVLTAETILKAGDNL 119  
QY 117 KIKQ-----NGNFYTSLSKDLDTLTSVGTETKLSFSANGKNVITSDTGLNFAKTAG 170  
DB 120 KIKQNDENTNASSFTYSLKELDTLTSVGTETKLSFSANGKNVITSDTGLNFAKTAG 179  
QY 171 TNGDTVHLNGIGSTLDTLNTGATNTVNDNTDDEKRAASVKNVLAAGNINIKVPC 230  
DB 180 TNGDTVHLNGIGSTLDTLNTGATNTVNDNTDDEKRAASVKNVLAAGNINIKVPC 239  
QY 231 GTTASDNVDFVRYDVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIEKDKGLV 290  
DB 240 GTTASDNVDFVRYDVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIEKDKGLV 289  
QY 291 GKDKGENGSTDEEGVLTAKVEIDAVNKGWRKTTTANGCGOAKFEFVTSGTWTF 350  
DB 300 GKDKGENGSTDEEGVLTAKVEIDAVNKGWRKTTTANGCGOAKFEFVTSGTWTF 359  
QY 351 ASGKGTATYSSKDOGNITWYDVNVGDALNVNOLQNSGNMLDSKAAVAGSSGKVISGNV 410  
DB 360 ASGKGTATYSSKDOGNITWYDVNVGDALNVNOLQNSGNMLDSKAAVAGSSGKVISGNV 419  
QY 411 PSKGMDETVNINAGNIEITRNKNIDTATSMTPPSSVSLGAGADAPTLVDGDALNV 470  
DB 420 PSKGMDETVNINAGNIEITRNKNIDTATSMTPPSSVSLGAGADAPTLVDGDALNV 479  
QY 471 GSKDKNRPVRTTNVAPVKEGDTNVAOLKGVAQNLNRRIDNVGNARAGIAOAIATAGL 530  
DB 480 GSKDKNRPVRTTNVAPVKEGDTNVAOLKGVAQNLNRRIDNVGNARAGIAOAIATAGL 539  
QY 531 VQAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGYQ 590  
DB 540 VQAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGYQ 599

RESULT 7  
Q930Y4 PRELIMINARY; PRT; 594 AA.  
AC Q930Y4;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel\_19, Last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxId=487;  
 RN [1]  
 RP  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=EG327.  
 RA Peak I.R., Stikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AF157605, AAK68866.1;  
 SO SEQUENCE 594 AA: 62297 MW: 9DD048B04B3A8EA2 CRC64;

Query Match	91.9%;	Score 2758.5;	DB 2;	Length 594;
Best Local Similarity	92.3%;	Pred. No. 1.8e-108;		
Matches 552;	Conservative 14;	Mismatches 21;	Indels 11;	Gaps 4

OY	1	MKKIRIIINSLNLMWVYVSELTRHNHTRKASTVTVATATLLPFTVVOASANNEDQEL	60
OY	1	MKKIRIIINSLNLMWVYVSELTRHNHTRKASTVTVATATLLPFTVVOASANNEDQEL	60
Db	1	MKKIRIIINSLNLMWVYVSELTRHNHTRKASTVTVATATLLPFTVVOASANNEDQEL	57
OY	61	YLDPVQRTAVVLIIVSDSEGTGEKKEKVEENSOMAAFYFNEKGVLTAIREILKAGDNLIKQ	120
Db	58	YLEPQRTAVVLIIVSDSEGTGEKKEKVEENSOMAAFYFNEKGVLTAIREILKAGDNLIKQ	116
OY	121	-----NCTNFTYSLKKDLTDLTSVGTSEKLSFANGKNKVNITSDFKGLNFAKETAGTNGD	174
Db	117	NTNEMTNASSFTYSLKKDLTDLTSVGTSEKLSFANGKNKVNITSDFKGLNFAKETAGTNGD	176
OY	175	TTVHLNGIGSTLTDTPLNTGATNTNTNDVTPDEKRRASVADVNLAGNNITGVKPGTTA	234
Db	177	TTVHLNGIGSTLTDTPLNTGATNTNTNDVTPDEKRRASVADVNLAGNNITGVKPGTTA	236
OY	235	SDNVDFVFRTPDVEFLSADTKTTTVNVESKDNKGKTEYVIGAKTSYIREKDGKLVYGRDK	294
Db	237	SDNVDFVFRTPDVEFLSADTKTTTVNVESKDNKGKTEYVIGAKTSYIREKDGKLVYGRDK	296
OY	295	GENSDTEDEGELVTAKEVIDAVNRKAGRMKTTTANGCGQADKFEYVSGTNVTFASGK	354
Db	297	GENSDTEDEGELVTAKEVIDAVNRKAGRMKTTTANGCGQADKFEYVSGTNVTFASGK	356
OY	355	GTTATVSKDDQGNITVTVDVNVGDLANVQNLNSGNNLDSKAVAGSSGKVIISGNVSPSKG	414
Db	357	GTTATVSKDDQGNITVTVDVNVGDLANVQNLNSGNNLDSKAVAGSSGKVIISGNVSPSKG	416
OY	415	KMDELVNINAGNNIETTRGKNIDTASMTPOFSSVSLGAGADAPLTLSDGCLALNVSGK	473
Db	417	KMDELVNINAGNNIETTRGKNIDTASMTPOFSSVSLGAGADAPLTLSDGCLALNVSGK	476
OY	474	KDNKVRITNVAPGKEGVTNVAOLKGAQVQNLNRINDVDGNARIGIQAQATATAGLVQA	533
Db	477	DANKVRITNVAPGKEGVTNVAOLKGAQVQNLNRINDVDGNARIGIQAQATATAGLVQA	536
OY	534	YLPGRSMALIGGCGTREGAGYALIGVSSISDGGNMWIIKGTASGNSRCHFPASASVGVQW	591
Db	537	YLPGRSMALIGGCGTREGAGYALIGVSSISDGGNMWIIKGTASGNSRCHFPASASVGVQW	594
RESULT	8		
ID	09JPS2	PRELIMINARY; PRT; 594 AA.	
AC	09JPS2		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		

OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=201757566; PubMed=10710308;  
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nisi S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteili H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.",  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1;  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A7BF53D256 CRC64;

Query Match	91.6%;	Score 2751.5;	DB 2;	Length 594;
Best Local Similarity	92.1%;	Pred. No. 3.5e-108;		
Matches 551;	Conservative 13;	Mismatches 23;	Indels 11;	Gaps 4;

QY	1	MNKIRIRIIN	SALN	AMVYVSEL	TRNH	KRAS	TVTAV	ATL	PLAT	VL	AVAS	ANNE	DEED	60	
Db	1	MNKIRIRIIN <td>SALN<td>AMVYVSEL<td>TRNH<td>KRAS<td>TVTAV<td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td></td></td></td></td></td>	SALN <td>AMVYVSEL<td>TRNH<td>KRAS<td>TVTAV<td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td></td></td></td></td>	AMVYVSEL <td>TRNH<td>KRAS<td>TVTAV<td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td></td></td></td>	TRNH <td>KRAS<td>TVTAV<td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td></td></td>	KRAS <td>TVTAV<td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td></td>	TVTAV <td>ATL<td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td></td>	ATL <td>PLAT<td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td></td>	PLAT <td>VL<td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td></td>	VL <td>AVAS<td>ANNE<td>DEED<td>57</td></td></td></td>	AVAS <td>ANNE<td>DEED<td>57</td></td></td>	ANNE <td>DEED<td>57</td></td>	DEED <td>57</td>	57	
QY	61	YLDPQR	IVAV	IV	ASD	KEG	TEK	EKE	VE	NS	MA	YF	EN	KG	120
Db	58	YLEPQR	IVAV	IV	ASD	KEG	TEK	EKE	VE	NS	MA	YF	EN	KG	116
QY	121	-----	NG	TN	F	Y	S	L	K	K	D	L	T	D	174
Db	117	NTDE	TM	AS	S	P	F	Y	S	L	K	K	D	L	176
QY	175	TTVHL	NG	I	G	S	T	L	D	T	L	M	T	G	234
Db	177	TTVHL	NG	I	G	S	T	L	D	T	L	M	T	G	236
QY	235	SDN	V	P	R	T	T	V	E	L	S	A	D	T	294
Db	237	SDN	V	P	R	T	T	V	E	L	S	A	D	T	296
QY	295	GEN	S	S	T	E	G	B	E	L	Y	A	K	E	354
Db	297	GEN	S	S	T	E	G	B	E	L	Y	A	K	E	356
QY	355	G	T	T	A	V	S	K	D	D	O	G	N	I	414
Db	357	G	T	T	A	V	S	K	D	D	O	G	N	I	416
QY	415	K	M	D	E	T	V	N	I	N	A	G	N	N	473
Db	417	K	M	D	E	T	V	N	I	N	A	G	N	N	476
QY	474	K	D	N	K	E	V	R	T	I	N	N	A	V	533
Db	477	D	A	N	K	E	V	R	T	I	N	N	A	V	536
QY	534	Y	L	P	G	S	M	A	I	G	G	T	R	G	591
Db	537	Y	L	P	G	S	M	A	I	G	G	T	R	G	594
RESULT	9														

OS *Neisseria meningitidis*.  
OC Bacteria: Proteobacteria: beta subdivision: Neisseriaceae: Neisseria  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND B2332;  
RX MEDLINE=20175756; Pubmed=10710308;  
RA Piazza M., Scarlato V., Masiugnani V., Giuliani M.M., Arico' B.,  
Comanucci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
Ralecchi C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blar E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.T., Granoff D.M., Venter C.,  
Moore E.R., Grandi G., Rappunoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.';  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -  
DR EMBL: AF226369; AAF42518.1; -  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04BA6 CRC64;

Query Match	91.58;	Score 2747.5;	DB 2;	Length 594;
Best Local Similarity	92.08;	Pred. No. 5.1e-108;		
Matches 550;	Conservative 13;	Mismatches 24;	Indels 11;	Gaps 4;

Qy	1	MNKTIRIIMNSALNAWYVSELITRNHKKRASAETKTVLTLTLEFATYQASANNEDBEDL	60
Db	1	MNKTIRIIMNSALNAWYVSELITRNHKKRASAETATVATLTLFATYQASATTD---DDDL	57
Qy	61	YLDPEVQRTVAVLIVNSDEKTEGKEKVEENSMAVYFENEKGVLTAREITLKAGDNLKIKO	120
Db	58	YLEPQORTAPALVSHADSEGEKEE-VTEDESMGVYFEDKGGVLTAGTITLKAGDNLKIKO	116
Qy	121	-----NOTNFTYSLKXDDLDLJTSVGEIKLSFSANGKKNVITTSPTKLNPAKETAINGSD	174
Db	117	NTDENYTNASSFTYSLEKKDDLDJTSVEITEKLSFGANGKKNVITTSPTKLNPAKETAINGSD	176
Qy	175	TTYVHLNGIGSTPLTDTLNTGATVNTVDNDYDDEKRAASVKDVLNAGMNLKGVKPGTTA	234
Db	177	TTYVHLNGIGSTPLTDTLNTGATVNTVDNDYDDEKRRASAASKVDVLNAGMNLKGVKPBTTA	236
Qy	235	SDNVDFVRTYDVEFLSADTKTTTVNVNESKDNKTEVKIGAKTSVIERKDGKLVYTKDK	294
Db	237	SDNVDFVRTYDVEFLSADTKTTTVNVNESKDNKTEVKIGAKTSVIERKDGKLVYTKDK	296
Qy	295	GENSSSTDEBEGGLYTAKEVIDAVNKAGKRAKTTTANGOTGQADKEFVYTSCTNVTFAKSG	354
Db	297	GENSSSTDEBEGGLYTAKEVIDAVNKAGKRAKTTTANGOTGADKEFVYTSCTKTVFASGN	356
Qy	355	GTTATVNSDDDGNTVYVDVWVAGALANVNOLONSGMNLDKSAVNGSSGKVISGVVPSKG	414
Db	357	GTTATVNSDDDGNTVYKIDVWVAGALANVNOLONSGMNLDKSAVNGSSGKVISGVVPSKG	416
Qy	415	KMDETVINAGNNIEITRNKNIDIASMTPQFSSVSLGAGADAPLTLSVGD-ALANYSK	473
Db	417	KMDETVINAGNNIEITRNKNIDIASMTPQFSSVSLGAGADAPLTLSVDEGLANYSK	476
Qy	474	KDNKPVRTTNVAPGVKESDVTNVAQLKGVAONLNNRIDVNDGNARAGIAQALATAGLYOA	533
Db	477	DANKPVRTTNVAPGVKEDVTNVAQLKGVAONLNNRIDVNDGNARAGIAQALATAGLYOA	536
Qy	534	YLPKGSMAIIGGGYRGAGAGATGSSSTSOGNMNITIGTASGNSRGHFGASASVGYOW	591
Db	537	YLPKGSMAIIGGGYRGAGAGATGSSSTSOGNMNITIGTASGNSRGHFGASASVGYOW	594

RESULT	10	
09JPH7		
ID	09JPH7	PRELIMINARY;
AC	09JPH7;	PRT; 594 AA.
DT	01-OCT-2000	(TREMBlrel. 15, Created)
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BZ198, AND 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scariato V., Masiгран V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santilli L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blar E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BZ198.  
RA Peak I.R., Stikhanata Y., Dieckelman M., Moxon R., Jennings M.P.,  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226368; AAF42517.1; -  
DR EMBL: AF226358; AAF42507.1; -  
DR EMBL: AF157604; AAK68865.1; -  
SQ SEQUENCE 394 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match	91.3%;	Score 2740.5;	DB 2;	Length 594;
Best Local Similarity	92.1%;	Pred. No. 1e-107;		
Matches 551;	Conservative 11;	Mismatches 25;	Indels 11;	Gaps 4.

Qy	1	MNKYIRITMNSALNAWVVSSELTNNHKKRASATVTKTAVLTPLTFATVOASANNNEQEDL	60
Qy	1	MNKYIRITMNSALNAWVVSSELTNNHKKRASATVTKTAVLTPLTFATVOASANNNEQEDL	60
Db	1	MNKYIRITMNSALNAWVVSSELTNNHKKRASATVTKTAVLTPLTFATVOASANNNEQEDL	57
Qy	61	YLDPORTVAVLINYSDEEGEKEKEEENDMAVYFENEKGVLAREITTLAKGDNLIKQ	120
Db	58	YLEPVQRTAAVYLSRSDKEGEGEGEDT-SMAVYVYDEDEKRYLKAGIITTLAKGDNLIKQ	116
Qy	121	-----NCTNFTSYLXKDLTDLTSVGTSEKLSFSANGKNVITSDPTKGLNFAKETAGTNGD	174
Db	117	NTNEMTNOSSFTYSLXKDLTDLTSVGTSEKLSFSANGKNVITSDPTKGLNFAKETAGTNGD	176
Qy	175	TTVHLNGIGSTLTDPLTLLTGATTNVDNVTDDEKKRAASVKDYLANGNHKGKPE8T7A	234
Db	177	PTVHLNGIGSTLTDPLTLLTGATTNVDNVTDDEKKRAASVKDYLANGNHKGKPE8T7A	236
Qy	235	SDNDFVATVYTVFELSADPTTNTVNVESKONGKKE7VKGAKSVYKENDGKLYTGKDK	294
Db	237	SDNDFVATVYTVFELSADPTTNTVNVESKONGKKE7VKGAKSVYKENDGKLYTGKDK	296
Qy	295	GENGSSTDEGEGLYTAKFEVIDAVNKKAGRMKTTTANGOTGADFEVTSGTNVTFA5GK	354
Db	297	DENGSTDEGEGLYTAKFEVIDAVNKKAGRMKTTTANGOTGADFEVTSGTNVTFA5GK	356
Qy	355	GTTATVSKDDGONTVMYDVNVGDLNVNOLONGSMNLD5KRAVAGSSGKVI5GCVSP5GK	414
Db	357	GTTATVSKDDGONTVMYDVNVGDLNVNOLONGSMNLD5KRAVAGSSGKVI5GCVSP5GK	416
Qy	415	KMDEVTNINAGNNIEITNGKNIDIA5MTQESVSYSIGAGADAPLT5VGDG-ALNVGSK	473
Db	417	KMDEVTNINAGNNIEITNGKNIDIA5MTQESVSYSIGAGADAPLT5VGDGALNVGSK	476
Qy	474	KDNKVFRTTNVAPGKESDVNVNOLKGVAONLNRRIDVNDGNNRAGIAOIAI7AGLYVOA	533
Db	477	DTNKKVFRTTNVAPGKESDVNVNOLKGVAONLNRRIDVNDGNNRAGIAOIAI7AGLYVOA	536



OY 534 YLPGKSMALIGGCTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 591  
|||||  
Db 537 YLPGKSMALIGGCTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRCHFGASASVGYQ 594

## RESULT 11

O9JPR9 PRELIMINARY; PRT; 598 AA.  
AC O9JPR9: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-NGH36;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226382; AAF42531.1;  
SQ SEQUENCE 598 AA: 62718 MW: 9095FBE31AD7C76D CRC64;

Query Match 91.2%; Score 2738.5; DB 2; Length 598;  
Best Local Similarity 91.5%; Pred. No. 1.2e-107;  
Matches 551; Conservative 11; Mismatches 25; Indels 15; Gaps 4;

OY 1 MNKIRIINNSALINAMVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
|||||  
Db 1 MNKIRIINNSALINAMVVSSELTRNHTKRASATVKTAVLATLLFATVOANATD---DDDL 57  
OY 61 YLDPVORTAVLIVNSDKRGTEGKEVEENSDMAVYFNEKGYLTAREITLKADNLIKIQ 120  
||:||||| || ||||| ||: ||||| || || ||||| |||||  
Db 58 YLEPVORTAVLIVNSDKRGTEGKEVEENSDMAVYFNEKGYLTAREITLKADNLIKIQ 116  
OY 121 -----NGINFTYSLKKDLTDLTSVGTETKLSFANGKNKNTSDTKGLNFAKETAG 170  
||:||||| || ||||| ||: ||||| || || ||||| |||||  
Db 117 NTNENTNENTNNTSSFTYSLKKDLTDLTSVGTETKLSFANGKNKNTSDTKGLNFAKETAG 176  
OY 171 TNGDTPVHLNGIGSTLTDLLTGATNTVNDVNDDEKRAASVYKDVLAGNNIKGVP 230  
|||||  
Db 177 TNGDTPVHLNGIGSTLTDLLTGATNTVNDVNDDEKRAASVYKDVLAGNNIKGVP 236  
OY 231 GTTASNDVDFVRYDVEELASDTKTTTVNVEESKDKKREVEIKAGTSYIKKEDKLYT 290  
|||||  
Db 237 GTTASNDVDFVRYDVEELASDTKTTTVNVEESKDKKREVEIKAGTSYIKKEDKLYT 296  
OY 291 GKDKGENSGTDEGEGLVTAKEVIDAVNKGAMKTTTANGOTGADKFEFTVSGTNVTF 350  
|||||  
Db 297 GKDKGENSGTDEGEGLVTAKEVIDAVNKGAMKTTTANGOTGADKFEFTVSGTNVTF 356  
OY 351 ASKGTTATVSKDDOGNITVMDVNVGDLNVLNQLONGSNGLDSKAVAGSSGKVISGNVS 410  
|||||  
Db 357 ASKGTTATVSKDDOGNITVMDVNVGDLNVLNQLONGSNGLDSKAVAGSSGKVISGNVS 416  
OY 411 PSKGDDEVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPLTVSDDEGALN 469  
|||||  
Db 417 PSKGDDEVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPLTVSDDEGALN 476  
OY 470 VGSKDKNKPVRTITNVPAGYEGDVTNVAOLKGVANQLNLRIDVNDGNARAGIAQAATATAG 529  
|||||

Db 477 VGSKDKNKPVRTITNVPAGYEGDVTNVAOLKGVANQLNLRIDVNDGNARAGIAQAATATAG 536  
OY 530 LVQAYLPGKSMALIGGCTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRCHFGASASVGY 589  
|||||  
Db 537 LVQAYLPGKSMALIGGCTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRCHFGASASVGY 596

OY 590 QW 591  
Db 597 QW 598

## RESULT 12

O9JPR0 PRELIMINARY; PRT; 598 AA.  
AC O9JPR0: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-2996;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226359; AAF42508.1;  
SQ SEQUENCE 598 AA: 62763 MW: 63A6A3BD7E0F2EE3 CRC64;

Query Match 90.8%; Score 2725.5; DB 2; Length 598;  
Best Local Similarity 90.9%; Pred. No. 4.3e-107;  
Matches 547; Conservative 13; Mismatches 27; Indels 15; Gaps 4;

OY 1 MNKIRIINNSALINAMVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEQEDL 60  
|||||  
Db 1 MNKIRIINNSALINAMVVSSELTRNHTKRASATVKTAVLATLLFATVOANATD---DDDL 57  
OY 61 YLDPVORTAVLIVNSDKRGTEGKEVEENSDMAVYFNEKGYLTAREITLKADNLIKIQ 120  
||:||||| || ||||| ||: ||||| || || ||||| |||||  
Db 58 YLEPVORTAVLIVNSDKRGTEGKEVEENSDMAVYFNEKGYLTAREITLKADNLIKIQ 116  
OY 121 -----NGINFTYSLKKDLTDLTSVGTETKLSFANGKNKNTSDTKGLNFAKETAG 170  
||:||||| || ||||| ||: ||||| || || ||||| |||||  
Db 117 NTNENTNENTNNTSSFTYSLKKDLTDLTSVGTETKLSFANGKNKNTSDTKGLNFAKETAG 176  
OY 171 TNGDTPVHLNGIGSTLTDLLTGATNTVNDVNDDEKRAASVYKDVLAGNNIKGVP 230  
|||||  
Db 177 TNGDTPVHLNGIGSTLTDLLTGATNTVNDVNDDEKRAASVYKDVLAGNNIKGVP 236  
OY 231 GTTASNDVDFVRYDVEELASDTKTTTVNVEESKDKKREVEIKAGTSYIKKEDKLYT 290  
|||||  
Db 237 GTTASNDVDFVRYDVEELASDTKTTTVNVEESKDKKREVEIKAGTSYIKKEDKLYT 296  
OY 291 GKDKGENSGTDEGEGLVTAKEVIDAVNKGAMKTTTANGOTGADKFEFTVSGTNVTF 350  
|||||  
Db 297 GKDKGENSGTDEGEGLVTAKEVIDAVNKGAMKTTTANGOTGADKFEFTVSGTNVTF 356  
OY 351 ASKGTTATVSKDDOGNITVMDVNVGDLNVLNQLONGSNGLDSKAVAGSSGKVISGNVS 410  
|||||  
Db 357 ASKGTTATVSKDDOGNITVMDVNVGDLNVLNQLONGSNGLDSKAVAGSSGKVISGNVS 416

Db	177	TNGDPYHLNIGIGSTLDDTLNTGATTTVNTDNYTDDEKKRAASVKDVLNMGWNIKGVP	236
Qy	231	GTASDNDVFRVTDYVEFLSADTKRTTTVNESKDNGKTEVKGAKTSVIREKDKLVT	290
Db	237	GTTASDNDVFRVTDYVEFLSADTKRTTTVNESKDNGKTEVKGAKTSVIREKDKLVT	296
Qy	291	GKDKGENGSTDEDEGLVTAKEVIDAVKAKGAKRAKTTTANQOTGADKFEVTVTSGTNTVF	350
Db	297	GKDKGENGSTDEDEGLVTAKEVIDAVKAKGAKRAKTTTANQOTGADKFEVTVTSGTNTVF	356
Qy	351	ASGKGTTATVSKDDOGNTTVTVADVVGALNVNOLONGSNWNLDSKAVVSGSGKTVISGWS	410
Db	357	ASGKGTTATVSKDDOGNTTVTKYDVNVGALNVNOLONGSNWNLDSKAVVSGSGKTVISGWS	416
Qy	411	PSKGMDETVINAGNNIETIRNGKNIDIASMTPQFSSVSLGAGADAPTLSVDPGD-ALN	469
Db	417	PSKGMDETVINAGNNIETIRNGKNIDIASMTPQFSSVSLGAGADAPTLSVDPGDALN	476
Qy	470	VGSKDKNRPVRTTVNAPGVKEDGYTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIAATAG	529
Db	477	VGSKDKNRPVRTTVNAPGVKEDGYTNVAQLKGVAQNLNRRIDNVDGNARAGIAQAIAATAG	536
Qy	530	LVQAVLPKSKMMAIGGGTYRGEAGYAIGYSSISDGCNNIICKTASGNSRGHFGAASAVGY	589
Db	537	LAQAVLPKSKMMAIGGGTYRGEAGYAIGYSSISDGNVWIKGTASGNSRGHFGAASAVGY	596
Qy	590	QW	591
Db	597	QW	598
RESULT	14		
Q930Y5		PRELIMINARY;	598 AA.
ID	Q930Y5		
AC	Q930Y5;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	NHHA OUTER MEMBRANE PROTEIN.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_Taxid=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-B210;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RL	membrane protein of Neisseria meningitidis.";		
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
EMBL:	AF157603; AAK68864.1; "		
SEQ	SEQUENCE 598 AA: 62687 MW; 18CEFFE6410A15DF CRC64;		

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QY 231 GTTASDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVYIGAKTSVYIKERDKLVT 290
DB 237 GTTASDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVYIGAKTSVYIKERDKLVT 296
QY 291 GKDKGENGSTDEGEGLYTAKEVIDAVNKGAMKTTTANGOTGADKFEETVSGTNVTF 350
DB 297 GKDKGENGSTDEGEGLYTAKEVIDAVNKGAMKTTTANGOTGADKFEETVSGTNVTF 356
QY 351 ASGKGTATVSKDDGNTITVMDVNVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVS 410
DB 357 ASGNGTATVSKDDGNTITVMDVNVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVS 416
QY 411 PSKGMDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLVSDGALN 476
DB 417 PSKGMDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLVSDGALN 476
QY 470 VGSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLNRRIDVNDGNARAGIAQALATAG 529
DB 477 VGSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLNRRIDVNDGNARAGIAQALATAG 536
QY 530 LVQAYLPGKSMAIIGGTYRGEAGYAIYSSISDGNMIITKTASGNSRHFAGASASVGY 569
DB 537 LVQAYLPGKSMAIIGGTYRGEAGYAIYSSISDGNMIITKTASGNSRHFAGASASVGY 569
QY 590 QW 591
DB 597 QW 598

RESULT 15
QY 09JPR8 PRELIMINARY: PRT: 599 AA.
AC 09JPR8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RA MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nili S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT *Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT *Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -
DR EMBL: AF157608; AAK68869.1; -
DR SEQUENCE 599 AA; 62844 MW; BBA16BEF53C1970C CRC64;

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Query Match 89.4%; Score 2685; DB 2; Length 599;  
 Best Local Similarity 89.4%; Pred. No. 2, 2e-105;  
 Matches 538; Conservative 16; Mismatches 34; Indels 14; Gaps 4;

QY 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKAVALATLLEFATVQASANNDEQEDL 60

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DB 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKAVALATLLEFATVQASANNDEQEDL 59
QY 61 YLDPVORTVAVLLVNSDKESTGEKEVEENSMAVYFENEKGVLTAREITLKADNLKIKO 120
DB 60 -LEPVRSALVLOFMIDKEGENEST -GNIGSIYYDNHNTLHGATVTLKADNLKIKO 117
QY 121 -----NGINFTYSILKKDLTDLTSVCTEKLSSANGKNKNTISDPKGLMFAKETAG 170
DB 118 NTKKNTNENTNDSFTYLSLKKDLTDLTSVCTEKLSSANGKNKNTISDPKGLMFAKETAG 177
QY 171 TNGDTVHLNGISSTLTDLTLNTGATTNVNDVTPDEKRAASVVDVNLNAGNNIGVKP 230
DB 178 TNGDTVHLNGISSTLTDLTLNTGATTNVNDVTPDEKRAASVVDVNLNAGNNIGVKP 237
QY 231 GTTASDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVYIGAKTSVYIKERDKLVT 290
DB 238 GTTASDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVYIGAKTSVYIKERDKLVT 297
QY 291 GKDKGENGSTDEGEGLYTAKEVIDAVNKGAMKTTTANGOTGADKFEETVSGTNVTF 350
DB 298 GKDKGENGSTDEGEGLYTAKEVIDAVNKGAMKTTTANGOTGADKFEETVSGTNVTF 357
QY 351 ASGKGTATVSKDDGNTITVMDVNVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVS 410
DB 358 ASGKGTATVSKDDGNTITVMDVNVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVS 417
QY 411 PSKGMDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLVSDGALN 476
DB 418 PSKGMDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLVSDGALN 477
QY 470 VGSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLNRRIDVNDGNARAGIAQALATAG 529
DB 478 VGSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLNRRIDVNDGNARAGIAQALATAG 537
QY 530 LVQAYLPGKSMAIIGGTYRGEAGYAIYSSISDGNMIITKTASGNSRHFAGASASVGY 569
DB 538 LVQAYLPGKSMAIIGGTYRGEAGYAIYSSISDGNMIITKTASGNSRHFAGASASVGY 569
QY 590 QW 591
DB 598 QW 599

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Search completed: July 3, 2002, 08:28:37  
 Job time: 1158 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:01 : Search time 168.6 Seconds

(without alignments)  
390.010 Million cell updates/sec

Title: US-09-771-382-2

Perfect score: 2987

Sequence: 1 MNRIYRINMSALNMYAVS.....TAGSNRGHGASASVGYQW 592

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Database :

Maximum Match 100%

Listing first 45 summaries

A.Geneseq\_032802:\*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2987	100.0	592	20	AAV23744
2	2987	100.0	592	22	AAU06172
3	2779	93.0	592	22	AAU06180
4	2743	91.8	592	20	AAV27203
5	2699.5	90.4	599	20	AAV23743
6	2699.5	90.4	599	22	AAU06176
7	2667	89.3	598	20	AAV23742
8	2667	89.3	598	22	AAU06177
9	2664	89.2	594	22	AAV23739
10	2664	89.2	594	22	AAU06179
11	2658	89.0	598	20	AAV23738

12	2658	89.0	598	22	AAU06178
13	2636	88.2	594	20	AAV23740
14	2636	88.2	594	21	AAV57044
15	2636	88.2	594	22	AAU06174
16	2581.5	86.4	591	21	AAV57045
17	2573.5	86.2	591	20	AAV27202
18	2573.5	86.2	591	20	AAV23746
19	2573.5	86.2	591	22	AAU06171
20	2554.5	85.5	591	20	AAV23741
21	2554.5	85.5	591	22	AAU06175
22	2552.5	85.5	591	22	AAU06183
23	2552	85.4	592	20	AAV23737
24	2490.5	83.4	589	20	AAV23745
25	2490.5	83.4	589	22	AAU06173
26	2407	80.6	512	22	AAU06182
27	2357	77.9	502	22	AAU06186
28	2216	74.2	604	22	AAU06181
29	2015.5	67.5	433	22	AAU06185
30	1869.5	62.6	407	22	AAU06184
31	1146	38.4	2353	17	AAU99393
32	1116	37.4	2411	21	AAU23860
33	1033	34.6	1094	21	AAU23858
34	1014	33.9	1098	17	AAU99392
35	945.5	31.7	679	17	AAU99394
36	945.5	31.7	679	21	AAU23855
37	887	29.7	245	20	AAV27201
38	732	24.5	1002	21	AAU23854
39	712	23.8	1004	21	AAU23857
40	663	22.2	1104	21	AAU23856
41	663	22.2	1104	21	AAU23859
42	580	19.4	116	21	AAU37832
43	391	13.1	2053	22	AAU69135
44	391	13.1	2123	22	AAU0701
45	383.5	12.8	1992	17	AAU04505

#### ALIGNMENTS

RESULT 1

AAV23744 standard; Protein; 592 AA.

AAV23744:

AC AAV23744:

DT 08-SEP-1999 (first entry)

XX

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; Infection; vaccine;

KW Immunoreactive peptide.

XX

OS Neisseria meningitidis.

XX

PN WO9931132-A1.

PD 24-JUN-1999.

XX

PF 14-DEC-1998: 98WO-AU01031.

XX

PR 12-DEC-1997: 97GB-0026398.

XX

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX

DR WPI: 1999-418754/35.

XX

DR N-PSDB: AAX85796.

XX

PT Neisseria meningitidis surface proteins useful for treating N.

XX

PT meningitidis infections

PS Claim 1; Page 118-120; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX Sequence 592 AA:

Query Match 100.0%; Score 2987; DB 20; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 4e-163;  
 Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIRIINMSALNANVAVSELTFRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEEL 60  
 DB 1 mkiyriilmasalnwaweselttrnhkkrasatvktavlatlflfatvqanatedeeseel 60  
 QY 61 ESVORSVVGSIQASMEGSVELETISLSMTNDSKEFVDPYIVYTLKAGDNKIKONTNENT 120  
 DB 61 esvovrsvvgisqasmegeveletislsmtndsketfvpdyivvltlkagdnkikqntent 120  
 QY 121 NASFEETSLKKDLTGLINVERTEKLSFGANGKKNVNIISDTKGLNFAKTAGTNGDTVHLN 180  
 DB 121 nasfeetyslkdlcglilnveeteksfgangkknvniisdtkglinfaktagntgdtvhlh 180  
 QY 181 GIGSTLDMLTNGATNTVNTDNTYDDEKKRAASVKDVLNAGWNIKGVKPGTASDNVDF 240  
 DB 181 gigtldmldntgatntvntdntynddtkkraasvkdvlagnwnikgvkpgtassdnvdf 240  
 QY 241 VRTDYVEFLSADTKTTTNNVESKDNKKTEVKGARTSVKEDGKRYTKRGGENSS 300  
 DB 241 vrtdyveflsadtktttnnveskdnkktevkgartsvkedgkrytkrggengss 300  
 QY 241 vrtdyveflsadtktttnnveskdnkktevkgartsvkedgkrytkrggengss 300  
 QY 301 TDEEGELVTAKEVIDAVNKAQMRMKTTPANGOTGOADKFEFTVSGTKVTFASGNGTATV 360  
 DB 301 tdeegeltakevidavnkagmrmttptangotgoadkfeftvsgtkvtfasgngttatv 360  
 QY 361 SKDDOGNITVRYDVNVDALNVNQLQNSGNWLDKRAVAGSSGKVLSCNVSPSKGMDFTV 420  
 DB 361 skddognitvrydvvnvdalnvvnqlqnsqwnldskravagssgkvlsqnvspskgmdetv 420  
 QY 421 NINAGNNIETRRNGKNIDIASMTPOESSVSLGAGADAPITLSYDDEGALNNGSKDANKPV 480  
 DB 421 ninagnnietrrngknidiatmtppqissvslgagadapitlsydegalnngskdankpv 480  
 QY 481 RITNVAPGVKEGDVTNNVQLKGVAQNLRNIDNNGNARAGIAQAIVTAVQVATLPKGS 540  
 DB 481 ritnvapgvkegdvtnnvqlkgvaqnlrnidnngnaragiaqavtavgaylpgks 540  
 QY 541 MMAIGCGTYLGEAGYALGYSSISAGNMWIKGTASGNSRGHFGASASVGYOM 592  
 DB 541 mmaigcgtylgeagyalgyssisagnmwikgtasgnsrghfgaasvgyom 592

RESULT 2  
 AAU06172 standard; Protein: 592 AA.  
 XX  
 AC AAU06172;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX N. meningitidis H41 surface antigen NhhA polypeptide sequence.  
 DE  
 XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
 KW  
 XX *Neisseria meningitidis* strain H41.  
 QS

XX	Key	Location/Qualifiers
EH	Peptide	1..51
FT	/label= signal_peptide	1..50
FT	Region	/label= C1
FT	/note= "Conserved region 1"	51..102
FT	Region	/label= V1
FT	/note= "Variable region 1"	52..592
FT	Protein	/label= Mature_NhhA
FT	/note= "Predicted mature protein, specifically claimed in claim 12"	
FT	Region	103..114
FT	/label= C2	
FT	/note= "Conserved region 2"	115..124
FT	Region	/label= V2
FT	/note= "Variable region 2"	125..188
FT	Region	/label= C3
FT	/note= "Conserved region 3"	189..210
FT	Region	/label= V3
FT	/note= "Variable region 3"	211..229
FT	Region	/label= C4
FT	/note= "Conserved region 4"	230..236
FT	Region	/label= V4
FT	/note= "Variable region 4"	237..592
FT	Region	/label= C5
FT	/note= "Conserved region 5"	
XX	W020015182-A1.	
PN	02-AUG-2001.	
PD	25-JAN-2001; 2001WO-AU00069.	
PF	25-JAN-2000; 2000US-0177917.	
XX	(UYOU ) UNIV QUEENSLAND.	
XX	Peak IRA, Jennings MP:	
XX	WPI: 2001-488774/53.	
DR	N-PSDB: AAS09162.	
XX	Claim 9; Fig 1; 91pp; English.	
PT	New NhhA surface antigen polypeptides and polynucleotides from	
PT	<i>Neisseria meningitidis</i> , useful in producing vaccines for treating or	
PT	preventing broad spectrum of <i>Neisseria meningitidis</i>	
XX		
PS		
XX	The present invention relates to the isolation of novel <i>Neisseria</i>	
CC	<i>meningitidis</i> mutant polypeptides of the surface antigen NhhA	
CC	(AAU06182-AAU06186). The modified or mutant NhhA polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnostics, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of N. meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen NhhA	
CC	from N. meningitidis strain H41 is 1 of 10 NhhA polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
CC	the present invention.	
XX	Sequence 592 AA:	
SO		

Query Match 100.0%; Score 2987; DB 22; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 4e-163;  
 Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKRIIRIINNSALNMVAVSELTRNHTKRASATVKAVALATLLEFAVQANANDEDEEEL 60
   |||||||
DB 1 mkklyrllwnsalnawavseltrnhtkrasatvkavalatllfavganadedeeel 60
QY 61 ESQSRVSGSIQASMEGSELEETISLSMTNDSKEFVDPYIVVTLKAGDMLKIKONTNEMT 120
   |||||||
DB 61 esvqsrsvsgisqasmegeleletislsmtndsketfdpyivvtrlkagdklkkqntnemt 120
QY 121 NASSFTYSLKQDLTGLINVERTEKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 180
   |||||||
DB 121 nassftyslkkdltglinveteklsfgangkkrvniisdtckglnfaketagngdtvtvhl 180
QY 181 GIGSTLTDLMLNTGATTNTNDNVTDDEKKRAASVADVLANAGMNIKGVKPGTTASDNVDF 240
   |||||||
DB 181 gigtstltdmlntgattntndnvtddekkraasvadvlanagmnikgvkpgttasdnvdf 240
QY 241 VRTYDVEFLSADFTTTTNNVESKDKGKTEYKIGAKTSVIEKDKGLTVTGKKGENGSS 300
   |||||||
DB 241 vrttydveflsadtftttttnvveskdkgteykigaktsviekdkglvtgkkgengss 300
QY 301 TDEGEGLYTAKEDVDAVNAKGRMKTTTANGOTGQADKEFVTSGTKTVPASGNGTTATV 360
   |||||||
DB 301 tdegelytakedvdaavnagrmttttangotgqadkefvtsgtkvtfasngttatv 360
QY 361 SKDDGNTIVKXYDVNVGDALNVNOLONGMNLDSKAVASSGKVIISGNTSPSKGMDENV 420
   |||||||
DB 361 skddgntlvkxydvngdalinvnqnswnldskavassgkvisgnvpskymdeenv 420
QY 421 NTNAGNNEITFPNGKNIDATSMTPQFSSVSLGACADAPTLSDDEGALNVGSKDANKPV 480
   |||||||
DB 421 ntngnneitfngknidatmtptqfssvslgagadaptlsvddegalnvgskdankpv 480
QY 481 RITNVAPEGVDVTNVAOLKGVNOLNLRIDNVNGNARAGIAQALATAGLVQAVLPGKS 540
   |||||||
DB 481 ritnvapegvdvtnvaolkgvnolnlnridnvngnaraagiataglvqavlpjgks 540
QY 541 NMAIGGTYLGEAGYALIGSSISAGSNMIIKGTASGNSGHRGASASVGYQW 592
   |||||||
DB 541 nmaiggytlygeagyaligssisaggnwlikgtasngsrghgaasvgyqw 592

```

RESULT 3  
 AAU06180  
 ID AAU06180 standard: Protein; 592 AA.  
 XX AAU06180;  
 AC  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis Z2491 surface antigen NhhA polypeptide sequence.  
 XX  
 KM Surface antigen NhhA; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain Z2491.  
 OS  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..102  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 103..114  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 115..124  
 FT /label= V2

FT /note= "Variable region 2"  
 FT 125..188  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 189..208  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 209..227  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 228..236  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 237..592  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 PN W020015182-A1.  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-AU00069.  
 XX  
 PR 25-JAN-2000; 2000US-0177917.  
 XX  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Peak IRA, Jennings MP;  
 XX  
 DR WPI: 2001-488774/53.  
 XX  
 DR N-PSDB; AAS09170.  
 XX  
 PT New NhhA surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX  
 PS Claim 9; Fig 1; 91pp; English.

The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen NhhA  
 CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC immunogens against a broader spectrum of N. meningitidis strains than  
 CC immunise against the mutant proteins when used as a vaccine can effectively  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen NhhA  
 CC from N. meningitidis strain Z2491 is 1 of 10 NhhA polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 SO Sequence 592 AA:

Query Match 93.0%; Score 2779; DB 22; Length 592;  
 Best Local Similarity 93.9%; Pred. No. 3.2e-151;  
 Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

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QY 1 MKRIIRIINNSALNMVAVSELTRNHTKRASATVKAVALATLLEFAVQANANDEDEEEL 60
   |||||||
DB 1 mkklyrllwnsalnawavseltrnhtkrasatvkavalatllfavganadedeeel 60
QY 61 ESQSRVSGSIQASMEGSELEETISLSMTNDSKEFVDPYIVVTLKAGDMLKIKONTNEMT 120
   |||||||
DB 61 esvqsrsvsgisqasmegeleletislsmtndsketfdpyivvtrlkagdklkkqntnemt 120
QY 121 NASSFTYSLKQDLTGLINVERTEKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 180
   |||||||
DB 121 nassftyslkkdltglinveteklsfgangkkrvniisdtckglnfaketagngdtvtvhl 180
QY 181 GIGSTLTDLMLNTGATTNTNDNVTDDEKKRAASVADVLANAGMNIKGVKPGTTA--SDNV 238

```





PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 XX  
 DR WPI: 1999-418754/35.  
 DR N-PSDB: AAX85795.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections  
 XX  
 PS Claim 1; Page 114-115; 132pp; English.  
 XX  
 CC The present sequence represents a surface protein of Neisseria  
 CC meningitidis which is approximately 62 kDa. The N. meningitidis  
 CC surface glycoproteins, nucleic acids, the primers and optionally  
 CC a thermostable polymerase, or antibodies are useful in a kit for  
 CC the detection or diagnosis of N. meningitidis infection in humans.  
 CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.  
 CC  
 XX Sequence 599 AA:  
 SQ  
 Query Match 90.4%; Score 2699.5; DB 20; Length 599;  
 Best Local Similarity 91.2%; Pred.No. 1.1e-146;  
 Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

OY 1 MNKIRIIMNSALNMAVAVSELTNRHTRKASATVKTAVLATLLEFATVQANATDEDEEEL 60  
 DB 1 mkiyriimsalnawavseltrnhtrkasatvktavlatllefatvqanadedeeel 60  
 OY 61 ESYQRS-VVGSIQASMEGSELEF--ISLSMTNDSKEFVDPIYVTLKAGNLKIKO-- 114  
 DB 61 epyvsrsalvlgfmldkegenesegnlsydhnlhg-actvlkagdnlikiknt 119  
 OY 115 --NTBENRNASSEFTYSLKKDLGLINVEREKLSFGANGKKVNIISPTKGLNFAKETAGCN 172  
 DB 120 nktntentdssfelyslkkdlcldlsveleklsifganqknvltsdtkylnfaketaagn 179  
 OY 173 GDTYHLNGIGSTLDMLNTGATTNVTNDNTYDDEKKRAASVVDVLAGMWNKIGVKKPST 232  
 DB 180 gdttrhnglgsstldlntgattcnvtrndntyddkkrasvkvdlagmwnlkvgkpgt 239  
 OY 233 TASDNDVFRYIVFEFLSADTKTTTVNESKDNCKTEVKGAKTSVIRKEDGKLVTGK 292  
 DB 240 tasdnvdfvhtydlveflsadtktctvnveskdngrtevkigaktsvirkedgklvtgk 299  
 OY 293 GKGEKSSPDEEGLYTAKREVDAVNAKGRMKTTTANGOTGOADKFEVTVSGTKVTFAS 352  
 DB 300 gkgengsspdegegltvtakevldavnkagwmktttlangqtgqadkfetvtsqtnvtfas 359  
 OY 353 GNGTATVSKDOGNITVYKDVNVDALNVNLONSGMWLDKAAVAGSSGKVIYGNVSPS 412  
 DB 360 gngtatvskddognitvyrndvndalnvnqngsmwldkavagssgkviysgnvps 419  
 OY 413 KKKMDETVNINAGNNIETRNCKNIDIAIATSWPQSSSVSLGAGADAPLTVSDEGALNVG 472  
 DB 420 kkgmdeetvniagnnietrncknidiatatwmpqsssvslgagadapltvsddkaglnvg 479  
 OY 473 SKDANKPRVITVAPGVKSGDVTNVAQLKGVANONLNMRIDNNGNRAIATAIATAGLV 532  
 DB 480 skdankprviltvapgvskevgtvnaqklgvagnlnmriddnngnragiaqatagltv 539  
 OY 533 QAYLPCKSMMAIGGTYLGEAGYAGYSSISAGNMWIIKGTASGNGRHFAGASASVGYWM 592  
 DB 540 qaylpgksmmaiggtlyrgeagyalgysisagnmwlikgtasngsrhfgasasvgywm 599

RESULT 6  
 AAU06176  
 ID AAU06176 standard; Protein; 599 AA.

XX  
 AC AAU06176;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.  
 XX  
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 XX  
 OS Neisseria meningitidis strain H38.  
 XX  
 XX  
 FT Key  
 FT Location/Qualifiers  
 FT Region  
 FT 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT 51..105  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 106..117  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 118..131  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 132..195  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 196..217  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 218..236  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 237..243  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 244..599  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 FT  
 FT Region  
 FT WO20015182-A1.  
 FT  
 FT 02-AUG-2001.  
 FT  
 FT 25-JAN-2001; 2001WO-AU00069.  
 FT  
 FT 25-JAN-2000; 2000US-0177917.  
 FT  
 FT (UYOU ) UNIV QUEENSLAND.  
 FT  
 FT Peak IRA, Jennings MP;  
 FT  
 FT WPI: 2001-488774/53.  
 FT N-PSDB: AAS09166.  
 FT  
 FT New Nhha surface antigen polypeptides and polynucleotides from  
 FT Neisseria meningitidis, useful in producing vaccines for treating or  
 FT preventing broad spectrum of Neisseria meningitidis -  
 FT  
 FT Claim 9; Fig 1; 91pp; English.

CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
CC the present invention.

XX Sequence 599 AA;

Query Match 90.4%; Score 2699.5; DB 22; Length 599;  
Best Local Similarity 91.2%; Pred. No. 1.1e-146;  
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

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QY 1 MNKIRIIMNSALNMAVAVSELTNRNHRKASATYKTAVALTLATLFAVQANATDEDEEEL 60
    |||||
    1 mnklyriimnsalnawavseltrnhkrasatvktavlatllfatvqanatedeeseel 60
D 1
QY 61 ESVORS-VVGSIOASMEGSVELET---ISLMTNDSKEFVPYIVTAKADNLKIKO-- 114
    |||||
    61 epyvrsalvqfmdkegenestgnigwsiydhntllng-atvclkaqdnlkiknt 119
D 61
QY 115 --NTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKKNVSIIDTKGLNFAKETAGTN 172
    |||||
    120 nktuentndsfyslkkdltdltsveteklsfgangknvtsdckglnfaketagtn 179
D 120
QY 173 GDTIVHLNGISTLTDLMLNTGATTNTNDVNTDEKRAASVSDVLAAGNINIKVPRGT 232
    |||||
    180 gdtivhngistltldtllngatlnvndvlddkkkrasavdvlnagwnikvprgt 239
D 180
QY 223 TASDNDVDFVRYTDYVEFLSADTKTTTVNESKDNKKTVEKIGAKTSYIKEDGKLVTK 292
    |||||
    240 tashndvdfvrytdyveflsadtktttnveskdngkrtrevkigaktsyikegkvlvrgk 299
D 240
QY 293 KGENGSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFEVTVSGTKVTPAS 352
    |||||
    300 kgenngsstdegeglvtakevidavnkagwrmkttlangqgqadkfetvcsqtnvtfas 359
D 300
QY 353 GNGTATATSKDQGNITRYKYVNVNGDALNVNQLQNSGNLDSKAVAGSSGAVISGNVSPS 412
    |||||
    360 gngtatatskddqgnitrykyvngvdalnvnqlqngswnldskavagssgavisgnvps 419
D 360
QY 413 KGMDETVNINAGNNIETTRNGKNIDTASMTPOFSSVSLGAGADAPLSVDDGALNVG 472
    |||||
    420 kymdetvniagnnielttrngknidatsmtprfssvslgagadaprlsvddgalnvrg 479
D 420
QY 473 SKDANKPVRITNVAAGVEGDVTNVAQLKGVAQNLNRRIDNVNNGARAGIAQAIATAGLV 532
    |||||
    480 skdankpvriltvnapgvkegdvtvnaqlkyvaqnlmrridnvngnaraglaqaiataglv 539
D 480
QY 533 QAYLPKGSMAAIGGTYLGEAGYAIGYSISAGGNWIIKGTASGNSRHFAGASASVGTOW 592
    |||||
    540 qaylpkgsmmaiaggtylgeagyaigysisadgnwilkgtasgnsrghfgasasvgtow 599
D 540
```

RESULT 7  
AAI23742  
ID AAI23742 standard; Protein: 598 AA.

XX AAI23742;

XX 08-SEP-1999 (first entry)

XX A surface protein of *Neisseria meningitidis*.

XX Surface protein: surface glycoprotein; infection: vaccine;

XX Immunoreactive peptide.

XX *Neisseria meningitidis*.

XX MO9931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98MO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-PSDB; AAX85794.

PT *Neisseria meningitidis* surface proteins useful for treating *N.*

PS meningitidis infections

PS Claim 1; Page 108-110; 132pp; English.

CC The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 598 AA;

Query Match 89.3%; Score 2667; DB 20; Length 598;  
Best Local Similarity 89.8%; Pred. No. 8.1e-145;  
Matches 544; Conservative 10; Mismatches 30; Indels 22; Gaps 6;

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QY 1 MNKIRIIMNSALNMAVAVSELTNRNHRKASATYKTAVALTLATLFAVQANATDEDEEEL 60
    |||||
    1 mnklyriimnsalnawavseltrnhkrasatvktavlatllfatvqanated-dddl 59
D 1
QY 61 ESVOR-SVGSIOASMEGSVELETISLMTNDSKEFDPYI-----VITKADNL 110
    |||||
    60 epyvrsalvqfmdkegenestgnigwsiydhntllng-atvclkaqdnlkiknt 112
D 60
QY 111 KIKONTNENTNA-----SFTYSLKKDLTGLINVEETKLSFGANGKKNVSIIDTKGLNFAK 166
    |||||
    113 kikontnentndsfyslkkdltdltsveteklsfgangknvtsdckglnfak 172
D 113
QY 167 ETAGNGDTIVHLNGISTLTDLMLNTGATTNTNDVNTDEKRAASVSDVLAAGNINIK 226
    |||||
    173 etagngdtpvhlngistldtllngatlnvndvlddkkkrasavdvlnagwnik 232
D 173
QY 227 GVKPGETIASDNDVRYTDYVEFLSADTKTTTVNESKDNKKTVEKIGAKTSYIKEDG 286
    |||||
    223 gvkpgetiasdndvrytdyveflsadtktttnveskdngkrtrevkigaktsyikeg 292
D 223
QY 287 KLVTKGKGENGSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGQTQADKFEVTVSGT 346
    |||||
    293 klvtkgkgenngsstdegeglvtakevidavnkagwrmkttlangqgqadkfetvcsqt 352
D 293
QY 347 KVFASGNGTATATSKDQGNITRYKYVNVNGDALNVNQLQNSGNLDSKAVAGSSGAVIS 406
    |||||
    353 kvftasngtatskddqgnitrykyvngvdalnvnqlqngswnldskavagssgavvis 412
D 353
QY 407 GNVSPSKGMDETVNINAGNNIETTRNGKNIDTASMTPOFSSVSLGAGADAPLSVDD 466
    |||||
    413 gnvspkskmdetvniagnnielttrngknidatsmtprfssvslgagadaprlsvdde 472
D 413
QY 467 GALVNGSKDANKPVRITNVAAGVEGDVTNVAQLKGVAQNLNRRIDNVNNGARAGIAQAI 526
    |||||
    473 galvngskdankpvriltvnapgvkegdvtvnaqlkyvaqnlmrridnvngnaraglaqai 532
D 473
QY 527 ATAGLVQAYLPKGSMAAIGGTYLGEAGYAIGYSISAGGNWIIKGTASGNSRHFAGASA 586
    |||||
    533 ataglvaylpkgsmmaiaggtylgeagyaigysisadgnwilkgtasgnsrghfgasa 592
D 533
QY 587 SVGTOW 592
    |||||
```

DB 593 svgyqw 598

RESULT 8

AAU06177

ID AAU06177 standard; Protein: 598 AA.

XX

AC AAU06177;

XX

DT 24-OCT-2001 (first entry)

XX

DE N. meningitidis H15 surface antigen Noha polypeptide sequence.

XX

KW Surface antigen Noha; meningococcal disease; meningitis vaccine.

OS Neisseria meningitidis strain H15.

XX

FH Key Location/Qualifiers

FT 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT 51..104

FT /label= V1

FT /note= "Variable region 1"

FT 105..116

FT /label= C2

FT /note= "Conserved region 2"

FT 117..130

FT /label= V2

FT /note= "Variable region 2"

FT 131..194

FT /label= C3

FT /note= "Conserved region 3"

FT 195..216

FT /label= V3

FT /note= "Variable region 3"

FT 217..235

FT /label= C4

FT /note= "Conserved region 4"

FT 236..242

FT /label= V4

FT /note= "Variable region 4"

FT 243..598

FT /label= C5

FT /note= "Conserved region 5"

XX

PN WO20015182-A1.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-AU00069.

XX

PR 25-JAN-2000; 2000US-0177917.

XX

PA (UYOU ) UNITV QUEENSLAND.

XX

PI Peak IRA, Jennings MP;

XX

XX WPI: 2001-488774/53.

DR N-PSDB; AAS09167.

XX

PT New Noha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

XX

PS Claim 9; Fig 1; 91pp; English.

XX

CC The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Noha

CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Noha

CC from N. meningitidis strain H15 is 1 of 10 Noha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX

SQ Sequence 598 AA:

Query Match 89.3%; Score 2667; DB 22; Length 598;

Best Local Similarity 89.8%; Pred. No. 8,1e-145;

Matches 544; Conservative 10; Mismatches 30; Indels 22; Gaps 6;

QY 1 MNKIYRIINWNLAMVAASELIRNHTKRASATVKTAVLATLFLFAVQANATDEDEEEL 60

DB 1 mkiyriiwnsalnawvvselttrnhtkrasatvatavlatlflfatvganad-dddlyl 59

QY 61 ESYQR-SVVGSIQASKEGSEVLETTISLSMTNDSKEFVPIY-----VPTLKAQDWL 110

DB 60 epvqrtaavylsfrsdkegfekeg-----tedsnawv-yfdekrvllkagaltlkagdnl 112

QY 111 KIKONTNENTNA-----SPTFYSLKRDNLGLINVEREKLSEFGANGKKVNTIISPTKGINPAK 166

DB 113 kikgnntnentndstfyslklkdltsveteleisfgangknvntlsdtkginfak 172

QY 167 ETAGTNGDTTVHLLNGIGSTLTFDMLNTGATTVNTNDVTDDEKKRAASYKDYLANAGMNR 226

DB 173 etagtngdptvlnhngistldtllntgatntvndnvddekkraasrkydlnagmnlk 232

QY 227 GVKPGTTASDNVDFVRYTVVEFLSADYRTTTVNVESKNGKTEVYICAKTSVYKEKG 286

DB 233 gvkpgttasdnvdfvrytveflsadtkttenveskngktevyikaktsvikekg 292

QY 287 KLVYTGKKGKENGSSDDEGBGIVTAKFVIDAVNKAAGRMKTTTANGOTGADKFEYTSGT 346

DB 293 kltvtygkdgengssldgeglvtakevidavnkagvrmtlttangtqgadfeytsgt 352

QY 347 KYTFASGNGTTAVSKDDOGNITVKYDVWVGDALANQLONSGMNDSKAVAGSSGKYS 406

DB 353 kvtfasngntatvskddogntlvkydvavgdalnnqdgngsmnldskavagssgkys 412

QY 407 GNVPSKGMDETVINAGNNIETTRNGKNIDIASMTPOFSSVSIGACADAPTLSDVDE 466

DB 413 gnvpskgykmdetvlnagnniettrngknidiatmtpqfssvsigadaptlsvdde 472

QY 467 GALNNGSKDANKPVRTTNAPGVKEDDYNNVAQLKVAONLNRRIDNVGNMRAAGIAQAI 526

DB 473 galnngskdankpvrtiltnvapgvkegdyvnnvaqlkvagpnlnrridnvgnnragiaqai 532

QY 527 ATAGLQVATLPKGSMAIGGTYGAGYAIGSSYSAGNMILIKTAGSNGSRHGAGASA 586

DB 533 ataglaqaylpgksmaiggytgyeagyaigysslsdgnvwiktagasnrghtgasa 592

QY 587 SVGYQW 592

DB 593 svgyqw 598

RESULT 9

AAU23739

ID AAU23739 standard; Protein: 594 AA.

XX

AC AAU23739;

XX

DT 08-SEP-1999 (first entry)

XX

DE A surface protein of Neisseria meningitidis.

XX

KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

XX Neisseria meningitidis.  
OS  
XX  
PN W09931132-A1.  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI: 1999-418754/35.  
DR N-PSDB; AAX85791.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 95-97; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX Sequence 594 AA;

Query Match 89.2%; Score 2664; DB 20; Length 594;  
Best Local Similarity 90.0%; Pred. No. 1.2e-144;  
Matches 542; Conservative 9; Mismatches 33; Indels 18; Gaps 5;

QY 1 MNKIRITINSLANWAVSELTRNHRKASATVKAVALLEFAVQANATDEDEEEL 60  
DB 1 mkkyrllmnsalnawvseltrnhktrasatvalatlillafatqanald-dddlyl 59  
QY 61 ESYOR-SVVGSIQASMEGSVELETISLMTNDSKFEVDPYI-----VYTLKAGDNL 110  
DB 60 epvqtlavvlfrsdkegtgekeg-----tedsnwv--yfdetkvlkagatlakagdl 112  
QY 111 KIKONTNENTNASSFTYSILKKDLTGLINVEFEKLSFGANGKKVNTISDTKGLNFAKETAG 170  
DB 113 kikqntnntndstfytglkkdltdltsveteklsfgangkvntlstdkgnfaketaag 172  
QY 171 TNGDTTVALNGIGSTLPJMLNTGATVNTDNTVTDDEKKRAASVQDVLMGNWIKGVKP 230  
DB 173 tngdptvlhnglgsfcltdcllntgatntvndnvddekkraasvkdvlmgwnlkgykp 232  
QY 231 GTTASDNDVFRVTYTFEFLSADTKTTVNESKDNKKTEKTIKAKTSVIREKKGKIVT 290  
DB 233 gttasdnvdfvrltyelveltsadtkttvnveskdnkktevkigaktsvirekkgklvt 292  
QY 291 GKKGKENSSTDEGEGLYTAKEVIDAVNKKAGRMKTTANGOTGADRFETVSGTKVTF 350  
DB 293 gkkgkengsstdegeglvtakevidavnkagymkttangotgqadkfeytsgtntvf 352  
QY 351 ASGNGTATVSKDDGNTTVKYVNVGDALNVNQLONSQWMLDSKAVAGSSGKTVISGANS 410  
DB 353 asgngttatvskddgnttkydvnnvgdalinvnqlnsgwmlsdskavagssgkvtisgnvs 412  
QY 411 PSKGMDETVINMAGNNIEITRNKGNIDIAISMTPOFSSVSIGACADAPTLSVDEGALN 470  
DB 413 pskgmdetvinnagnnietrngknidiatismapqfssvsigadadapltlsvdegaln 472

QY 471 VGSKDKANKPVRITNVAPGKVEDYTNVAQLKGVAONLNRRIDNVNGNARACIAQALATAG 530  
DB 473 vgsdkdnknpvritnvapgvkegdrvtnvqglkyvaqnlmrridnvdngnaragjaqalataag 532  
QY 531 LVQATLPKSSMMAIGGCTYLCDEAGYATGYSSISAGGNWITKGTASGNSRGHFGASASVGY 590  
DB 533 lvqaylpgkssmmaigdtylrgdeagyaigyssisdggnwlkgtasgnrghfgasasvgy 592  
QY 591 QW 592  
DB 593 qw 594  
  
RESULT 10  
AAU06179  
ID AAU06179 standard; Protein: 594 AA.  
AC AAU06179;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis B2198 surface antigen Nhba polypeptide sequence.  
XX  
KW Surface antigen Nhba; meningococcal disease; meningitis vaccine.  
OS Neisseria meningitidis strain B2198.  
XX  
FH Key  
FT Region  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..104  
FT /label= V1  
FT /note= "Variable region 1"  
FT 105..116  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 117..126  
FT /label= V2  
FT /note= "Variable region 2"  
FT 127..190  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 191..212  
FT /label= V3  
FT /note= "Variable region 3"  
FT 213..231  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 232..238  
FT /label= V4  
FT /note= "Variable region 4"  
FT 239..594  
FT /label= C5  
FT /note= "Conserved region 5"  
  
W0200155182-A1.  
PD 02-AUG-2001.  
XX  
PP 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI: 2001-488774/53.  
DR N-PSDB; AAS09169.  
XX  
PT New Nhba surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of *Neisseria meningitidis* -  
XX  
PS Claim 9; Fig 1; 9pp; English.  
XX

CC The present invention relates to the isolation of novel *Neisseria*  
CC meningitidis mutant polypeptides of the surface antigen Nha  
CC (AAU06182-AAU06186). The modified or mutant Nha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of *N. meningitidis*, and in designing and/or screening of  
CC immunise against a broader spectrum of *N. meningitidis* strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nha  
CC from *N. meningitidis* strain B2198 is 1 of 10 Nha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
CC the present invention.  
XX  
SO Sequence 594 AA:

Query Match 89.2%; Score 2664; DB 22; Length 594;  
Best Local Similarity 90.0%; Pred. No. 1.2e-144;  
Matches 542; Conservative 9; Mismatches 33; Indels 18; Gaps 5;

QY 1 MNKIYRIINMSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 mkiylriinmsalnnavvseltrnhtkrasatvatavlatllfatvganad-dddlyl 59  
QY 61 ESVQR-SVVGSIQASMEGSELETTISLMTNDSKEFVDPI-----VYLRKAGDNL 110  
DB 60 epvqrtaavslsfrsdegekeg-----tedsnwav--yfdkrylkgagatlkgadnl 112  
QY 111 KIKQNTNENTNASSFTYSLKDDLTGLINYTEKLSFGANGKKVNIISDTRKGLNFAKETAG 170  
DB 113 ktkqntnentndssfyslkkdltgltsveteklsfgangknvnltsdtkylnfaketag 172  
QY 171 TNGDTVHLANGISTITDMLNTGATTNTNDVNTDDEKKRAASVADVNLACNNTIGVPR 230  
DB 173 tngdtpvhlngistitdclntgattntndvntddekkraasvadvnlnacnntigvpr 232  
QY 231 GPTASDNVFEVRTYDVEFLSADTKTTTNNVESKONGKTEVIGAKTSVIREKDKLVT 290  
DB 233 gptasdnvfvrtlydveflsadtktttvnveskngkktevlgaktsvirekdgklyt 292  
QY 291 GKKGNGSGSTDEGELVTAKEVIDAVNRAGRMKTTTANGOTGADKFEVTSGRVT 350  
DB 293 gkgkngsgstdegeglvtakevidavnragrmktttangotgqgdkfetvsgtnvlf 352  
QY 351 ASGNGTTAIVSKDDGNTVYKVDVNGALNVQNLONGMNLDSKAVAGSSGKVIISGNVS 410  
DB 353 asgngttaivskddgntlvykvdvngaldnvqnlngmsgnldskavagssgkviisgnvs 412  
QY 411 PSKGRDEFTVNIAGNNIETTRNGKNIDIASMTPOFSSVIGAGADAPLISVDDGALN 470  
DB 413 pskgrmedevniagnniettrngknidiatcmtpofssvlgagadapllisvddgala 472  
QY 471 VGSKADANKPVRTTNVAPGVKEGDVTNVAQLKGVAQMLNNRIDVNNARAGIAQAATATAG 530  
DB 473 vsgkadenkpvritnvapgvkegdvtnvaqlkgyaqlnnridvngdnaraglaqatag 532  
QY 531 LVQATVLPKSSMAIGGTYLGEAGYAIYSSISAGGNIITKTAAGNSRGHFGASASVGT 590  
DB 533 lvqatvlpkssmaiggytlylgeagyaigyssisdggnwllkgtaasnsrgfhgaasavgy 592  
QY 591 QW 592  
DB 593 qw 594

RESULT 11  
AAV23738

ID AAV23738 standard; Protein; 598 AA.  
XX

AAV23738;  
XX

08-SEP-1999 (first entry)  
XX

A surface protein of *Neisseria meningitidis*.  
DE

Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX

*Neisseria meningitidis*.  
XX

W09931132-A1.  
XX

24-JUN-1999.  
XX

14-DEC-1998; 98WO-AU01031.  
XX

12-DEC-1997; 97GB-0026398.  
XX

(ISIS-) ISIS INNOVATION LTD.  
PA (UYOU) UNIT QUEENSLAND.  
XX

Jennings MP, Moxon ER, Peak IRA;  
XX

WPI; 1999-418754/35.  
DR

N-PSDB; AAV85790.  
XX

*Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
XX

Claim 1; Page 91-93; 132pp; English.  
PS

The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX

Sequence 598 AA:  
SO

Query Match 89.0%; Score 2658; DB 20; Length 598;  
Best Local Similarity 89.4%; Pred. No. 2.7e-144;  
Matches 542; Conservative 11; Mismatches 31; Indels 22; Gaps 6;

QY 1 MNKIYRIINMSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 mkiylriinmsalnnavvseltrnhtkrasatvatavlatllfatvganad-dddlyl 59  
QY 61 ESVQR-SVVGSIQASMEGSELETTISLMTNDSKEFVDPI-----VYLRKAGDNL 110  
DB 60 epvqrtaavslsfrsdegekeg-----tedsnwav--yfdkrylkgagatlkgadnl 112  
QY 111 KIKQNTNENTNASSFTYSLKDDLTGLINYTEKLSFGANGKKVNIISDTRKGLNFAKETAG 170  
DB 113 ktkqntnentndssfyslkkdltgltsveteklsfgangknvnltsdtkylnfaketag 172  
QY 171 TNGDTVHLANGISTITDMLNTGATTNTNDVNTDDEKKRAASVADVNLACNNTIGVPR 230  
DB 173 tngdtpvhlngistitdclntgattntndvntddekkraasvadvnlnacnntigvpr 232  
QY 231 GPTASDNVFEVRTYDVEFLSADTKTTTNNVESKONGKTEVIGAKTSVIREKDKLVT 290  
DB 233 gptasdnvfvrtlydveflsadtktttvnveskngkktevlgaktsvirekdgklyt 292  
QY 291 GKKGNGSGSTDEGELVTAKEVIDAVNRAGRMKTTTANGOTGADKFEVTSGRVT 350  
DB 293 gkgkngsgstdegeglvtakevidavnragrmktttangotgqgdkfetvsgtnvlf 352  
QY 351 ASGNGTTAIVSKDDGNTVYKVDVNGALNVQNLONGMNLDSKAVAGSSGKVIISGNVS 410  
DB 353 asgngttaivskddgntlvykvdvngaldnvqnlngmsgnldskavagssgkviisgnvs 412  
QY 411 PSKGRDEFTVNIAGNNIETTRNGKNIDIASMTPOFSSVIGAGADAPLISVDDGALN 470  
DB 413 pskgrmedevniagnniettrngknidiatcmtpofssvlgagadapllisvddgala 472  
QY 471 VGSKADANKPVRTTNVAPGVKEGDVTNVAQLKGVAQMLNNRIDVNNARAGIAQAATATAG 530  
DB 473 vsgkadenkpvritnvapgvkegdvtnvaqlkgyaqlnnridvngdnaraglaqatag 532  
QY 531 LVQATVLPKSSMAIGGTYLGEAGYAIYSSISAGGNIITKTAAGNSRGHFGASASVGT 590  
DB 533 lvqatvlpkssmaiggytlylgeagyaigyssisdggnwllkgtaasnsrgfhgaasavgy 592  
QY 591 QW 592  
DB 593 qw 594  
QY 287 KLVWGKKGNGSGSTDEGELVTAKEVIDAVNRAGRMKTTTANGOTGADKFEVTSGR 346  
DB 287 klvwgkkgngsgstdegeglvtakevidavnragrmktttangotgqgdkfetvsgt 346

```
Db 293 klvtgkqgengsstdegeglvtakevidavnkagwmkttlangqlgqadkfetvtsqt 352
OY 347 KVFASGNGTTATVSKDDQGNITVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKYIS 406
    |||||
Db 353 kvtfasngttatvskddqgnltvkvdydvngdalinvgqlqnsqwnldskavagsgkyis 412
OY 407 GNVSPSKGKMDETVINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDE 466
    |||||
Db 413 gnvpskqkmdetvlnagmnielttrngknidiatsmtpqfssvslgagadaptilsvdde 472
OY 467 GALNNGSKDANKPVRITVNAVPGVKEGDTVNAQLKGVAQNLNRRIDNVNNGNARAGIAQAI 526
    |||||
Db 473 galnvgsdkdankpvriltvnapgvkegdvlnvaqllkyvaqnlunnridnvdnaraglaqai 532
OY 527 ATAGLVQAVILPGKSMMAIGGCTYLGEGYALGYSISAGNMIIKGTASGNSRGHFGASA 586
    |||||
Db 533 ataglaqaylpgksmmaiggctyrgaayalgyssistdgnwvlkgtasgnsrghfgasa 592
OY 587 SVGYQW 592
    |||||
Db 593 svgyqw 598

RESULT 12
AAU06178
ID AAU06178 standard; Protein: 598 AA.
XX
AC AAU06178;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis BZ10 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
OS Neisseria meningitidis strain BZ10.
XX
FH Key
FT Location/Qualifiers
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..130
FT /label= V2
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FT 195..216
FT /label= V3
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FT /label= C4
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FT /label= V4
FT /note= "Variable region 4"
FT 243..598
FT /label= C5
FT /note= "Conserved region 5"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
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XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI: 2001-488774/53.
XX
DR N-PSDB: AAS09168.
XX
PT New NhhA surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen NhhA
CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhhA
CC from N. meningitidis strain BZ10 is 1 of 10 NhhA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 598 AA:
XX
Query Match 89.0%; Score 2658; DB 22; Length 598;
Best Local Similarity 89.4%; Pred. No. 2,7e-144;
Matches 542; Conservative 11; Mismatches 31; Indels 22; Gaps 6;
OY 1 MNKIIRIINSNALNMAVAVSELTRNHTKRASATYKAVLATLLEFATYQANNTDEDEEEL 60
    |||
Db 1 mknkiriinmsalnaavvsselttrnhtkrasatavlatllefayqanadt-dddlyl 59
OY 61 ESVQR-SVYGSIQASMEBSVELETISLSMTNDSKEFVPIY-----VYTLKAGNLT 110
    |||
Db 60 epvqrtaavlvrfsrdskeglgekeg-----tedsnaw--yidekrvllkagallkagahl 112
OY 111 KIKONTNENTNA---SSFTYSLKDLTGLINVERTEKLSFGANGKKNVITIDTKGLNPAK 166
    |||||
Db 113 ktkqntnententndssftyslkkdlctlsvekeklsfngangknvltstdtqglntak 172
OY 167 ETAGTNGDTVHLNGIGSLTIDMLNLTGATTNVTNDNTDDEKKRAASVKDVLNAGNMIK 226
    |||||
Db 173 etagntngdptvhlngigstlctllnltgatlntvndntddekkrasvkvdlnaqwnik 232
OY 227 GYKRGCTTASDNVDVRYRTDYVEFLSADTKTTTVNVESDNKKRTFKGATSVYKEDG 286
    |||||
Db 223 gvkpqtltasdhvdivrlydvelflsadtkcttvnveskxngkrtevkigaktsvlkekdq 292
OY 287 KLVNKGKGENGSPTDFEGGLVTAKEDVIDAVNKAQWRKTTTANGQTQADKFETVTSQT 346
    |||||
Db 293 klvtgkqgengsstdegeglvtakevidavnkagwmkttlangqlgqadkfetvtsqt 352
OY 347 KVFASGNGTTATVSKDDQGNITVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKYIS 406
    |||||
Db 353 kvtfasngttatvskddqgnltvkvdydvngdalinvgqlqnsqwnldskavagsgkyis 412
OY 407 GNVSPSKGKMDETVINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDE 466
    |||||
Db 413 gnvpskqkmdetvlnagmnielttrngknidiatsmtpqfssvslgagadaptilsvdde 472
OY 467 GALNNGSKDANKPVRITVNAVPGVKEGDTVNAQLKGVAQNLNRRIDNVNNGNARAGIAQAI 526
    |||||
Db 473 galnvgsdkdankpvriltvnapgvkegdvlnvaqllkyvaqnlunnridnvdnaraglaqai 532
OY 527 ATAGLVQAVILPGKSMMAIGGCTYLGEGYALGYSISAGNMIIKGTASGNSRGHFGASA 586
```

Db 533 ataglagaylpqksmma1gggtyrgeagya1gyss1sdgtgnw1klytaagnsrghfsta 592  
 QY 587 SVGYQM 592  
 Db 593 svgyqm 598

## RESULT 13

AAV23740  
 ID AAV23740 standard; Protein; 594 AA.

AC AAV23740;

DT 08-SEP-1999 (first entry)

DE A surface protein of *Neisseria meningitidis*.

KW Surface protein; surface glycoprotein; infection; vaccine;

XX immunoreactive peptide.

OS *Neisseria meningitidis*.

PN WO9931132-A1.

PD 24-JUN-1999.

PE 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PI (UNYU) UNIV QUEENSLAND.

PL Jennings MP, Moxon ER, Peak IRA;

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

PT *Neisseria meningitidis* surface proteins useful for treating *N.*

PS *meningitidis* infections

CC Claim 1; Page 100-101; 132pp; English.

CC The present sequence represents a surface protein of *Neisseria*

CC *meningitidis* which is approximately 62 kDa. The *N. meningitidis*

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of *N. meningitidis* infection in humans.

CC The *N. meningitidis* surface glycoproteins can also be used to

CC prevent or treat *N. meningitidis* infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

CC

CC

CC

CC

Sequence 594 AA;

Query Match 88.2%; Score 2636; DB 20; Length 594;

Best Local Similarity 89.3%; Pred. No. 4.8e-143;

Matches 536; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

QY 1 MKIRIRIINNSALNMWVAASELIRNHTKRASATVKTAVLATLLEFATVQANANDEDEEEL 60

Db 1 mkkiririlwnsalnmwvaseilrnlhkrasatvalatallfavgastld-dddl1 59

QY 61 ESVQR-SVVGSIQASMEGSVELETLISMTNDS-----KEFVDPYIVVTAKAGDNLEKI 112

Db 60 evqrlavvlfrsldkgegeke-----vledsnwgyvdfkgyvlagtiltlkagdnlti 114

QY 113 KONTNENTNASSFTYSLKADLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTN 172

Db 115 kntnenntnassfyslkkdldtltsvgtelksfsansknvtsldtkglnfakktlaetn 174

QY 173 GDTVHLANGISLTLDMLNTGATTNVTNDNTDEKKRAASYKVYLAAGWNIKGVKPGT 232  
 Db 175 gdtvhlngisltldmlntgattnvntndntdeekkraasvkvylagwnikgvkpgt 234  
 QY 233 TASDNVDVFRYTDVVEELSADTKTTTVNVEKDNKGTTEVKIGAKTSVIREKDGKLVTK 292  
 Db 235 tasdnvdfvrytdvveelsadctkttnveskdngrtevkigaktsvirekdgkltvk 294  
 QY 293 GKGENSSVDEGEGLVTAKEVIDAVNKAQRKTTTANQOTGQADKEFVTSCTKTFPS 352  
 Db 295 dkgenssldkgeglvtakevidavnkagvrmtltanqgtqadkefvtsgtlnltas 354  
 QY 353 GNGTATVSKDOGNITTVYDVNVGDALNVNOLONGMNLDSKAVAGSSGKTVSGNVSPS 412  
 Db 355 gngtatvskdognitvymdvngdalinvnqlngsmwnldskavagssgkvtsgnvsp 414  
 QY 413 KGRMDETIVINAGNNIEIRNRGNKIDIASMTPOFSSVSLGAGADAPTLVDEGALNVG 472  
 Db 415 kgmdetvlnagnnietlrngknidiatmtpfssvslgagadaptlsvdegalnv 474  
 QY 473 SKDANKPVRIITVAPGVKRGDVTNVAQLKGVANLNRIDNNGNRRACIAQAIATAGLV 532  
 Db 475 skdanpvrlitvapgvgkdvtlnvaqlkvgvagnlnhldnvgnaraglaqalatl 534  
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 Db 535 qaylpqksmma1gggtyrgeagya1gyssisdggnw1klytaagnsrghfstaasvgyqm 594

## RESULT 14

AAV57044  
 ID AAV57044 standard; Protein; 594 AA.

AC AAV57044;

DT 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from *N. meningitidis* strain ATCC13090.

KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;

XX infection; treatment; prevent; antibacterial drug.

OS *Neisseria meningitidis*.

FT Key Location/Qualifiers

FT Misc-difference 104 /note= "Encoded by AATC"

PN WO9958683-A2.

PD 18-NOV-1999.

PE 07-MAY-1999; 99WO-EP03255.

PR 13-MAY-1998; 98GB-0010276.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Ruelle J;

DR WPI; 2000-053103/04.

DR N-PSDB; AA239864.

PT New polypeptide from *Neisseria meningitidis* useful for diagnosis,

PS treatment or prevention of bacterial infections in mammal

CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from

CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the

CC Haemophilus influenzae surface fibril (HSF) protein. The invention

CC relates to BASB029 polynucleotide sequences (AA239864-239865) and

CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.

CC BAS029 polypeptides are useful in a method of diagnosing a *Neisseria*  
 CC meningitidis infection in a mammal. Compositions containing BAS029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BAS029 is useful in treating humans with *Neisseria*  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BAS029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.

CC XX  
 CC Sequence 594 AA:

Query Match 88.2%; Score 2636; DB 21; Length 594;

Best Local Similarity 89.3%; Pred. No. 4.8e-143;  
 Matches 536; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

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 Db 60 epvgrlvsvfisdkgelgeke-----vledsmgyvfdkkgvltgcltkagdnk 114  
 QY 113 KONNENTNASSFTYSLKDLGLINVEKLSFGANGKKNIISDTRKGLNFAKETAGTN 172  
 Db 115 kqntentnassfyslkdldtltsvgtelksansknktsdtkglnfaktaetn 174  
 QY 173 GDTVHLNGISLTLDMLNTGATTNTNDVNDDEKKRAASVKDVLNAGNNIKGVFET 232  
 Db 175 gdtvhlngisltldtlinlgatlnvndvtdckkraasvkdvlngvnlkvgvpgt 234  
 QY 233 TASNNDVPRVRYDVEFISATKTNTTVNESKDNKKREVIKATSYRKDKGLVGR 292  
 Db 235 tashndvprvrydvefisdktctvneskdngkrtvknigaktsvirkdglvgr 294  
 QY 293 GKGENGSTDEGEIYVTAKEVIDAVNKAEMKTTTANGQTGOADKEETVSGTRVTFAS 352  
 Db 295 dkgenstdegeidvtakevndavnkagvrmkttanqgsgqdkfctvsgntvfas 354  
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 QY 413 KGKMDPEYNINAGNNIETRRGNKNDIATSMTPPESSVSLAGADAPRLSLVDDGALVWG 472  
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RESULT 15

AAU06174  
 ID AAU06174 standard; Protein: 594 AA.

AC AAU06174;

XX 24-OCT-2001 (first entry)

XX N. meningitidis EG327 surface antigen Nhba polypeptide sequence.  
 DE

XX XX  
 XX Surface antigen Nhba; meningococcal disease; meningitis vaccine.  
 KW N. meningitidis strain EG327.  
 OS *Neisseria meningitidis* strain EG327.  
 XX  
 FH Key  
 FT Location/Qualifiers  
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 FT /note= "Conserved region 1"  
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 FT /label= C5  
 FT /note= "Conserved region 5"  
 PN W020015182-A1.  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYOU ) UNIV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI WPI: 2001-488774/53.  
 DR N-PSDB: AAS09164.  
 DR  
 XX New Nhba surface antigen polypeptides and polynucleotides from  
 PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
 PT preventing broad spectrum of *Neisseria meningitidis* -  
 PS  
 XX Claim 9; Fig 1; 91pp: English.  
 XX  
 CC The present invention relates to the isolation of novel *Neisseria*  
 CC meningitidis mutant polypeptides of the surface antigen Nhba  
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of *N. meningitidis*, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of *N. meningitidis* strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhba  
 CC from *N. meningitidis* strain EG327 is 1 of 10 Nhba polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
 CC the present invention.  
 CC XX  
 SO Sequence 594 AA;



Query Match 88.2%; Score 2636; DB 22; Length 594;  
 Best Local Similarity 89.3%; Pred No. 4.8e-143;  
 Matches 536; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

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   |||||
Db 1 mkiyrlimnsalnawavseltrhrhtkrasatvktavlatlifatvqstcd-dddiyl 59
   |||||

OY 61 ESVQR-SYVGSIQASMEGSVELETTISLSTNDS-----KEFVDPRIYVTLKAGDNKI 112
   |||||
Db 60 epvqrlavlsfrsdkegtgeke-----vtedsnwvyvfdkkgvltagtlitlkagdnli 114
   |||||

OY 113 KONTNENTNASFTYSLKKDLGLINVEEKLSPGANGKKNIIISDTKGLNFAKEFAGFN 172
   |||||
Db 115 knntnntnassfctylkldldlsvgleklsfnsnknltscdkylnfakktaeln 174
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OY 173 GDTVHLNGIGSTLDMNLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPQT 232
   |||||
Db 175 gdtvhlngigstlcllntgattcnvndvtddekkraasvkdvlngwnlkgvqpt 234
   |||||

OY 233 TASDWDVFRRTDYEFELASDRTTNNVESKDNKTEFKIGAKTSYKEKDKLYTGK 292
   |||||
Db 235 tasdwdvfrtydveflsadtlttnveskdngrtevkigaktsylkekdklytgk 294
   |||||

OY 293 GKENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTATTANGOTGADKFEFVTSGTKVTFAS 352
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   |||||

OY 353 GNGTTATVSKDDQGNITVKKYDVNVGDALNVNQLQNSGWNLDKRAVAGSSGKYISGNVSPS 412
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Db 355 gngttatvskddqgnltvmgydvngdahnvnglqnswnldskavagsgkylsgnvsp 414
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OY 413 KKKMDETVNINAGNNIEITRNKNIDIASMTPOFSSVSLGADAPTLSPVDEGALNNG 472
   |||||
Db 415 kkmdeetvnninagnnietlrngknidiasmtpfssvslgagadaptlsvddegalnvg 474
   |||||

OY 473 SKDANKPVRITVAPGVKGGDVTNVAOLKGVAQNINNRIDNVNGNARAGIAQAIAATAGLV 532
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OY 533 QAYLPKSMMAIGGTYLQAGYAIGYSSISAGNMWIKGTASGNSRGHFGASASVGYOW 592
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Db 535 qaylpqksmmaiggytlygagyaigysisddgnwilkgtasgnsrghfgasaavgyqw 594
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Search completed: July 3, 2002, 08:09:03  
 Job time: 489 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:12 ; Search time 64.11 Seconds

Title: US-09-771-382-2

Perfect score:

Sequence: 1 MNKIYRIIWSALNAWVAVS.....TASGNSRGHEGASASVGYQM 592

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Total number of hits satisfying chosen parameters: 231628

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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| 8          | 2658   | 89.2        | 594    | 4  | US-09-669-974-7  | Sequence 7, App1  |
| 9          | 2658   | 89.0        | 598    | 4  | US-09-377-155-5  | Sequence 5, App1  |
| 10         | 2658   | 89.0        | 598    | 4  | US-09-669-974-5  | Sequence 5, App1  |
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| 22         | 1146   | 38.4        | 2353   | 4  | US-08-913-942-4  | Sequence 4, App1  |
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| 44 | 712    | 23.8 | 1004 | 4 | US-09-268-347-30 | Sequence 30, April |
| 45 | 663    | 22.2 | 1104 | 4 | US-09-268-347-38 | Sequence 38, April |

## ALIGNMENTS

## RESULT 1

US-09-377-155-17

; Sequence 17, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

PEAK, Ian Richard Anselm

APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard

1. TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

FILE REFERENCE: 065064/0128

CURRENT APPLICATION NUMBER: US/09/377,155

;; CURRENT FILING DATE: 1999-08-15

PRIOR APPLICATION NUMBER: PCI/A098/01031

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEO ID NOS: 33

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; NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0

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SEO ID NO 17

LENGTH: 592

TYPE: PRT

ORGANISM: *Neisseria meningitidis*

US-09-377-155-17

| Query Match | Similarity   | 100.0%                                                         | Score 2987         | DB 4 | Length 592 |
|-------------|--------------|----------------------------------------------------------------|--------------------|------|------------|
| Best Local  | Similarity   | 100.0%                                                         | Pred. No. 2,9e+229 |      |            |
| Matches     | Conservative | 0                                                              | Mismatches         | 0    | Indels     |
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## RESULT 2

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US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17
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Query Match 100.0%; Score 2987; DB 4; Length 592;

Best Local Similarity 100.0%; Pred. No. 2,9e-229;

Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 RITNVAPEGKGDYTNVAQLKGVAQNLRIDNVNGNARAGIAQAIAATAGLVQAYLPKGS 540
Oy 541 MAAIGGCTYLEAGYAGTSSISAGGNWITKGTASGNSRGHFGASASVGYOM 592
Db 541 MAAIGGCTYLEAGYAGTSSISAGGNWITKGTASGNSRGHFGASASVGYOM 592
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## RESULT 3

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US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
```

Query Match 90.4%; Score 2699.5; DB 4; Length 599;

Best Local Similarity 91.2%; Pred. No. 2e-206;

Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

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Oy 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLEFATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLEFATVOANATDEDEEEL 60
Oy 61 ESVQSRVSGIOASMEGSVELETTISLSMTNDSKEFVDPYIVYTLKAGNLIKIKONT 114
Db 61 ESVQSRVSGIOASMEGSVELETTISLSMTNDSKEFVDPYIVYTLKAGNLIKIKONT 114
Oy 115 --NINENINASSFTYSLKKDLGLINVEETKLSFGANGKKNVNIISDTKGLNFAKETAGT 172
Db 120 NKNINENINASSFTYSLKKDLGLINVEETKLSFGANGKKNVNIISDTKGLNFAKETAGT 179
Oy 173 GDTYVHLNGISSTLMDLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMNIKGVRPGT 232
Db 180 GDTYVHLNGISSTLMDLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMNIKGVRPGT 239
Oy 232 TASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKKTEYKIGAKTSVIEKDKGLVTGK 292
Db 240 TASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKKTEYKIGAKTSVIEKDKGLVTGK 299
Oy 293 GKGENGSTTDEEGLVTAKEVIDAVNKKAGMRKMTTANGOTGQADKFEVTSGTKVTFAS 352
Db 300 GKGENGSTTDEEGLVTAKEVIDAVNKKAGMRKMTTANGOTGQADKFEVTSGTKVTFAS 359
Oy 353 GNGTTATVSKDDOGNITTVYDVNVGALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPS 412
```

| Query Match           | 90.4%           | Score 2699.5                                                  | DB 4     | Length 599 |
|-----------------------|-----------------|---------------------------------------------------------------|----------|------------|
| Best Local Similarity | 91.2%           | Pred. No. 2e-206                                              |          |            |
| Matches 547           | Conservative 11 | Mismatches 33                                                 | Indels 9 | Gaps 4     |
| Oy                    | 1               | MKKIRIINWSLNMWVAASELIRHHTKASATVTAVALATLTFATVQANATDEDEEEL      | 60       |            |
| Db                    | 1               | MKKIRIINWSLNMWVAASELIRHHTKASATVTAVALATLTFATVQANATDEDEEEL      | 60       |            |
| Oy                    | 61              | ESVORS-VVGSIOASMEGSLELET--ISLMTNDSKEFVDPIYVTLTACGDNLKIKQ--    | 114      |            |
| Db                    | 61              | EPVVSALVLOQMIDKEGSENEGNIQMSIYDQNHNTLHG-AYVTLKAGDNLKIKQNT      | 119      |            |
| Oy                    | 115             | --NTNENTNASSFTYSLKKDLTGLINVETEKISFGANGKKVNIISDTKLNPAKETAGTN   | 172      |            |
| Db                    | 120             | NKNTNENTNDSFPTYSLKLDLTDLTSVETEKLSFGANGKKNVITSPTKLNPAKETAGTN   | 179      |            |
| Oy                    | 173             | GQTVYHLNGISITLDMLLNTGATNTVNTDNTDDEKKRAASVKDYLANGNMIRKGYKPGT   | 232      |            |
| Db                    | 180             | GQTVYHLNGISITLDMLLNTGATNTVNTDNTDDEKKRAASVKDYLANGNMIRKGYKPGT   | 239      |            |
| Oy                    | 233             | TASDNDVFERTDYEEFLSADFKTTTVNVESKDNCKKTEVKIGAKTSYKKEKDGKLVTK    | 292      |            |
| Db                    | 240             | TASDNDVFERTDYEEFLSADFKTTTVNVESKDNCKKTEVKIGAKTSYKKEKDGKLVTK    | 299      |            |
| Oy                    | 293             | GKGENGSSTDEGEGLVTAKEVIDAANKAGWRKTTTANGQTQADKFEVTSIGTKVTPAS    | 352      |            |
| Db                    | 300             | GKGENGSSTDEGEGLVTAKEVIDAANKAGWRKTTTANGQTQADKFEVTSIGTNTFAS     | 359      |            |
| Oy                    | 353             | GNGTATVYSKDDQGNITVYKVDYVNGDALNVNOLQNSGMNLDSKAAVSSGKVIISGNVSPS | 412      |            |

| Query Match | Similarity   | 89.3%                                                         | Score 2667         | DB 4      | Length 598 |
|-------------|--------------|---------------------------------------------------------------|--------------------|-----------|------------|
| Best Local  | Similarity   | 89.8%                                                         | Pred. No. 7.8e+204 |           |            |
| Matches 544 | Conservative | 10                                                            | Mismatches 30      | Indels 22 | Gaps 6     |
| QY          | 1            | MNKIRIINMSALNMAVAASELTNRHTRKASATVKRAVLATLIFAVQANATDEDEEEL     | 60                 |           |            |
| DB          | 1            | MNKIRIINMSALNMAVVYSELTRNHTKASATVAVALATLILFVAVQANATD-DDLT      | 59                 |           |            |
| QY          | 61           | ESVQR-SVYGSIQASMEGSEVELETISLSMTNDSKEVPYI-----VYTLKGDML        | 110                |           |            |
| DB          | 60           | EVQORTAAVVLSPRSDKEGKEGEGE-----TEDSNMAV--YFDEKRYLKAGATILKKGDML | 112                |           |            |
| QY          | 111          | KIKONTNENTNA-----SEFTSYLKKDLTGLINVERTKLSFGANGKKVNIISPTKGAFNAK | 166                |           |            |
| DB          | 113          | KIKONTNENTNENTNDSSTFYSLKKDLTDLTVEFEKLSFGANGKNVNIITSDTKGLNFAK  | 172                |           |            |
| QY          | 167          | EPAGTNGDTVHLNLGISTLTDMLNTGATTVNTDNTDDEKKRAASYKVDYLNAGMNIK     | 226                |           |            |
| DB          | 173          | EPAGTNGDPTVHLNLGISTLTDLTNTGATTVNTDNTDDEKKRAASYKVDYLNAGMNIK    | 232                |           |            |
| QY          | 227          | GKPGGTASDANDVPEVYTYTVEFLASDPTTNYNVSCKNGKKEVYKIAKTSVIREKGG     | 286                |           |            |
| DB          | 233          | GKPGGTASDANDVPEVYTYTVEFLASDPTTNYNVSCKNGKKEVYKIAKTSVIREKGG     | 292                |           |            |
| QY          | 287          | KLVTVGKKGENGSSTDEGEGLVTAKEVIDAVNAKAGRMKTTTANGOTGADKFEIVTSGT   | 346                |           |            |
| DB          | 293          | KLVTVGKKGENGSSSTDEGEGLVTAKEVIDAVNAKAGRMKTTTANGOTGADKFEIVTSGT  | 352                |           |            |
| QY          | 347          | KYTFPAGNQTTPVNSDDOGNTTVKDVAVGALANYNOLONGSMNLDKSAVAGSSGKAYS    | 406                |           |            |
| DB          | 353          | KYTFPAGNQTTPVNSDDOGNTTVKDVAVGALANYNOLONGSMNLDKSAVAGSSGKAYS    | 412                |           |            |
| QY          | 407          | GNVSPSKGMDATVNIAGNNIEIRNGKNIDIAISMTQFSSVLGAGADAPTSLVDDE       | 466                |           |            |

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|||||
Db 413 GNVSPSKGKMEETVINAGNNIEITRNCKNIDITASMTPOESSVSLGAGAPLTSVDE 472
Oy 467 GALVNGSKDANKPVRITVAVPGVEGDVTNVAOLKGVAQONLNRRIDNVNGNARAGIAOI 526
Db 473 GALVNGSKDANKPVRITVAVPGVEGDVTNVAOLKGVAQONLNRRIDNVNGNARAGIAOI 532
Oy 527 ATAGLQAQYILPGKSMMAIGGGTYLGEAGYAIGYSSISAGCMMIITKGTASGNSRHFAGASA 586
Db 533 ATAGLQAQYILPGKSMMAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRHFAGASA 592
Oy 587 SVGYOW 592
Db 593 SVGYOW 598

RESULT 6
US-09-669-974-13
: Sequence 13, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: PRIOR FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 13
: LENGTH: 598
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-13
```

```
Query Match 89.3%, Score 2667; DB 4; Length 598;
Best Local Similarity 89.8%; Pred. No. 7.8e-204;
Matches 544; Conservative 10; Mismatches 30; Indels 22; Gaps 6;

Oy 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATYKTAVALTLLEFATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATYKTAVALTLLEFATVOANATD-DDDLXL 59
Oy 61 ESVQR-SVYGSIOAMESSVELETISLMTNDSKEFVDPYI-----VYTLKAGNLT 110
Db 60 EPOVQTAVALSFRSDKEGTGEGE-----TEDSNMAV--YFDEKRVLKAGATTLKAGNLT 112
Oy 111 KIKONTNENTNA---SSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDTKGLNFAK 166
Db 113 KIKONTNENTNENTNDSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDTKGLNFAK 172
Oy 167 ETAGTNGDTVHLNGISGTLTDMLTNGATNTVNDNTDDEKKRAASVQDVLNAGWNIK 226
Db 173 ETAGTNGDTVHLNGISGTLTDMLTNGATNTVNDNTDDEKKRAASVQDVLNAGWNIK 232
Oy 227 GVKPCTTASDNVDFVRYTDVYEFELASDTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDG 286
Db 233 GVKPCTTASDNVDFVRYTDVYEFELASDTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDG 292
Oy 287 KLVTKGKGNGSSSTDEEGGLYTAKEVIDAVNKAQRKMTTANGOTGOADFEETVTSKTYF 346
Db 293 KLVTKGKGNGSSSTDEEGGLYTAKEVIDAVNKAQRKMTTANGOTGOADFEETVTSKTYF 352
Oy 347 KYTFASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIYS 406
Db 351 ASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIYS 410
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Db 353 KYTFASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIYS 412
Oy 407 GNVSPSKGKMEETVINAGNNIEITRNCKNIDITASMTPOESSVSLGAGAPLTSVDE 466
Db 413 GNVSPSKGKMEETVINAGNNIEITRNCKNIDITASMTPOESSVSLGAGAPLTSVDE 472
Oy 467 GALVNGSKDANKPVRITVAVPGVEGDVTNVAOLKGVAQONLNRRIDNVNGNARAGIAOI 526
Db 473 GALVNGSKDANKPVRITVAVPGVEGDVTNVAOLKGVAQONLNRRIDNVNGNARAGIAOI 532
Oy 527 ATAGLQAQYILPGKSMMAIGGGTYLGEAGYAIGYSSISAGCMMIITKGTASGNSRHFAGASA 586
Db 533 ATAGLQAQYILPGKSMMAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRHFAGASA 592
Oy 587 SVGYOW 592
Db 593 SVGYOW 598

RESULT 7
US-09-377-155-7
: Sequence 7, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-7
```

```
Query Match 89.2%, Score 2664; DB 4; Length 594;
Best Local Similarity 90.0%; Pred. No. 1.3e-203;
Matches 542; Conservative 9; Mismatches 33; Indels 18; Gaps 5;

Oy 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATYKTAVALTLLEFATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATYKTAVALTLLEFATVOANATD-DDDLXL 59
Oy 61 ESVQR-SVYGSIOAMESSVELETISLMTNDSKEFVDPYI-----VYTLKAGNLT 110
Db 60 EPOVQTAVALSFRSDKEGTGEGE-----TEDSNMAV--YFDEKRVLKAGATTLKAGNLT 112
Oy 111 KIKONTNENTNA---SSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDTKGLNFAK 170
Db 113 KIKONTNENTNENTNDSFTYSLKDLTGLINVEETKLSFGANGKKNVNIISDTKGLNFAK 172
Oy 171 TNGDTTVALNGISGTLTDMLTNGATNTVNDNTDDEKKRAASVQDVLNAGWNIKGVK 230
Db 173 TNGDPTVHLNGISGTLTDMLTNGATNTVNDNTDDEKKRAASVQDVLNAGWNIKGVK 232
Oy 231 GTTASDNVDFVRYTDVYEFELASDTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDGKTYF 290
Db 233 GTTASDNVDFVRYTDVYEFELASDTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDGKTYF 292
Oy 291 GKGKNGSSSTDEEGGLYTAKEVIDAVNKAQRKMTTANGOTGOADFEETVTSKTYF 350
Db 293 GKGKNGSSSTDEEGGLYTAKEVIDAVNKAQRKMTTANGOTGOADFEETVTSKTYF 352
Oy 351 ASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIYS 410
Db 351 ASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVIYS 410
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Db 353 ASGKGTATATVSKDDGNTITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKAVISGNVS 412
QY 411 PSKGMDEVTYNINAGNNIETTRNGKNIDTATSKTPOFSSVSLGAGADAPTLVSVDDEGALN 470
Db 413 PSKGMDEVTYNINAGNNIETTRNGKNIDTATSKTPOFSSVSLGAGADAPTLVSVDDEGALN 472
QY 471 VSKDANKPVRITNVAPGVKEDGVTNVQOLKGVAQNLNRRIDNVNGNARAGIAQALATAG 530
Db 473 VSKDANKPVRITNVAPGVKEDGVTNVQOLKGVAQNLNRRIDNVNGNARAGIAQALATAG 532
QY 531 LVQAYLPGKSMMAIGGDTYRGEAGYAIYSSISDGSNMIIKGTASGNSRCHFGASASVGY 590
Db 533 LVQAYLPGKSMMAIGGDTYRGEAGYAIYSSISDGSNMIIKGTASGNSRCHFGASASVGY 592
QY 591 QW 592
Db 593 QW 594

```

## RESULT 8

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US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

```

Query Match 89.2%; Score 2664; DB 4; Length 594;

Best Local Similarity 90.0%; Pred. No. 1.3e-203; Matches 542; Conservative 9; Mismatches 33; Indels 18; Gaps 5;

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QY 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 ESVQR-SVVGSIQASMEGSVELETISLSMTNDSKEFYDPI-----VTLKAGDNL 110
Db 60 EPQORTAVVLSFRSDEKTEGEGEKG-----TEDSNMAV--YFDEKRYLKAGATILKAGDNL 112
QY 111 KIKONTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKVNITSDPKGLNFAKETAG 170
Db 113 KIKONTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKVNITSDPKGLNFAKETAG 172
QY 171 TNGDTPVHLNGIGSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVLNAGNINIKGVK 230
Db 173 TNGDTPVHLNGIGSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVLNAGNINIKGVK 232
QY 231 GTTASNDVFPVRTYDVEFLSADTKTTYNVESKONGKTEVKIGAKTSVIRKDGKLYT 290
Db 233 GTTASNDVFPVRTYDVEFLSADTKTTYNVESKONGKTEVKIGAKTSVIRKDGKLYT 292
QY 291 GKGKGNGSSTDEGELVTAKEVIDAVNKGWMMKTTTANGOTGQADKFEETVTSGRKVPF 350

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Db 293 GKGKGNGSSTDEGELVTAKEVIDAVNKGWMMKTTTANGOTGQADKFEETVTSGRKVPF 352
QY 351 ASGNGTTATVSKDDGNTITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKAVISGNVS 410
Db 353 ASGKGTATATVSKDDGNTITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKAVISGNVS 412
QY 411 PSKGMDEVTYNINAGNNIETTRNGKNIDTATSKTPOFSSVSLGAGADAPTLVSVDDEGALN 470
Db 413 PSKGMDEVTYNINAGNNIETTRNGKNIDTATSKTPOFSSVSLGAGADAPTLVSVDDEGALN 472
QY 471 VSKDANKPVRITNVAPGVKEDGVTNVQOLKGVAQNLNRRIDNVNGNARAGIAQALATAG 530
Db 473 VSKDANKPVRITNVAPGVKEDGVTNVQOLKGVAQNLNRRIDNVNGNARAGIAQALATAG 532
QY 531 LVQAYLPGKSMMAIGGDTYRGEAGYAIYSSISDGSNMIIKGTASGNSRCHFGASASVGY 590
Db 533 LVQAYLPGKSMMAIGGDTYRGEAGYAIYSSISDGSNMIIKGTASGNSRCHFGASASVGY 592
QY 591 QW 592
Db 593 QW 594

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## RESULT 9

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US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

```

Query Match 89.0%; Score 2658; DB 4; Length 598;

Best Local Similarity 89.4%; Pred. No. 4e-203; Matches 542; Conservative 11; Mismatches 31; Indels 22; Gaps 6;

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QY 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 ESVQR-SVVGSIQASMEGSVELETISLSMTNDSKEFYDPI-----VTLKAGDNL 110
Db 60 EPQORTAVVLSFRSDEKTEGEGEKG-----TEDSNMAV--YFDEKRYLKAGATILKAGDNL 112
QY 111 KIKONTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKVNITSDPKGLNFAKETAG 166
Db 113 KIKONTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKVNITSDPKGLNFAKETAG 172
QY 167 ETAGTNGDTPVHLNGIGSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVLNAGNINIK 226
Db 173 ETAGTNGDTPVHLNGIGSTLTDLMLNTGATTNTNDVNTDDEKKRAASVADVLNAGNINIK 232
QY 227 GVKPGTTASNDVFPVRTYDVEFLSADTKTTYNVESKONGKTEVKIGAKTSVIRKDGK 286
Db 233 GVKPGTTASNDVFPVRTYDVEFLSADTKTTYNVESKONGKTEVKIGAKTSVIRKDGK 292
QY 287 KLVTKGKGNGSSTDEGELVTAKEVIDAVNKGWMMKTTTANGOTGQADKFEETVTSGRKVPF 346

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|||||
Db 293 KLVYTGKGGKENGSSSTDEBGLVTAKEVIDAVNRAGRMKRTTANQGTGADKRETYTSGT 352
OY 347 KVFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNCGMNLDSKRVASSGKVIS 406
Db 353 KVFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNCGMNLDSKRVASSGKVIS 412
OY 407 GNVSPSKGKMDDEVYNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDVE 466
Db 413 GNVSPSKGKMDDEVYNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDVE 472
OY 467 GALNVGSKDANKPVRITNVAPGVKEGDTVVAOLKGYAQLNNRIDNVNNGNARAGIAOI 526
Db 473 GALNVGSKDANKPVRITNVAPGVKEGDTVVAOLKGYAQLNNRIDNVNNGNARAGIAOI 532
OY 527 ATAGLVAOYLPGKSMMAIGGGTYLGEAGYAIAGYSSISAGSNMIIKKTASGNSRCHFGASA 586
Db 533 ATAGLVAOYLPGKSMMAIGGGTYLGEAGYAIAGYSSISDTGNMVIKGTASGNSRCHFGTSA 592
OY 587 SVGYOW 592
Db 593 SVGYOW 598
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RESULT 10
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5
```

```
Query Match 89.0%; Score 2658; DB 4; Length 598;
Best Local Similarity 89.4%; Pred. No. 4e-203;
Matches 542; Conservative 11; Mismatches 31; Indels 22; Gaps 6;

OY 1 MNKIRIIMNSALNAWVAVSELTNRNHTKRASATYKTAVALATLLPATYQANATDEDEEEL 60
Db 1 MNKIRIIMNSALNAWVAVSELTNRNHTKRASATYKTAVALATLLPATYQANATD-DDDLYL 59
OY 61 ESVOR-SVYGSIOASMESVLEETISLSMTDSKEFVDPYI-----VYTLKAGNLI 110
Db 60 EPOVOTAVLVSFRSDKEGTGEKE-----TDSMNAV--YDEDEKRVLKAGAITLKAGDNL 112
OY 111 KIKONTNNTNA---SSEFTYSLKDLTGLINVERTKLSFGANGKRVNIISDTKGLNFAK 166
Db 113 KIKONTNNTNNTNDSSFTYSLKDLTDLISVETKLSFGANGKRVNIISDTKGLNFAK 172
OY 167 ETAGTNGDTYHLNGIGSTLDMLTNGATNTVNDVNTDDEKKRAASVKDYLANGNWIK 226
Db 173 ETAGTNGDPTYHLNGIGSTLDMLTNGATNTVNDVNTDDEKKRAASVKDYLANGNWIK 232
OY 227 GVKPGTTASDNVDVRYDYVEFLSADTKTTTVNVEKDNCKTEVYIGAKTSVKEKDG 286
Db 227 GVKPGTTASDNVDVRYDYVEFLSADTKTTTVNVEKDNCKTEVYIGAKTSVKEKDG 286
```

```
Db 233 GVKPGTTASDNVDVRYDYVEFLSADTKTTTVNVEKDNCKRTEVYIGAKTSVKEKDG 292
OY 287 KLVYTGKGGKENGSSSTDEBGLVTAKEVIDAVNRAGRMKRTTANQGTGADKRETYTSGT 346
Db 293 KLVYTGKGGKENGSSSTDEBGLVTAKEVIDAVNRAGRMKRTTANQGTGADKRETYTSGT 352
OY 347 KVFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNCGMNLDSKRVASSGKVIS 406
Db 353 KVFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNCGMNLDSKRVASSGKVIS 412
OY 407 GNVSPSKGKMDDEVYNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDVE 466
Db 413 GNVSPSKGKMDDEVYNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDVE 472
OY 467 GALNVGSKDANKPVRITNVAPGVKEGDTVVAOLKGYAQLNNRIDNVNNGNARAGIAOI 526
Db 473 GALNVGSKDANKPVRITNVAPGVKEGDTVVAOLKGYAQLNNRIDNVNNGNARAGIAOI 532
OY 527 ATAGLVAOYLPGKSMMAIGGGTYLGEAGYAIAGYSSISAGSNMIIKKTASGNSRCHFGASA 586
Db 533 ATAGLVAOYLPGKSMMAIGGGTYLGEAGYAIAGYSSISDTGNMVIKGTASGNSRCHFGTSA 592
OY 587 SVGYOW 592
Db 593 SVGYOW 598
```

```
RESULT 11
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9
```

```
Query Match 88.2%; Score 2636; DB 4; Length 594;
Best Local Similarity 89.3%; Pred. No. 2.2e-201;
Matches 536; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

OY 1 MNKIRIIMNSALNAWVAVSELTNRNHTKRASATYKTAVALATLLPATYQANATDEDEEEL 60
Db 1 MNKIRIIMNSALNAWVAVSELTNRNHTKRASATYKTAVALATLLPATYQASTTD-DDDLYL 59
OY 61 ESVOR-SVYGSIOASMESVLEETISLSMTDS-----KEFVDPYIIVYTLKAGDNLKI 112
Db 60 EPOVOTAVLVSFRSDKEGTGEKE-----VTDSDMNGVYFDKKGVLVLAAGTITLKAGDNLKI 114
OY 113 KONTNENTNASSFTYSLKDLTGLINVERTKLSFGANGKRVNIISDTKGLNFAKETAETN 172
Db 115 KONTNENTNASSFTYSLKDLTDLISVETKLSFGANGKRVNIISDTKGLNFAKETAETN 174
OY 173 GDTYVHLNGIGSTLDMLTNGATNTVNDVNTDDEKKRAASVKDYLANGNWIKGVKPGT 232
Db 175 GDTYVHLNGIGSTLDMLTNGATNTVNDVNTDDEKKRAASVKDYLANGNWIKGVKPGT 234
OY 233 TASDNVDVRYDYVEFLSADTKTTTVNVEKDNCKTEVYIGAKTSVKEKDGKLVYIGK 292
Db 233 TASDNVDVRYDYVEFLSADTKTTTVNVEKDNCKTEVYIGAKTSVKEKDGKLVYIGK 292
```



```
|||||
Db 235 TASDNVDFVRYDTVEFLSADTKTTTVNVESSKNGKREVEIKAGTSVIEKEDGKLVTK 294
OY 293 GKGENSSSTDEBGLVYAKAEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTKYTFAS 352
Db 295 DKGENSSSTDKGGLVYAKAEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTKYTFAS 354
OY 353 GNGTTATVSKDDOGNTTVKDVVNGDALNVNOLONGSMNLSKRAVAGSSGKVSIGNVSPS 412
Db 355 GKGTATVSKDDOGNTTVKDVVNGDALNVNOLONGSMNLSKRAVAGSSGKVSIGNVSPS 414
OY 413 KGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLVDEGALNVG 472
Db 415 KGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLVDEGALNVG 474
OY 473 SKDANKPVRITTVNAPGVKEDDVTNVAOLKGYAONLNRRINDVNGNARAGIAQAIATAGLV 532
Db 475 SKDANKPVRITTVNAPGVKEDDVTNVAOLKGYAONLNRRINDVNGNARAGIAQAIATAGLV 534
OY 533 QAYLPKSKMMAIGGGTYLGEAGYALIGYSSISAGNNIITKGTASGNSRGHFGASASVGYOM 592
Db 535 QAYLPKSKMMAIGGGTYLGEAGYALIGYSSISAGNNIITKGTASGNSRGHFGASASVGYOM 594
```

## RESULT 12

US-09-669-974-9

```
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9
```

Query Match 88.2%; Score 2636; DB 4; Length 594;

Best Local Similarity 89.3%; Pred. No. 2.2e-201;

Matches 536; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

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OY 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFAVQANATDEDEEEL 60
Db 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFAVQASTTQ-DDDLXL 59
OY 61 ESQVR-SVSGISQAMGSELETTISLMTNDS-----KEFVDPIYVITLAKGDNLIK 112
Db 60 EPQQRRAVVLSPRSDKEGGEKE-----VTEDSNMGVYEPKKGVLATGTTTLAAGDNLIK 114
OY 113 KONTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKKNVITSDTGLNPAKETAGTN 172
Db 115 KONTNENTNASSFTYSLKKDLTGLISVTEKLSFSANSNKNVITSDTGLNPAKTAETN 174
OY 173 GDDTVHLNGISLTDLMLNTGATTNVTNDNVYDDEKKRAASVKDVLNAGMNIKGVKPGT 232
Db 175 GDDTVHLNGISLTDLMLNTGATTNVTNDNVYDDEKKRAASVKDVLNAGMNIKGVKPGT 234
OY 233 TASDNVDFVRYDTVEFLSADTKTTTVNVESSKNGKREVEIKAGTSVIEKEDGKLVTK 292
|||||
```

```
Db 235 TASDNVDFVRYDTVEFLSADTKTTTVNVESSKNGKREVEIKAGTSVIEKEDGKLVTK 294
OY 293 GKGENSSSTDEBGLVYAKAEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTKYTFAS 352
Db 295 DKGENSSSTDKGGLVYAKAEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTKYTFAS 354
OY 353 GNGTTATVSKDDOGNTTVKDVVNGDALNVNOLONGSMNLSKRAVAGSSGKVSIGNVSPS 412
Db 355 GKGTATVSKDDOGNTTVKDVVNGDALNVNOLONGSMNLSKRAVAGSSGKVSIGNVSPS 414
OY 413 KGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLVDEGALNVG 472
Db 415 KGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLVDEGALNVG 474
OY 473 SKDANKPVRITTVNAPGVKEDDVTNVAOLKGYAONLNRRINDVNGNARAGIAQAIATAGLV 532
Db 475 SKDANKPVRITTVNAPGVKEDDVTNVAOLKGYAONLNRRINDVNGNARAGIAQAIATAGLV 534
OY 533 QAYLPKSKMMAIGGGTYLGEAGYALIGYSSISAGNNIITKGTASGNSRGHFGASASVGYOM 592
Db 535 QAYLPKSKMMAIGGGTYLGEAGYALIGYSSISAGNNIITKGTASGNSRGHFGASASVGYOM 594
```

## RESULT 13

US-09-377-155-21

```
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
```

Query Match 86.2%; Score 2573.5; DB 4; Length 591;

Best Local Similarity 87.5%; Pred. No. 2e-196;

Matches 524; Conservative 23; Mismatches 37; Indels 15; Gaps 6;

```
OY 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFAVQANATDEDEEEL 59
Db 1 MNKIYRIINNSALNANVAVSELTRNHTKRASATVKTAVLATLLFAVQANANDEDEEDL 60
OY 60 -LESQVR-SVSGISQAMGSELETTISLMTNDSKEFVDPIYV----VTLKAGDNLIK 113
Db 61 YLDPVQRTAVVLLVNSDKEGGEKEVE-ENSDMAVVFENKGVLTAREITLTKAGDNLIK 119
OY 114 QNTNENTNASSFTYSLKKDLTGLINVEETKLSFGANGKKNVITSDTGLNPAKETAGTN 173
Db 120 Q-----NGTNPYSLKKDLTGLISVTEKLSFSANGKKNVITSDTGLNPAKETAGTN 173
OY 174 DTTVHLNGISLTDLMLNTGATTNVTNDNVYDDEKKRAASVVDVLNAGMNIKGVKPGT 233
Db 174 DTTVHLNGISLTDLMLNTGATTNVTNDNVYDDEKKRAASVVDVLNAGMNIKGVKPGT 233
OY 234 ASDNVDFVRYDTVEFLSADTKTTTVNVESSKNGKREVEIKAGTSVIEKEDGKLVTKG 293
Db 234 ASDNVDFVRYDTVEFLSADTKTTTVNVESSKNGKREVEIKAGTSVIEKEDGKLVTKGD 293
OY 294 KGGENSSSTDEBGLVYAKAEVIDAVNKAQKRMKTTTANGOTGADKFEYTSCTKYTFASG 353
|||||
```

|    |     |                                                                 |     |
|----|-----|-----------------------------------------------------------------|-----|
| Db | 294 | KGENSSSTDEGEGLVTTAKVEYIDAVNFKGWMRKTTTAGQGTQADKFEFTVSGTWVPEASG   | 353 |
| Oy | 354 | NGTATVTSKDIOGMITATKYDYNVDALINVNOLMSGNLDSKAVAGSSGVTIGSNVPSK      | 413 |
| Db | 354 | KGTATVTSKDIOGMITATKYDYNVDALINVNOLMSGNLDSKAAVAGSSGVTIGSNVPSK     | 413 |
| Oy | 414 | GKMDPEVYNINANNIETTRNKNKIDATISMTPOEVSYSILGADAPLTLYSDDEGALNVGS    | 473 |
| Db | 414 | GKMDPEVYNINANNIETTRNKNKIDATISMTPOEVSYSILGADAPLTLYSDGD-ALNVGS    | 472 |
| Oy | 474 | KDAKKPVKITVAVARGVEGDVNTVAOLKGYAONLNPNFIDNVNCGARAGIAQOATATAGTVO  | 533 |
| Db | 473 | KKDKKPVKITVAVARGVEGDVNTVAOLKGYAONLNPNFIDNVNCGARAGIAQOATATAGTVO  | 532 |
| Oy | 534 | AYLPQKSMALITGGGTITGEGAGYATIGSYSSISAGCMMIITKPTASGNSRHFQASASVGTOM | 592 |
| Db | 533 | AYLPQKSMALITGGGTITGEGAGYATIGSYSSISDGGMIIITKPTASGNSRHFQASASVGTOM | 591 |

```

RESULT 14
US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAR, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/A098/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

```

| Query Match           | 86.2%           | Score 2573.5                                                    | DB 4      | Length 591 |
|-----------------------|-----------------|-----------------------------------------------------------------|-----------|------------|
| Best Local Similarity | 87.5%           | Pred. No. 2e-196                                                |           |            |
| Matches 524           | Conservative 23 | Mismatches 37                                                   | Indels 15 | Gaps 6     |
| QY                    | 1               | MKKIRIIMNSLNMWVSELTRNHTKASATVTAVALTLLFATVQANANDEDEE             | 59        |            |
| Db                    | 1               | MKKIRIIMNSLNMWVSELTRNHTKASATVTAVALTLLFATVQASANNEDEED            | 60        |            |
| QY                    | 60              | -LESVQRSV-VGSIQASGSEVELETTISLSMDNKEFPDPIV---VTLKAGDLKIK         | 113       |            |
| Db                    | 61              | YLDPIQRTVAVLIVNSDEGTEGKEKVE-ENSDMAVIFNEKGVLTRARETTLAAGDLKIK     | 119       |            |
| QY                    | 114             | QNTNENTAASTPTYSILKKDLDTGLINVEETEKLSPGANGKKNVITISPTKGINFAKETAGTG | 173       |            |
| Db                    | 120             | Q-----NGNTNPTYSILKKDLDTGLISVGTGFKLSFGSANGKNVNTISPTKGINFAKETAGTG | 173       |            |
| QY                    | 174             | DTVYHLNGISGTLTMDLINTGATINVTNDNVTYDDEKKRAASYKDVILNAGMNIKGVRPQTT  | 233       |            |
| Db                    | 174             | DTVYHLNGISGTLTDLTLNTGATINVTNDNVTYDDEKKRAASYKDVILNAGMNIKGVRPQTT  | 233       |            |
| QY                    | 234             | ASDNVDFVRYTDVFEVLSADTKTTTVINVESKDKNGKTEYVIGAKTSVIREKDGKLVYTGK   | 293       |            |
| Db                    | 234             | ASDNVDFVRYTDVFEVLSADTKTTTVINVESKDKNGKTEYVIGAKTSVIREKDGKLVYTGK   | 293       |            |
| QY                    | 294             | KGENSSSTDEGBGLVTAKEVIDAVNKKAGRMKTTTIANGTGQADKFEYVTSGETKYTFASG   | 353       |            |

|    |     |                                                               |      |
|----|-----|---------------------------------------------------------------|------|
| Db | 294 | KGENSSSTDEGEJVTAKREVDAVNRKAGWRMKTTTANGQGTQADKFEVTASGTVTFPASC  | 353  |
| Qy | 354 | NGTATVSKSDQGNITVYKYVDNALVNOLOJNSGNHDSKAVAGSSGKVIISGNVSPSK     | 4133 |
| Db | 354 | KGTATVSKSDQGNITVYVDVNBDAALVNOLOJNSGNHDSKAAVAGSSGKVIISGNVSPSK  | 4133 |
| Qy | 414 | GKMEVTVINAGNNIETIRNKNIDIAITSMTPOFSSVSLGAGADAPLTVDDEGALVWGS    | 4737 |
| Db | 414 | GKMEVTVINAGNNIETIRNKNIDIAITSMTPOFSSVSLGAGADAPLTVDGD-ALNVGS    | 4727 |
| Qy | 474 | KDANKPVKITVNAFVKEGDTVNAOLKGVAAQNLNBRIDNVNAGARAGIAQAIATAGLVQ   | 5333 |
| Db | 473 | KDKDKPVKITVNAFVKEGDTVNAOLKGVAAQNLNBRIDNVNAGARAGIAQAIATAGLVQ   | 5323 |
| Qy | 534 | AYLEBKSMMAIGGGTYTJGCAQYATIGYSSISAGGMMWIIKGTASGSRBHPFASASVGVQW | 592  |
| Db | 533 | AYLEBKSMMAIGGGTYKREAGYATIGYSSISDGGMMWIIKGTASGSRBHPFASASVGVQW  | 591  |

```

RESULT 15
US-09-377-155-11
: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAR, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-11

```

| Query Match           | 85.5%           | Score 2554.5                                                   | DB: 4     | Length 591 |
|-----------------------|-----------------|----------------------------------------------------------------|-----------|------------|
| Best Local Similarity | 87.0%           | Pred. No. 6.6e-195                                             |           |            |
| Matches 521           | Conservative 24 | Mismatches 39                                                  | Indels 15 | Gaps 6     |
| Qy                    | 1               | MKKIRITINSLNMAWVAVSELTRHHTRKASVTATVATLLPFTVQANATDEDEEE-        | 59        |            |
|                       | :               |                                                                |           |            |
|                       | 1               | MNELIRITINSLNMAWVAVSELTRHHTRKASVTATVATLLPFTVQANANDEEDL         | 60        |            |
| Qy                    | 60              | -LESVQRSA-VGSIDASMEGSVELEPTISLMSNDSEKEFDPIYV----VTLKAGDLKTK    | 113       |            |
|                       | :               | :                                                              | :         | :          |
| Db                    | 61              | YLDPLRITVAALIVIVSDXEGTEGKEKVE-ENSDMAVYENERGCVLTAREITLQAGDLKTK  | 119       |            |
| Qy                    | 114             | QNTNENTVAASPFYSLKDDLTGLINWETREKLSFGANGKVKVNIISDTKGLNFAKETAGTNG | 173       |            |
|                       | :               | :                                                              | :         | :          |
| Db                    | 120             | Q-----NGNTNFTYSLKDDLDITVSGTEKLSFGANGKVKVNIISDTKGLNFAKETAGTNG   | 173       |            |
| Qy                    | 174             | DTTVHLNIGSFLTPMLLNTGATVWTDNDVNDDEKKRAASVQDVLNAGMNLKGVKPGTT     | 233       |            |
|                       | :               | :                                                              | :         | :          |
| Db                    | 174             | DTTVHLNIGSFLTDTLLNTGATVWTDNDVNDDEKKRAASVQDVLNAGMNLKGVKPGTT     | 233       |            |
| Qy                    | 234             | ASDNDVFRVTVDFEFLSADTKTTTVNVNESKONGKRTVEKIGAKTSVIREKDGKLVYTGKG  | 293       |            |
|                       | :               | :                                                              | :         | :          |
| Db                    | 234             | ASDNDVFRVTVDFEFLSADTKTTTVNVNESKONGKRTVEKIGAKTSVIREKDGKLVYTGKD  | 293       |            |
| Qy                    | 294             | KGENGSSDTDEGEGLTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTKVTFPASG   | 353       |            |
|                       | :               | :                                                              | :         | :          |
| Db                    | 294             | KGENGSSDTDEGEGLTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNTVTFPASG  | 353       |            |
| Qy                    | 354             | NGTTATVSKDDGNTTVKRYVNVNGDALNVNOLNSGWNLSKAVAGSSGKVIISGNAVSPSK   | 413       |            |

```

Db 354 KGTATVSKDDGNTVMTDVNVGDALNVLQNSGMNLDKAVAGSSGKVTISGNVSPSK 413
QY 414 GKMDETVINAGNNEITRNGKNIDIAFMTPOFSSVSLGAGADAPTLVDEGALNVGS 473
Db 414 GKMDETVINAGNNEITRNGKNIDIAFMTPOFSSVSLGAGADAPTLVDCD -ALNVGS 472
QY 474 KDANKPVRTTNVAPGVKEGDTVNVQNLKGVQNLNRRIDNVNGNARAGTQAATATAGLVQ 533
Db 473 KDKNKPVRTTNVAPGVKEGDTVNVQNLKGVQNLNRRIDNVNGNARAGTQAATATAGLVQ 532
QY 534 AYLPGRSMMAIGGTYLGEGYALIGYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 592
Db 533 AYLPGRSMMAIGGTYRGEGYALIGYSSISDGNWIKGTASGNSRGHFGASASVGYQW 591

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Search completed: July 3, 2002, 08:10:14  
 Job time: 526 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:11:59 ; Search time 95.27 Seconds

(without alignments)  
597.091 Million cell updates/sec

Title: US-09-771-382-2

Perfect score: 2987

Sequence: 1 MNKIRIINMSALNMAVAVS.....TASGNSRGHFGASASVGYCW 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2779   | 93.0        | 592    | 2  | probable surface f |
| 2          | 2573.5 | 86.2        | 591    | 2  | adhesin NMB0992 (I |
| 3          | 591    | 19.8        | 298    | 2  | adhesin homolog HI |
| 4          | 392.5  | 13.1        | 2059   | 2  | surface protein XF |
| 5          | 379.5  | 12.7        | 1588   | 2  | probable adhesin Z |
| 6          | 379.5  | 12.7        | 1588   | 2  | probable adhesin E |
| 7          | 373.5  | 12.5        | 1107   | 2  | probable autotrans |
| 8          | 371    | 12.4        | 1190   | 2  | surface protein XF |
| 9          | 321.5  | 10.8        | 658    | 2  | probable surface p |
| 10         | 256    | 8.6         | 1004   | 2  | surface-exposed ou |
| 11         | 243.5  | 8.2         | 1325   | 2  | Ydek protein - Esc |
| 12         | 231    | 7.7         | 1535   | 2  | high-molecular-we  |
| 13         | 226.5  | 7.6         | 1343   | 2  | hypothetical prote |
| 14         | 225    | 7.5         | 1109   | 2  | surface-array prot |
| 15         | 223.5  | 7.5         | 1343   | 2  | hypothetical prote |
| 16         | 223.5  | 7.5         | 4919   | 2  | hypothetical prote |
| 17         | 220.5  | 7.4         | 1091   | 2  | hypothetical prote |
| 18         | 214    | 7.2         | 1910   | 2  | probable adhesin h |
| 19         | 214    | 7.2         | 3705   | 2  | AD0123             |
| 20         | 212    | 7.1         | 1018   | 2  | probable autotrans |
| 21         | 211.5  | 7.1         | 1655   | 2  | probable adhesin p |
| 22         | 211.5  | 7.1         | 2249   | 2  | hypothetical prote |
| 23         | 210.5  | 7.0         | 5188   | 2  | 190K surface antiq |
| 24         | 209.5  | 7.0         | 5291   | 2  | probable RTX fami  |
| 25         | 209    | 7.0         | 949    | 2  | hypothetical prote |
| 26         | 209    | 7.0         | 1005   | 2  | AIDA-I adhesin-lik |
| 27         | 208.5  | 7.0         | 1366   | 2  | probable adhesin z |
| 28         | 208    | 7.0         | 3029   | 2  | Iga-specific metal |
| 29         | 206.5  | 6.9         | 1238   | 2  | hypothetical prote |
|            |        |             |        |    | probable exported  |

|    |       |     |      |   |        |                    |
|----|-------|-----|------|---|--------|--------------------|
| 30 | 203.5 | 6.8 | 2232 | 2 | T34434 | hypothetical prote |
| 31 | 203   | 6.8 | 1286 | 2 | S28634 | adhesin AIDA-I pre |
| 32 | 203   | 6.8 | 1651 | 2 | JC1340 | outer membrane pro |
| 33 | 201   | 6.7 | 1577 | 2 | A35140 | hemolysin A precu  |
| 34 | 200.5 | 6.7 | 1477 | 2 | B43855 | high-molecular-we  |
| 35 | 200   | 6.7 | 1275 | 2 | T33369 | hypothetical prote |
| 36 | 199   | 6.7 | 936  | 2 | I40711 | sapB protein - Cam |
| 37 | 198   | 6.6 | 2020 | 2 | C48399 | ABC-type transport |
| 38 | 197.5 | 6.6 | 4152 | 2 | T31102 | filamentous hemagg |
| 39 | 197   | 6.6 | 1417 | 2 | A83080 | hypothetical prote |
| 40 | 194.5 | 6.5 | 920  | 2 | I40614 | surface array prot |
| 41 | 193.5 | 6.5 | 1361 | 2 | T03415 | S-layer protein -  |
| 42 | 193   | 6.5 | 1430 | 2 | AF0351 | probable autotrans |
| 43 | 192   | 6.4 | 1327 | 2 | B90674 | AIDA-I adhesin-lik |
| 44 | 192   | 6.4 | 1349 | 2 | E85524 | probable beta barr |
| 45 | 192   | 6.4 | 1428 | 2 | AC2224 | hypothetical prote |

## ALIGNMENTS

|                                                                                         |                                                                                       |  |
|-----------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|--|
| RESULT                                                                                  | 1                                                                                     |  |
| A81888                                                                                  | probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain z |  |
| C:Species: Neisseria meningitidis                                                       |                                                                                       |  |
| C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001             |                                                                                       |  |
| C:Accession: A81888                                                                     |                                                                                       |  |
| R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo   |                                                                                       |  |
| ; Holtroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre |                                                                                       |  |
| Nature 404, 502-506, 2000                                                               |                                                                                       |  |
| A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z491   |                                                                                       |  |
| A:Reference number: A81775; MUID:20222556                                               |                                                                                       |  |
| A:Accession: A81888                                                                     |                                                                                       |  |
| A:Status: preliminary                                                                   |                                                                                       |  |
| A:Molecule type: DNA                                                                    |                                                                                       |  |
| A:Residues: 1-592 <PAR>                                                                 |                                                                                       |  |
| A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84461.1; PID:9737   |                                                                                       |  |
| C:Experimental source: serogroup A, strain z491                                         |                                                                                       |  |
| C:Genetics:                                                                             |                                                                                       |  |
| A:Gene: NMA1200                                                                         |                                                                                       |  |
| Query Match                                                                             | 93.0%; Score 2779; DB 2; Length 592;                                                  |  |
| Best Local Similarity                                                                   | 93.9%; Pred. No. 1.2e-131;                                                            |  |
| Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;                           |                                                                                       |  |
| QY 1 MNKIRIINMSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVQANATDEDEEEL 60                      |                                                                                       |  |
| DB 1 MNKIRIINMSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVQANATDEDEEEL 60                      |                                                                                       |  |
| QY 61 ESYQSRVSGSIQASMEGSELETSLSMTNDSKEFPDPIYVTLKAGDNLIKQNTNEMT 120                      |                                                                                       |  |
| DB 61 ESYQSRVSGSIQASMEGSELETSLSMTNDSKEFPDPIYVTLKAGDNLIKQNTNEMT 120                      |                                                                                       |  |
| QY 121 NASSFFYSLKDDTGLINVEKELSPGANGKKNISDPKGLFAFETAGTNDTIVHLN 180                       |                                                                                       |  |
| DB 121 NASSFFYSLKDDTGLINVEKELSPGANGKKNISDPKGLFAFETAGTNDTIVHLN 180                       |                                                                                       |  |
| QY 181 GIGSTLTDLMLTGATNTVNDVTDEKRAASVQDVINAGNIRKVGRTTA--SDNV 238                        |                                                                                       |  |
| DB 181 GIGSTLTDLMLTGATNTVNDVTDEKRAASVQDVINAGNIRKVGRTTA--SDNV 238                        |                                                                                       |  |
| QY 239 DRYRTDYVEFLSADTKTTTVNVNESKDNGKTEVKIGATSVYKEKDGKLYTGKGGENG 298                    |                                                                                       |  |
| DB 239 DRYRTDYVEFLSADTKTTTVNVNESKDNGKTEVKIGATSVYKEKDGKLYTGKGGENG 298                    |                                                                                       |  |
| QY 299 SSTDEEGGLVTAKEVIDAVNKAQMKRTTANGQOQADKFEVTSQFVTPFASGNGTTA 358                     |                                                                                       |  |
| DB 299 SSTDEEGGLVTAKEVIDAVNKAQMKRTTANGQOQADKFEVTSQFVTPFASGNGTTA 358                     |                                                                                       |  |
| QY 359 TVSKDQGNITKYKVDVNVGDALNVNOLQNSGWLDSKRAVAGSSGKVISGNVSPSKKMD 418                   |                                                                                       |  |
| DB 359 TVSKDQGNITKYKVDVNVGDALNVNOLQNSGWLDSKRAVAGSSGKVISGNVSPSKKMD 418                   |                                                                                       |  |



A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF8438.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Bilones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, M.A.; Silva Jr., W.A.; da Silveir  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1529

Query Match 13.1%; Score 392.5; DB 2; Length 2059;  
Best Local Similarity 24.8%; Pred. No. 9.5e-12;  
Matches 173; Conservative 98; Mismatches 225; Indels 201; Gaps 32;  
58 EELESYQSRVSVGSIQASMEGVELETISLMTNDSKEFVDPYIVYTLKAGD-NLKIKONT 116  
1402 EETDAVNFSQLSISTAYD---QGTTLTASGANGSK--VASGTYDLKKTGNTLITSKSG 1456  
117 NENTNASSFTYSLKRDGLINVEKELFGANGKVV--NIISDTKGLNFAKETACT--- 171  
1457 DSDNDVFNLEDLKEKSIIVGTQIDK---DGVKSSNVLLDSNELVITSSHSSTSVK 1511  
172 ---NGDTYH---LNGIGSTLTDML-----LNTGA--TTNVT--- 200  
1512 TLANESVYVNRVTVNGDGVNIDVYVNDLGLIIVGASLITSGINAGSHKITTNTAGTE 1571  
201 -NDNTYDDEKRAASYKVDVNLNAGMNI-----KGVRGTASDNDV-----FVRTY 244  
1572 DTDVAVNFSQLK---SVSEAVNDKGMVLTITASGANGSKVSGTYDLKKTGNTLITSKSGDN 1628  
245 DTFEFLSADTK-----TTTVNESKDNKRTKTEVKGITAKVSIKEKDKLTKGKNGEN 297  
1629 DVFVNLKSKFKYDEVYAGTAVNTDGVKVG--SDVSLGAMGLFIANGPVTASGFAAGK 1686  
298 -----GSTDGEGELVYAKVYDAVNAKGMKTTTANGTG-----QADKFEV 342  
1687 VISHAVAGMADPDVAVNFSQLKQAVOSVTKATRYSTINDGTGOGNVDGCGATGAKAIAA 1746  
343 TSGTKVT-----FASNGGTT--ATVSKD-----DGC-----NTTVK 372  
1747 GVGTOASGCGAANAAGSAAASGKSTAIGRMAIASADGVALGDGAKDGKGAESTYTKY 1806  
373 D-----VNVG-----DALVNTQI-----QNSGMNLS----- 394  
1807 SCGVNNTVGTAVGDAKGETRISINVDAKEMDAVNLROLDVAYAKQNLITDDMRHEI 1866  
395 -----KAVAGSGKVIISGANSPEKGMDETIVINA---GNNIETRN-----GNNDI 439  
1867 NNIEDVFKITKGDSSASVVG-----MGVNAAGITNAAVSGTESVALGKNTNV 1914  
440 ATSMTPQSFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITTVAPVKEGDVTNVVQ 499  
1915 SMD-----NAVAIGMSVA-----DRANSVSVSGGSEH--OVTNVAATATDIDAVNVQ 1962  
500 LKGVANLNLRIDNVNGNR---AGIAQAITAGIYVATLPKSKMMAIGGGTYLGEAGY 555  
1963 LMGGITAKQYTDGMVGNLRRTSGGVAALATPANIPLQAYVYGRGRTSVGVSSTGQGSAT 2022  
556 AIGYSISAGCMMIIGKTASGNSRGHFGASASVGYOM 592  
2023 AVGSVAVSESGHMVFKFSGSANTRSHVGVAGVGYOM 2059

RESULT 5  
A86036  
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialianta, E.; Potamoustis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MID:21074935; PMID:11206551  
A:Accession: A86036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN0145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029

Query Match 12.7%; Score 379.5; DB 2; Length 1588;  
Best Local Similarity 24.8%; Pred. No. 3e-11;  
Matches 162; Conservative 94; Mismatches 289; Indels 109; Gaps 23;  
33 TYKTAVALTLFATYQANATDEDEBEL--ESVQSRVSVGSIQASMEGVELET--ISLSM 88  
950 TAPPTYIAAEVNNV--GDALDLADNALLMDETANGACAAYNASHDGKASITTNVANGSI 1008  
89 TNSKEFVDPYIVYTLKADNLKIKONT---NENTNASSFTYSLKRDGLINVEF--RK 143  
1009 SEDSDAVNG-----SOLNMTNMIENQNTIOLNAGNTATY-IOENGAGINTVRRNDG 1063  
144 LSF-----GANGKRVNIISDTKGLNFAKETAGTNGDTTVHNLGISTLTMLNTGA--T 196  
1064 LAFNDASQGVGATATGYNVSAKGDSSVALIGGYSYDVTGIALGSSVSRIAGKSHD 1123  
197 TINTNDNV-----TDDEKRAASYD-----VLNAGNNIKGVKGTITASDNDVPEVRY 244  
1124 TITENGVIYGYDTTDELLGALSTIGDDKRYRIIN-----VADGSEAHDAVT--VRL 1175  
245 DTFEFLSADTKTTTVVESKDNK---KTEVKGITAKVSIKEKDKLTKGKNGEN 290  
1176 QNAIGAVATTPKRYFRANSTEDSLAVGTDSLAMGKKTIVNGDKIGTIGYAVDANALN 1235  
291 GKQGE-----NGSTDGEGELVYAKVYDAVNAKGMKTTTANGQ----- 332  
1236 GIAISGNAQVHVNSIAIGNGSTTRGAQNTAYVMDAPONSVEFVSADGQHQITN 1295  
333 --TGADKFEYVTSKTVTFASGNGTTATVSKDQ-----GNTTVYDVNVGDAL----- 380  
1296 VAAGSADTDVAVNVGQLKVTDAQVSOVTOSITNLDNVTNLDSTVNTIENGIGIVTTGST 1355  
381 -----NVNOLONGMNLDSKAVAGSSGKVIISGNSPEKGM---DETVINAGNNIETRN 432  
1356 KYFKTITDQVDSAQCKDSVALIGSGSIAAADSVALGTSVATEENTISVSGSTNRRT 1415  
433 N---GNNDIATSMTPQSFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITTVAPGV 489  
1416 NVAAGKNATDVAVNAQLKSEAGVYRDTFKADOSIDYSNITLGGGNG--TTRISNVAGV 1474  
490 KEGDVTNVAQLKGVQO-----NLNRLDENVNGNARAGIAQAITAGIYVATLPK 538  
1475 NNNDVNVYVQLOKQSVQETQYTDORVAVENDNLSKSTESKLSGSIASAMAMTGILPAQYTTG 1534  
539 KSMMAIGGGTYGEAGYAGTISAGNMIIKKTASGNSRGHFGASASVGYOM 592  
1535 ASMASIGGTYTGESAVALGVSNVANGRMVYTKLGSTNSQGEYSALAGIOW 1588

RESULT 6  
H91188  
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain R

C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kubhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genoc  
A:Reference number: A96629; MUID:21156231; PMID:11558796  
A:Accession: H91188  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <NAV>  
A:Cross-references: GB:BA000007, PIDN:BA837903.1, PID:913363955, GSPDB:GM00154  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: ECs4480

```

Query Match Summary      12.7%: Score 379.5: DB 2: Length 1568;
Best Local Similarity   24.8%: Pred. No. 3e-11;
Matches 162: Conservative 94: Mismatches 269: Indels 109: Gaps 23;

OY      33  TTKVATLTLFATVQAAATDEDEEEEL--ESVORSVYSGIOASMEGSVELET--ISLSM 88
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      950  TAPPTIANAEEYNN--GDALDALDNDALLMDETANGAGAYVASHDGKASITTVANGSI 1008

OY      89  TNDSEFPDPRIVLVTLKKAGDNLTKONT--NENNASFFYSLKDKDLGLNVT--EK 143
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1009 SEDSDYANG--SOLANMIMLEONTQIILNOLAGNTDAY--IOENAGINIVYTNDDG 1063

OY      144  LSF-----GANGKKVNIISDTKGLNFAKETAGTGTTHLNGISLTLMALNTGA-T 196
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1064 LAFNDASAGVGATAIGNSYAKGDDSSVALIGGGSYSDVDTGIALGSSSVSSVIAKKSRD 1123

OY      197  TNYTNDNV-----TDDEKKRAASYKD-----VNAAGNIKGVPRTGASDNDFVPTY 244
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1124 TSITENGVVIGIDYTDIGELGLALSTIGDGKRYROIIN-----VADGSEADHAYT-VHQL 1175

OY      245  DTFVELSADFTKTYTVNVESKDNKG---KTEYKIGAKTSVIEK-----DGKLVY 290

DB      1176 QNAIGAVATTPPKYRPHANSTEDSLAVGDSLAMGAKITVNGDKIGIGAYVDANLN 1235

OY      291  GKQKE-----NGSDEGEGLYAKAYIDAIVAKAGRMKTTTANGO----- 332

DB      1236 GAIISNMQVHVNSIAIGNGSTTTRGAOTNTAYANMAPONSVEEFSVGSADGROITN 1295

OY      333  --TGQADKEFEYTSCTKYTFASGNGTFAVSKDPD-----GNITKYDVNVGDAL----- 380

DB      1296 VAAGSADPDVAIVVGOLKTYDAVYSONTOSITNLDKRYTNLDSRYVINIENGIDITYTGST 1355

OY      381  ----NVNOLONGSNLDSKAVAGSSGKVISGNVSPSKGM---DETVNINAGNIEETR 432

DB      1356 KYFKNTNGVPSAAGKKSVAIGSGSIAAADNSVALIGSVATEENTISVGSSTQMRBIT 1415

OY      433  N--GKNIDIASMTPOPSVSVLGGADAPLTSLVDEGALVNGSKDARKPVITTVARV 489
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1416 NYAAGKNAATDAVANAQLKSSSEAGVRYPTKADGSLIDYSNITLGGNGG--TTRISVNSGV 1474

OY      490  KEGDVTVNAQLKGAQ-----NLNFRIDVNGNARAGIAOAIATAGLVQVYLP 538
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1475 NNNDVYVNAQLKOSVOETKOYTDORMVEMDNKLSTESKLSGSIASAMAMGLPQATYPG 1534

OY      539  KSMALIGGGTYLGEAGYALGYSSISAGGNWIIITKTAAGNSNRHFPASASVGYQW 592
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1535 ASMAISGGTIGESAVVALGVSMVSAANGRWYKTLGGSTNSOGEYSAAALGAGIOW 1568

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RESULT      7
AC0976
probable autotransporter sabp [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhi
C:date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

```

C:Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.  
N:ature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se  
A:Reference number: AB0502; PMID:11677608  
C:Accession: AC0976  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176  
C:Genetics:  
A:Gene: sapB

|                       |                 |                   |            |             |
|-----------------------|-----------------|-------------------|------------|-------------|
| Query Match           | 12.5%           | Score 373.5       | DB 2       | Length 1107 |
| Best Local Similarity | 21.3%           | Pred. No. 3.7e-11 |            |             |
| Matches 181           | Conservative 11 | Mismatches 261    | Indels 295 | Gaps 31     |

|    |     |                                                                 |      |
|----|-----|-----------------------------------------------------------------|------|
| Db | 273 | TFPSARNGSASRKTINILAACTLADSDVAVNGSOLYETNOKVQNTSALADINTSI--TN     | 329  |
| QY | 81  | LETSLSMTNDSKREFVDPY-----IVYILKAD-----NLKIKONTN                  | 117  |
| Db | 330 | LSNDLSNLETTFNSFSASHSSSTTKITVNAAGELSEESTDAVNGSOLFETNEKQDONTT     | 389  |
| QY | 118 | E--NT-----NASSFTYSLKDDTLGI-----NYETEKLSGAKKKVYNTIS              | 157  |
| Db | 390 | DIANTNTINQNSALINLNTSVSDINTSITGLTDNALLMBDDTGAFSANHGGSSTKITN      | 449  |
| QY | 158 | DTKGLINAKETACTNG-----DTHVLNGISITLTDMLTGCATTVNTDNTDDEKKRAA       | 213  |
| Db | 450 | VAAALSSEDSTDAVNGSOLYETNOKVQNTSALAD--INT--SITNLGTDALSMBDEEAF     | 506  |
| QY | 214 | SVKDVLANGMWIKVKVKGCTASDNVFPV--RTYDT-----VEFLSADTKTTTVN          | 260  |
| Db | 507 | SASHGTSQTKITVNAAGELASDSTDAVNGSOLYETNMLISOYNESISLADTSETIYT       | 566  |
| QY | 261 | -----VESKDNKGTEVKIKAKTSVIREKDKGLVTKG--KGENGSTDEG----            | 304  |
| Db | 567 | ENGTVGKYIRINDNGLEGQDAVATGNGATPVGDAVASGACIALGQNSSSIEGSIALG       | 626  |
| QY | 305 | -----EGLY-----TAKVIDAVNKA-----GMRKTTANGOGQ                      | 335  |
| Db | 627 | SGSTSNRAITTTGIRETSATSDGVIGVNTDFRLGLALSGLDGBESYRQITVNAAGSEAO     | 686  |
| QY | 336 | -----ADKFETVTSIGFVTPASGNGTATVASKDDQGITVVKKDVAVNG                | 377  |
| Db | 667 | DAVYVRQLOMAGVATTPPKYYHANSTEDSLAVGTDSLMBGAK-----TIVNADAIG        | 741  |
| QY | 378 | DALVYNOLQ--SGWNLDSRAVAGSSGKYISGVNSP-----                        | 411  |
| Db | 742 | IGLNTVLVADALINGIALIGSABARAHANSIAMGNSQOTRGAOTDYAYNMDTPQNSVGEF    | 801  |
| QY | 412 | SKGKMD--ETVNNNAQ-------NIETRRGKNI-----                          | 437  |
| Db | 802 | SVSDEGQORQITTVNAAGSADTDVAVNVGQLKVTDAYQVSRATQSTINLNTQVSNLDTRVNI  | 861  |
| QY | 438 | -----DIATSMTPQF-----SSVSLGAGADAP-----TLSTVDE--GA                | 468  |
| Db | 862 | ENGIGDIYTCSTPYFTNTNDGDADANAQGDASVALISSGSIAAENSVALGTCSVADDEANT   | 921  |
| QY | 469 | LNVGSKDANKPVRITTVNAPGVKEGQDVTVNAQLK-----                        | 501  |
| Db | 922 | VSVSSSTQOOR--RTTNVAAGVNNTDAVNAQLKASEAGSVRYRETNAAGGSVNTSVNLGDG   | 979  |
| QY | 502 | -----GVAQ-----MLNMRIDVNNCNAAGIAQ                                | 524  |
| Db | 980 | SGGTTIRIGNVSAAYNDTDVAVNYAQLKRSVEEANTYTTDQKMGKENSISIKIENKMSGGIAS | 1039 |



OY 525 AATGATGVOAYTPKSGSMMAIGCGTTCAGCAAGCAGTSSISACGNNTIRIKCTAGSNGRHGCA 584  
| | | | | | | | | | | | | | | | | | | | | | : | | : |  
Db 1040 AAAGAAGLQDAPATPAGANMTSLTAGGTTFNGESAVAIQSVMSSESGGWYRKUQTSTNSQGDYSA 1099

OY 585 SASVGYOW 592  
: | | |  
Db 1100 AATGACGFW 1107

RESULT 8

A82615  
surface protein Xr1981 [imported] - xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615

R:Anonymous, "The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000

A:title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615

A:Molecule type: DNA  
A>Status: preliminary  
A:Residues: 1-1190 <SIM>

A:Cross-references: GB:A004017; GB:AE003849; MID:G9107083; PIDN:AAF84783.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Brlones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Falcinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laizy  
chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, B  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
A:Genetics:

:Gene: Xr1981

[illegible]

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Db      886 -EGATAVSSGAASAASKGTAIGRNAVVASADSVALGD-GAKDGCARGAESTTGTSGLONN 943
Qy      343 TSGTKVTFEASGNGTATATYTSKDDOGNIIVKYVDVNGDALNVL-----QNSGMWLDKAVA 398
Db      944 TVGTVSVGDASKGETRTVS-----NVADAKREAT--DAVNLRLQDRVAQDANRYVDNKIES 996
Qy      399 GSSGCVVIGSNVSPSKGKMDFTVINIAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADA 458
Db      997 LSEGQTF-----VKVNSLNN-----SAPPLIAGVDATAIIGVATA 103
Qy      459 -----PLTSDVEGAL-----NWGSKDANKPVRTITNAPVCKREDVT 495
Db      1032 SGADSIAMGNKASASADANAIGHHSVADRANTVSVSSASSER--QYTNVAAAGTAPTDPAV 108
Qy      496 NVAOLKGAQNLNNEFIDNVNGMAR---AGIAQAIAATAGLVQALPCKSMALIGGCTYLG 551
Db      1090 NVSQLNOGLITAKYQTTDGVVSLRRDRDGGVAAAIATATANLPQAIYIPRGMTSVGVSSTRG 114
Qy      552 EAGYALIGYSSISAGCNWLIIRKTAAGNSNGHGHCASAVSYGYOW 592
Db      1150 QSAIAVGVSVSESGRWFKFSGSANTRSQVIGAGVGYOW 1190

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RESULT 9  
AH0110  
probable surface protein (partial) YP00902 [imported] - *Yersinia pestis* (strain CO92)  
C:Species: *Yersinia pestis*  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarragat, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586350  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <kur>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YP00902

| Query Match           | 10.8%            | Score 321.5                    | DB 2:                         | Length 658:            |
|-----------------------|------------------|--------------------------------|-------------------------------|------------------------|
| Best Local Similarity | 23.0%            | Pred. No. 7.5e-09:             |                               |                        |
| Matches 138:          | Conservative 71: | Pred. Matches 214:             | Indels 177:                   | Gaps 21:               |
| QY                    | 115              | NNNNNNASSFFSYSLKKDITGLIINE---- | TEKLSPGANGKKV----             | NIISDRKL-----NF 164    |
| Db                    | 114              | SSTSDAVVSGSLXNLVQDSTRIFHANSVNP | STSLASGLETI                   | AVGPATTVSGDNGVIGWT 173 |
| QY                    | 165              | AKETAGTNGDTTVHLNGIGSTLT-----   | DMILNTGATTVTNDNVTD            | 207                    |
| Db                    | 174              | ALVGAAGATGIAI-----GFTQYVTA     | GATATIGSMAQGAQGAISALGAVTSQAN  | 229                    |
| QY                    | 208              | EKKRAASVQV-----                | LNAGH-----                    | NIKGVPCTTASDNDVPR 242  |
| Db                    | 230              | ---AASITVVAOSSYSAYALTAPQASVGE  | IGIGTALGNRRITGVAASASSADAVNAQO | 285                    |
| QY                    | 243              | -----TYDVEFLSADTKTTTV--        | NYESKDN-----                  | KKEVYIGATSVY 281       |
| Db                    | 286              | LTAVGDOVQONTANITSLGCRVTT       | IEGSMASLANGGVYVFHANS          | TOPDPSVASGINSVAI 345   |
| QY                    | 282              | -----KEKMDGLVYCKGKGENGS        | STDEBEGVLTAKEVID              | 315                    |
| Db                    | 346              | GPASLASGNAALASGAGAVAI          | DGAASAASDGSVAIGQSGDNGRVE----- | 392                    |
| QY                    | 316              | AVNKGWRMRKTTTANGQTSQADKFE      | TVYSIGTVTFASGNGTTATYSK        | DOGNITVYKIDVN 375      |
| Db                    | 393              | -----NYTKYSNASNTSSGTSV         | GTATGATGRTTYSVNAVD-----       | LQ 430                 |

|    |  |                                                                                             |                                                                                                                                                                  |     |
|----|--|---------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| Oy |  | 376                                                                                         | VGDALNVLQNGSGNNLDSKAAVSSGKYVISGSWSPSKGMDETVINAGNNI-EITNG                                                                                                         | 434 |
| Dd |  | 431                                                                                         | ATDAVNLMQLDQS-----IAASIYVENNNVSGCLONGTDGMEQVANNSSGLAKPSATG                                                                                                       | 480 |
| Oy |  | 435                                                                                         | KNIDI--ATSMTPPFSSVSLGAGADAPPLS-----VDDEGALNVGSKDANKPVRIT                                                                                                         | 483 |
| Dd |  | 481                                                                                         | ANSATGGAGSVASGNNSHTAFEGSAKATAANSALGANSVADRANVSIVSGVNER--OIT                                                                                                      | 538 |
| Oy |  | 484                                                                                         | NVAFCVKEGDTVTNAOLKGVAQN-----LNNRIDNVNGNAR-----AGIQAQITACLV                                                                                                       | 532 |
| Dd |  | 539                                                                                         | NVAPRYTGTDAVNFQDLKSISNOTNAYTNORSELRKODLRKONSVLASIGIASMSASTLT                                                                                                     | 598 |
| Oy |  | 533                                                                                         | QAVLGKSGMMAIGGGTYTGCAGYAIGCVSISAGCMMWIIKGFSCGNSRCHFGCASASGYOM                                                                                                    | 592 |
| Dd |  | 599                                                                                         | OPYTSGSSMTTITGAASVTRKQASLSGVSSISDSGRHWVSKLQASSNTQGDFFGICGVGYOW                                                                                                   | 658 |
|    |  | RESULT                                                                                      | 10                                                                                                                                                               |     |
|    |  | C82672                                                                                      |                                                                                                                                                                  |     |
|    |  | surface-exposed outer membrane protein Xf1516 [Imported] - Xylella fastidiosa (strain 96-1) |                                                                                                                                                                  |     |
|    |  | C:Species:                                                                                  | Xylella fastidiosa                                                                                                                                               |     |
|    |  | C:Date:                                                                                     | 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000                                                                                              |     |
|    |  | C:Accession:                                                                                | C82672                                                                                                                                                           |     |
|    |  | R:Anonymous:                                                                                | The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence                                                                                    |     |
|    |  | Nature 406,                                                                                 | 151-157, 2000                                                                                                                                                    |     |
|    |  | A>Title:                                                                                    | The genome sequence of the plant pathogen Xylella fastidiosa.                                                                                                    |     |
|    |  | A:Reference number:                                                                         | A82515; MUID:20365717                                                                                                                                            |     |
|    |  | A>Note:                                                                                     | For a complete list of authors see reference number A59328 below                                                                                                 |     |
|    |  | A:Accession:                                                                                | C82672                                                                                                                                                           |     |
|    |  | A>Status:                                                                                   | preliminary                                                                                                                                                      |     |
|    |  | A:Molecule type:                                                                            | DNA                                                                                                                                                              |     |
|    |  | A:Residues:                                                                                 | 1-1004 <STM>                                                                                                                                                     |     |
|    |  | A:Cross-references:                                                                         | GB:AEO03981; GB:AEO03849; NID:g9106543; PIDN:AAFB4325.1; GSPDB:GN000                                                                                             |     |
|    |  | A:Experimental source:                                                                      | Strain 945c                                                                                                                                                      |     |
|    |  | R:Simpson, A.J.G.;                                                                          | Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brliones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargu, L.E.A.; Carreiro, D.M.; Carreir, H. |     |
|    |  | as-Neto, E.;                                                                                | Docena, C.; El-Dorry, H.; Facincanl, A.P.; Ferreira, A.J.S.                                                                                                      |     |
|    |  | submitted to GenBank,                                                                       | Cui 2000                                                                                                                                                         |     |
|    |  | A:Authors:                                                                                  | Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm                                                                                    |     |
|    |  | J.D.;                                                                                       | Junqueira, M.L.; Kemper, E.L.; KlafJim, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig                                                                                 |     |
|    |  | Chado, M.A.;                                                                                | Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, I                                                                                      |     |
|    |  | A:Authors:                                                                                  | Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Palmeiri, D.                                                                        |     |
|    |  | ; F.G.;                                                                                     | Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Sakasai                                                                         |     |
|    |  | Rodrigues, V.;                                                                              | Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal                                                                                        |     |
|    |  | A:Authors:                                                                                  | da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve                                                                                      |     |
|    |  | M.;                                                                                         | Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;                                                                               |     |
|    |  | A:Reference number:                                                                         | A59328                                                                                                                                                           |     |
|    |  | A:Contents:                                                                                 | annotation                                                                                                                                                       |     |
|    |  | C:Genetics:                                                                                 |                                                                                                                                                                  |     |
|    |  | A:Gene:                                                                                     | Xf1516                                                                                                                                                           |     |
|    |  | Query Match                                                                                 | 8.6%; Score 256; DB 2; Length 1004;                                                                                                                              |     |
|    |  | Best Local Similarity                                                                       | 22.1%; Pred. No. 2, 4e-05;                                                                                                                                       |     |
|    |  | Matches                                                                                     | 162; Conservative 90; Mismatches 280; Indels 200; Gaps 32.                                                                                                       |     |
| Oy |  | 2                                                                                           | NKIYRIIMNSALNAVVAASELTRNH-----TKRASATVKTAVALTLFPAVQOANTDED                                                                                                       | 55  |
| Dd |  | 4                                                                                           | NOIYRFKMILSIGSWSVASHMTNDGCSDVYLHRSVGSRNRSJVLAIQALTSTVTHA----                                                                                                     | 59  |
| Oy |  | 56                                                                                          | EFEELSESORSVYGSIQAMESGVELE---TISLSMTNDSKE-----                                                                                                                   | 94  |
| Dd |  | 60                                                                                          | -----OSVASPMANVTASKYVAHVBSOVNRTADRIPTGSGSELMMHMALDMKFPPPGNNS                                                                                                     | 114 |
| Oy |  | 95                                                                                          | -----FVDYIVYVTTKLAKGDNLIKONTNENTN-ASSFTYSLKDKLTGLINTETKLSFGA                                                                                                     | 148 |
| Dd |  | 115                                                                                         | IAlGYSKAFAPRNAILAGVNSSYTQSANNVAGALSSTVS-----GVNSVALGACS                                                                                                          | 165 |
| Oy |  | 149                                                                                         | NGKVNIISDTGLNFAKETAGTNGDTTVHLNGISGTLTMDMLINTGATTNVDNYTDE                                                                                                         | 208 |
| Dd |  | 166                                                                                         | MASELNVISVGG-----DGVTGPVARRIYVWG----DGIGNDAVANUKSOLDGVTAGV                                                                                                       | 214 |
| Oy |  | 209                                                                                         | KRRASVKKVL-----MGAMNIKGVKPGTTA-SDNADVPRITDYEE-----                                                                                                               | 249 |

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Db 215 NDVAASYKTIALTQNTGSSVASASGKESTALIGSQAQAVADN-----TVAFGGRALA 266
OY 250 -----LSADT-----KTTTVNYESKD-----NGKTEVKIGAKTSVIK 282
Db 267 NAVGASALGFSPSHAKGINSTTVGTQSVSLGQGVSLIGVSNFVEBGSFNGIALSNSLTVLL 326
OY 283 EKDGKLVYTKR-----KGENGSTDEGEGE--VTAKEVI-----DAVKAQWRMKTTT 328
Db 327 QGVDSVALGSSMSAEPNVVSVSGDGLRGPAVRIRYVNWGDGIGNNDVAVKSSQLDGVYAS 386
OY 329 ANGOTGQADKEFEV--TSGTKVFTEASGNTTAT--VSKDDGQNTITVKYDVNVGALVYNOL 385
Db 387 VNDVYASVKINAGAIQTITGSCVASVSQDSTPAAGASAQAAGDSSIA---LGARSRANAII 442
OY 386 QNSGNND-----SKRNVGSSKRYISGNVSPBKGMDETVNIAGNNIIEIRNGCNID 438
Db 443 GSSALGVGDGHALGANSTPALGQSTALIBEGTSLG--YNSFVGQSAFNGIALGSN----- 494
OY 439 IATSMTPQFSSVSIAGAGADAPTLISVDEDEGALNVGSKD--ANKPV--RTITNAPVQKEGDTV 495
Db 495 ---ATVSCVNSVALGAGVASSELV-----ISVGGGCGVTCGPAVRKIRVYVWDDGIGNNDAY 546
OY 496 NVAQLKEVQAQMLNN---RIDVWVNGNAR---AGIAQAI--ATAGLVQAYLLPGRSMAIG- 545
Db 547 NKSQLDGVTASVNDVYASVKIKVITQITGSGVASALIGKDSATGASQAQVGDSSVALGT 606
OY 546 -----GGTYLGEAGYATIGSSISAGGNMIIR-----GTAASNSR 579
Db 607 RATAANAIGSSVILGYDSRARGINSTALGRHOSNAIDGVSISLEFNSFVRQSGEHHVALGTDA 666
OY 580 GHFGA--SASVGY 590
Db 667 GYSGKDSIALGT 678

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RESULT 11.  
A64905  
ydek protein - Escherichia coli  
N:Alternate names: protein T  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
C:Accession: A64905: 152440; S34315  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
A.: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: A64905  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1325 <BLAT>  
A:Cross-references: GB:AE000248; GB:U00096; NID:g187783; PIDN:AACT4583.1; PID:g187777  
A:Experimental source: strain K-12, substrain MO155  
R:Cartwright, P.; Timms, M.; Lithgow, T.; Hoj, P.; Hoogenraad, N.  
Biochim. Biophys. Acta 1153, 345-347, 1993  
A:Title: An Escherichia coli gene showing a potential ancestral relationship to the g  
A:Reference number: 152440; MUID:94100243  
A:Accession: 152440  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <RES>  
A:Cross-references: EMBL:X73295; NID:g312392; PIDN:CA51730.1; PID:g312393  
A:Note: The difference in length is due to a frameshift error at pos 653  
C:Genetics:  
A:Gene: ydek  
C:Function:  
A:Description: probably involved in protein translocation apparatus  
C:Keywords: nucleotide binding, P-loop  
E:712-719/Region: nucleotide-binding motif A (P-loop)

Query Match 8.2%; Score 243.5; DB 2; Length 1325;

[illegible][illegible]

QY 61 ESVORSVGSIOASMEGV---ELETISLMTN-DSKEFVDPYI-----VYTLKAGDN 109  
 Db 46 -----RLTLGVLLA-LSGSVSGASLEVDNGOITNIDTVAADAYLVGWYGTGLNLLAGGN 100  
 QY 110 LKIKONTNENMNASFFYSLKDKDLGLIN--ETEKL-SFGANGKKVNI-ISDRKGLNFA 165  
 Db 101 ASL-----TTTTSVIGNEDESEGTAVNLGCTWRLYDSGNNAKPLNVGOSGTGLNIK 153  
 QY 166 KE-----TAGTN--GDTTVHLNGIGSTLTDMLNTGATTNTNDNVTDDEKKRAASV 215  
 Db 154 OKGVHDGCLRLGTQAAGVGTAVNEGEDSVLTTFELFEG-SYGTGSLNITD----- 203  
 QY 216 KDVLNAGMNIKVKPPTTASNDVFRYTVPEFLSADYTTTNYVNSKDKNGKTEVAKIG 275  
 Db 204 -----KG-----YYTSSIVA-----ILGYQANSNGKVVVEKGG 231  
 QY 276 AKTSVIEKDGKLVTKGKKEGNSSTDEGELVYAKEDIVANVAGRMKTTTANGTQ 335  
 Db 232 --EWLKNNDSSIEFOJGNOGTGATIREGLITAEHTTIGGNATG---VGTINVO--- 282  
 QY 336 ADKPEYTSKTYTFASNGTGTATVSKDOGNITVK-YD-VNVDALN--VNOLONSGMN 391  
 Db 283 -DQDSVITVRRLNYGTFGNG--AVNISNMLNNKEXSLVGVODGSHGVVNTVDKGMN 338  
 QY 392 L-----DSKAVAGSSGKVIISGNVSPSKGMDFTVINAGN-----NIE 429  
 Db 339 FLGTGEAFRYIYIGDAGDDELINVSREGKVDGSIITAG---MKET---GTGMLTVKDKNSV 392  
 QY 430 ITRNGKNDIATSMTPPSSVSLGAGADAPLTVSDDEGALNV-----GSKRANKPVRTN 484  
 Db 393 ITNIGTMLGYDGHGEMNISMGVLVNSGSSLGGETGVGKVSITTTGIMVNNKRVYTTI 452  
 QY 485 VAPGVKEGDYTNVAKGVAQNLNRRIDNVNGNARAGIAQIATAGLVQAYLP--GKSM 542  
 Db 453 GVAGVGNLNIISDGG--KFVSGNITFLGDKASGIGTILNIMDATTSEPDYIVGIVNGSGIV 510  
 QY 543 AIGGTYLGEAGYAI-----GYSSISAGNMIIKGTASGNSR 579  
 Db 511 NVNGATLNSTGYGFIGGNASGKGIIVNSTDLNMLK-TSSTNAQ 554  
 RESULT 14  
 A56143  
 surface-array protein homolog sapa2 - Campylobacter fetus (strain 82-40 LP3)  
 C:Species: Campylobacter fetus  
 C:Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 08-Oct-1999  
 C:Accession: A56143  
 R:Dworkin, J.; Tumuru, M.K.R.; Blaser, M.J.  
 J. Bacteriol. 177, 1734-1741, 1995  
 A:Title: A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein  
 A:Reference number: A56143; MUID:95204338  
 A:Accession: A56143  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1109 <DMO>  
 A:Cross-references: GB:576860; NID:9913763; PIDN:AAB3871.1; PID:9913764  
 C:Note: this gene appeared to be silent in strain 82-40 LP3  
 C:Genetics:  
 A:Gene: sapa2

Query Match 7.5%; Score 225; DB 2; Length 1109;  
 Best Local Similarity 25.0%; Pred. No. 0.00098;  
 Matches 152; Conservative 76; Mismatches 221; Indels 158; Gaps 35;

QY 55 DEEBELSVQSVGSIOASMEGV--LETISLMTNDSKEFVDPYI-VYTLKAGDN 112  
 Db 330 DGSADVONLKNVYGAKGASVAITADKIETLNLN-TTGSQSFVSADVASISVKGANLNL 388  
 QY 113 KONTNENTNASSFTYSLKDKDLGLIN--ETEKL-SFGANGKKVNI-ISDRKGLNFA 171  
 Db 389 ATGAKTTTLDASSFGALDADLSTASVTSIK---GGNGNDKITYIKDV-AVNVAID-GGA 443

QY 172 NGDTTVHLNGIGSTLTDMLNTGATTNTNDVTD--EKKRAASYKDYVLNAGMNIKGV 228  
 Db 444 GNELVYIKGSGTADLLOPLTN--IEKVTIDGNTKDLTSLKKAQSVTEL-----SKNI 495  
 QY 229 -KPGTASDNVDFVRYDYFEFL--SADFTKTTYNVNES-----KDNCKTEVAKIGA 276  
 Db 496 AKYTESNGNV-----ETYNIIANNATDKAVYINDESLKTINSDVDDG-----ASVAA 545  
 QY 277 KTSVIEKDKLVYTKGK-----GENSGTDEGELVYAKEDIV----- 315  
 Db 546 KGLIVADKATLEFLINSKVTYLASDAVQAAATKID---INAKDVTGLTGGVAKLTID 601  
 QY 316 -AVNKAQRKAKTTTANG-----QTGAQKPEFTVS-----GTVTASG 353  
 Db 602 LTVNNKG-APALGANATDLDVKNLSVNEGAFSIAFASLKLNNLSLNGVSADINSV 660  
 QY 354 NGTATVASKDO-----GNITVKYDV-----NVGALANVOLONGSMINDSKAVA 398  
 Db 661 NVGTATLASLEANINVSGERLGTITAKGDYDENLVG-ALTIGALITSSIGNA-SVATIS 718  
 QY 399 GSSGKVIISGNVSPSKGMDFTVINAGNIEITRNGKNDIATSMTPPSSVSLGAGADA 458  
 Db 719 SATGNVTLGAVSATQNL---TLNAGNTL-----GNITIGA-LKG 754  
 QY 459 PTLVSDDEGALNVSKANPEVRLTNVAPGVKEGDT-----NVAOLKGA--QNLN 508  
 Db 755 DIVSVLDGVLGTINSANNNKVSITS-----NEVYVGEISKNVYEITAAAGTDLN 807  
 QY 509 NRIDNVNGNARAGIAQIATAGLVQAYLPKSMAGGTFYLGAGYVAGSSISAGNM 568  
 Db 808 AQ---VIGGAADADLTLTGKDTOTITASD---LSGGITLTLTERTKLSLIDISG-- 859  
 QY 569 IIKGTASGN 577  
 Db 860 -VKG-ITGN 866  
 RESULT 15  
 D85724  
 hypothetical protein ydek [imported] - Escherichia coli (strain O157:H7, substrain ED  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: D85724  
 R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 Niller, L.; Grobbeck, E.J.; Davis, N.W.; Jlm, A.; Dimalanta, E.; Potamousis, K.; Apoda  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: D85724  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1343 <STO>  
 A:Cross-references: GB:AE005174; NID:912515159; PIDN:AAG56256.1; GSPDB:GN00145; UMGCP:  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: ydek

Query Match 7.5%; Score 223.5; DB 2; Length 1343;  
 Best Local Similarity 24.0%; Pred. No. 0.0015;  
 Matches 154; Conservative 79; Mismatches 257; Indels 153; Gaps 32;

QY 1 MNKIRITMNSALNAVAVSELTNRHTRKASATYKTAVALTLFATVQANATDEDEBEL 60  
 Db 1 MNRITRYMNTCTLOVFOACSELTRRVGKTSVNLKSSGLTKTS----- 45  
 QY 61 ESVORSVGSIOASMEGV---ELETISLMTN-DSKEFVDPYI-----VYTLKAGDN 109  
 Db 46 -----RLTLGVLLA-LSGSVSGASLEVDNGOITNIDTVAADAYLVGWYGTGLNLLAGGN 100  
 QY 110 LKIKONTNENTNASSFTYSLKDKDLGLIN--ETEKL-SFGANGKKVNI-ISDRKGLNFA 165  
 Db 101 ASL-----TTTTSVIGNEDESEGTAVNLGCTWRLYDSGNNAKPLNVGOSGTGLNIK 153

```
OY 166 KE-----TAGTN--GDTVHNGISSTLMDLNTGATNTVNDVDEKRRASV 215
Db 154 QKGVHDGTYLRLGTQAGVTVNVEGEDSVLTTELFEIG-SYGTGSLNTD----- 203
OY 216 KDVLNAGWNKGVKPGTASDNVDFVRFDYVEFLSADTKTTVNVESKDNCKTEVKIG 275
Db 204 -----KG-----YVTSIYA-----ILGYQANSNGKVVVEKGG 231
OY 276 AKTSYKEKDGKLVTKGKGNGSSTDEBGLVTAKEVIDAVNKAQWRKTTTANGQTGQ 335
Db 232 --EWLIKNNDSIEFQIGNQGTGEATIREGLITAENTIIIGNATG---VGLNVQ--- 282
OY 336 ADKEFTVSGTFTVFASGNGTATATVSKDOGNITVK-YD-VNVGDALN--VNQLONSGN 391
Db 283 -DQDSVITVRRLYNGYFGNG--AVNISNNGLINNKEYSLVGVDGSHGVNVVTDKGHN 338
OY 392 LDSKAVA-----GSSGKVIKGNVSPSK-GKMDETVINAG-----NNIET 431
Db 339 FLGTGEAFPRYIYIGDAG--XGELNVSRGKVDSCI-ITAGMKETGTGNLTVKDKNSVIT 394
OY 432 RNGKNIDIATSKTPOFSSVSLGAGADAPTLVSDGALNV-----GSKDANKPVRTNYA 486
Db 395 NLGTMLGYDGHGEMNISNEGVLVNSGSSIGYGETGVGVKSITTGIMEVKNKNTYTTIGV 454
OY 487 PGVKEGDTNNVAQLKGVAQNLNRRIDNVNNGNARAGIAAIAIATAGLYQATLP--GKSMAAI 544
Db 455 AGVGNLNLISDGG--KEVSQNIIFLDGDKASIGITLNLMDATSSFDYVGINVNGSGGIYV 512
OY 545 GGGTYLGEAGYAI-----GYSSISAGGNWIIKGTASGNSR 579
Db 513 SNGATLNSTGYGFIGGNASGKIIVNISTDSLNLK-TSSTNAQ 554
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Search completed: July 3, 2002, 08:12:05  
Job time: 427 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:29:38 ; Search time 48.34 Seconds

(without alignments)  
474.182 Million cell updates/sec

Title: US-09-771-382-2

Perfect score: 2987

Sequence: 1 MNKIYRIMNSALNAMYAVS.....TASGNSKGHGASASVGYQW 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 243.5 | 8.2         | 1325   | 1 YDEK_ECOLI | P32051 escherichia  |
| 2          | 220.5 | 7.4         | 1039   | 1 AG43_ECOLI | P39180 escherichia  |
| 3          | 212   | 7.1         | 1655   | 1 OMPB_RICCN | O9Kk43 r outer mem  |
| 4          | 211.5 | 7.1         | 2249   | 1 OMPA_RICRI | P15921 rickettsia   |
| 5          | 206.5 | 6.9         | 1654   | 1 OMPB_RICRI | O53047 r outer mem  |
| 6          | 203   | 6.8         | 1286   | 1 AIDA_ECOLI | Q03155 escherichia  |
| 7          | 201   | 6.7         | 1577   | 1 HUYA_PROMI | P14666 proteus mir  |
| 8          | 198   | 6.6         | 2003   | 1 YDBA_ECOLI | P33666 escherichia  |
| 9          | 197   | 6.6         | 1656   | 1 OMPB_RICJA | O06653 r outer mem  |
| 10         | 190   | 6.4         | 1645   | 1 OMPB_RICTY | P96989 r outer mem  |
| 11         | 190   | 6.4         | 2021   | 1 OMPA_RICCN | P34460 r outer mem  |
| 12         | 188   | 6.3         | 1953   | 1 BIGA_SALTY | O52657 rickettsia   |
| 13         | 187   | 6.3         | 1300   | 1 120K_RICRI | P25927 salmonella   |
| 14         | 184   | 6.2         | 933    | 1 SLAP_CAME  | P14914 rickettsia   |
| 15         | 183   | 6.1         | 1608   | 1 HUYA_SERMA | P35827 campylobact  |
| 16         | 182   | 6.1         | 1643   | 1 OMPB_RICPR | P15320 seetratia ma |
| 17         | 180.5 | 6.0         | 1861   | 1 APD1_THETU | Q53020 r outer mem  |
| 18         | 178   | 6.0         | 1025   | 1 SLAP_CANDR | P38536 t amylopull  |
| 19         | 174   | 5.8         | 1567   | 1 ICEN_XANCT | P31828 caulobacter  |
| 20         | 170.5 | 5.7         | 1153   | 1 PVDB_PLAKN | P50493 plasmodium   |
| 21         | 170   | 5.7         | 814    | 1 SLAI_BACAN | P40051 bacillus an  |
| 22         | 170   | 5.7         | 1569   | 1 YPRA_ECOLI | P52143 escherichia  |
| 23         | 166.5 | 5.6         | 918    | 1 YWCB_CAEEL | P34487 caenorhabdi  |
| 24         | 166   | 5.6         | 550    | 1 FLIC_SHIFL | Q08860 shigella fl  |
| 25         | 165.5 | 5.5         | 2334   | 1 WAPA_BACSU | Q07833 bacillus su  |
| 26         | 160   | 5.4         | 1005   | 1 Y456_CHLTR | O84462 chlamydia t  |
| 27         | 160   | 5.4         | 1770   | 1 PMPC_CHLFR | O84419 chlamydia t  |
| 28         | 159.5 | 5.3         | 948    | 1 HP1L_DEIRA | P56867 deinococcus  |
| 29         | 159   | 5.3         | 1694   | 1 IGA0_HAETN | P44969 haemophilus  |
| 30         | 159   | 5.3         | 1702   | 1 IGA2_HAETN | P45384 haemophilus  |
| 31         | 157.5 | 5.3         | 1034   | 1 ICEN_PANAN | Q47879 pantoea ana  |
| 32         | 157   | 5.3         | 1723   | 1 PM20_CHLPP | O92812 chlamydia p  |
| 33         | 156.5 | 5.2         | 1007   | 1 Y741_CHLMU | O9p1t6 chlamydia m  |

|    |       |     |      |              |                    |
|----|-------|-----|------|--------------|--------------------|
| 34 | 156   | 5.2 | 917  | 1 HXA3_HAETN | P45355 haemophilus |
| 35 | 155.5 | 5.2 | 504  | 1 FLIC_SALBU | O06969 salmonella  |
| 36 | 155.5 | 5.2 | 928  | 1 HXA2_HAETN | P45354 haemophilus |
| 37 | 155.5 | 5.2 | 928  | 1 PM10_CHLPP | O92865 chlamydia p |
| 38 | 155.5 | 5.2 | 1322 | 1 ICEA_PANAN | P20469 pantoea ana |
| 39 | 155.5 | 5.2 | 2329 | 1 YS89_CAEEL | Q09624 caenorhabdi |
| 40 | 155   | 5.2 | 762  | 1 SLAP_ACERI | P22258 acetogenium |
| 41 | 155   | 5.2 | 1310 | 1 VAC3_HELPY | O48253 helicobacte |
| 42 | 155   | 5.2 | 1902 | 1 P2P_LACPA  | O02470 lactobacill |
| 43 | 154.5 | 5.2 | 512  | 1 FLA4_HELPF | O94038 helicobacte |
| 44 | 154.5 | 5.2 | 575  | 1 FLA2_CAME  | P22251 campylobact |
| 45 | 153.5 | 5.1 | 671  | 1 ALYS_ENTFA | P37710 enterococcu |

## ALIGNMENTS

```

RESULT 1
YDEK_ECOLI
ID YDEK_ECOLI STRAND: PRT: 1325 AA.
AC P32051: P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28,040.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
[3]
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Tibbels M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
[4]
RN [4]
RP SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
[5]
RN [5]
RP SIMILARITY: TO E-COLI YEAL.
[6]
RN [6]
RP SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
[7]
RN [7]
RP CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
-----
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CC -----  
 DR EMBL: AB000248; AAC74583.1; -  
 DR EMBL: D50793; BAA15190.1; ALT\_INIT.  
 DR EMBL: D90794; BAA15197.1; ALT\_INIT.  
 DR EMBL: X73295; CAA51730.1; ALT\_FRAME.  
 DR PIR: S34315; S34315.  
 DR Ecogene: EG11780; Ydek.  
 DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
 KM Complete proteome.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
 FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT CONFLICT 884 884 N -> K (IN REF. 3).  
 FT CONFLICT 1317 1317 M -> S (IN REF. 3).  
 SQ SOURCE 1325 AA; 136514 MW; 26A3A06FA19ADDYD CRC64;

Query Match 8.2%; Score 243.5; DB 1; Length 1325;  
 Best Local Similarity 23.8%; Pred. No. 9.8e-05;

Matches 133; Conservative 79; Mismatches 259; Indels 151; Gaps 29;

QY 1 MNKIRIINNSALNAAVAVSELEFRNHTKASATVKTAVLATLLEATVOANATDEDEEEL 60  
 1 MNRIRYIMNCTLOVQACSELEFRACKTSVNLKRSSGLTKRSRLT----- 49  
 QY 61 ESORSVAGSIQSMESSELETSLSMTN-DSKEFYDPI-----VYTKAGDMLKI 112  
 50 -----GYLLALSGSAGA-SLEVDNDITNDVDVADAYDAVGVGTGVNILLAGNANSL 103  
 QY 113 KONTNENTNASSFYLSLKDITGLIN--ETEKL-SFGANGKKYNI-ISDTHKGLN----- 163  
 104 -----TTTTSYIGANEDSEGTANVGGTWRLYDSGNARPLNVGOSGTGILNIOKG 156  
 QY 164 -----FAKETAGTNGDTVHLNGISLTLDMLTGTATTVNTDNDVDEKKRAASVYDV 218  
 157 HVDGGLRLSSSTGCVTVNVEGDSVLTTELFIG-SYTGSLNITD----- 203  
 QY 219 LNAAGNITKVKPCTTASDNDVFTYDTVELSLADDTTYYNVSKDKNGKTEVKIGAKT 278  
 204 -----KG-----YVTSIVA-----ILGYAGSGNGQYVVEKGG--E 232  
 QY 279 SVIEKDGKLVTKGKGEGSSSTDEGGLVAKVIDAVNAGRMKTTTANOGTGOADK 338  
 233 WLKNNDSSIFQJGNGTGEATIREGLVTAENTIIIGNATG-----IGTLNV-----DQ 284  
 QY 339 FEVTSGLKVTFAASNGTATATSKDDGNITVK-YD-VNNGDALN-VNQLONGMNL-- 392  
 285 DSVITVRLVNGYFNG--TVNISNNGLINNKREYSLVGVDDSHGVVNVTDKGMWFLG 341  
 QY 393 -----DSKAVAGSSGKVIISGNVSPKGMDELVINAGN-----NIETLR 432  
 342 TGEAFRYIIGDADGELINVSSEKGVDSGITAG--MKET--GTGTIVTKRNSVITN 395  
 QY 433 NGKNIDATSMTPQFSSVSLGAGADAPLISVDDEGALNV-----GSKRANKPVRTINAP 487  
 396 LGTULGIDGHEGNISNGGLVNSGSLGEGGVGVNSTTGGMMVNNVNTTIGVA 455  
 QY 488 GVRKGDVYVNLQKGVANLNRIDNVGNARAGIAQIATAGIQAVALP--GKSMAG 545  
 456 GVGKLNISDGC--KFSVGNITFLDKASGIGTILNMDATSSFDYGVINGVNGSGIVAVS 513  
 QY 546 GGYVLGAGYAI-----GYSSISAGNWIIGTASGNSR 579  
 514 NGATLNSTGYGFIGGNASGKGIIVNSTDLNMLK-TSSTNAQ 554  
 DB

RESULT 2  
 AG43\_ECOLI STANDARD; PRT; 1039 AA.

AC P39180; P76360; P75614; P97241; Q46771;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Antigen 43 precursor (AG43) (Fluffing protein).  
 GN FLU OR B2000.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 NCBI\_Taxid=562;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=9742617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RT Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97251358; PubMed=9097040;  
 RA Iton T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
 RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
 RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,  
 RA Yamamoto Y., Horiiuchi T.;  
 RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 40.1-50.0 min region on the linkage map.";  
 RT DNA Res. 3:379-392(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ML 308-225;  
 RA Henderson I.R., Owen P.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP PRELIMINARY SEQUENCE OF 53-78.  
 RC STRAIN-ML 308-225;  
 RX MEDLINE=89291704; PubMed=2661530;  
 RA Caffrey P., Owen P.;  
 RT "Purification and N-terminal sequence of the alpha subunit of antigen  
 RT 43, a unique protein complex associated with the outer membrane of  
 RT Escherichia coli.";  
 RT J. Bacteriol. 171:3634-3640(1989).  
 RN [5]  
 RP SEQUENCE OF 53-63.  
 RC STRAIN-K12 / EWG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12.";  
 RT Electrophoresis 18:1259-1313(1997).  
 RN [6]  
 RP GENE NAME.  
 RX MEDLINE=97257509; PubMed=9103983;  
 RA Henderson I.R., Meehan M., Owen P.;  
 RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
 RT determines colony morphology and autoaggregation in Escherichia coli  
 RT K-12.";  
 RT FEMS Microbiol. Lett. 149:115-120(1997).  
 CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY  
 CC FUNCTION AS AN ADHESIN.  
 CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
 CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
 CC CHAIN).  
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.  
 CC -1- SIMILARITY: TO ADHESIN AIDA-I AND TO BORDETELLA PERTACTIN.  
 CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AE000291; AAC75061.1; ALT\_INIT.  
DR EMBL: D90838; BAA15825.1; ALT\_INIT.  
DR EMBL: D90839; BAA15832.1; ALT\_INIT.  
DR EMBL: U24429; AAB47869.1; -.

DR Ecocore: E812686; Flu.  
KM Outer membrane; Signal; Complete proteome.

FT SIGNAL 1 52  
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.  
FT VARIANT 552 1039 K -> N (IN STRAIN ML 308-225).  
FT VARIANT 2 2 SL -> FF (IN STRAIN ML 308-225).  
FT VARIANT 41 42 T -> K (IN STRAIN ML 308-225).  
FT VARIANT 46 46 W -> L (IN STRAIN ML 308-225).  
FT VARIANT 157 157 V -> F (IN STRAIN ML 308-225).  
FT VARIANT 188 188 ATN -> STI (IN STRAIN ML 308-225).  
FT VARIANT 303 305 A -> T (IN STRAIN ML 308-225).  
FT VARIANT 320 320 N -> Q (IN STRAIN ML 308-225).  
FT VARIANT 372 372 E -> V (IN STRAIN ML 308-225).  
FT VARIANT 493 493 S -> N (IN STRAIN ML 308-225).  
FT VARIANT 497 497 H -> K (IN STRAIN ML 308-225).  
FT VARIANT 585 585 M -> T (IN STRAIN ML 308-225).  
FT VARIANT 709 709 GHL -> SHE (IN STRAIN ML 308-225).  
FT VARIANT 721 721 S -> P (IN STRAIN ML 308-225).  
FT VARIANT 751 753 A -> V (IN STRAIN ML 308-225).  
FT VARIANT 803 803 C -> S (IN STRAIN ML 308-225).  
FT VARIANT 815 815 LNLVHTS -> MNLVHTS (IN STRAIN ML 308-225).  
FT VARIANT 824 824  
FT VARIANT 829 835  
FT VARIANT 845 847 OGT -> LGA (IN STRAIN ML 308-225).  
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).  
FT VARIANT 888 888 S -> L (IN STRAIN ML 308-225).  
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).  
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).  
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647CDBDEBEO CRC64;

Query Match 7.4%; Score 220.5; DB 1; Length 1039;  
Best Local Similarity 20.6%; Pred No. 0.00095;  
Matches 138; Conservative 84; Mismatches 255; Indels 193; Gaps 29;

OY 1 MKRIYRIINWSALNMAVAVSELTNRHTRKASATVKTAVLATLFAVAVQANADEDEEEL 60  
DB 5 LMTCYRLVNMHTGAFVAVSELARARGKGVAVALSIAVTSLPVLADIYVHPE--- 61  
OY 61 ESVQSVSVCSIASMGSEVELETSLSMTNDSKEFVDPYVTLKAGDNKIKONTNENT 120  
DB 62 -----TWNGG-----TLNHDNDQIYFGTNGMT 84  
OY 121 NASFTYSLKDDTLGLINTEKLSFGANGKRVNIISDTKGLFAKETAGTDDTVHLN 180  
DB 85 ISTGLEYGDN-----ANTGGQVWDGDTANKTTVTS--GLQ-RVNPQGSVDIYISG 137  
OY 181 GIGSTLTDLMLNTG-----ATTNTNDVNTDEKRAASVDVYNAGNINIG 227  
DB 138 G-GOSLOGRAVNTTLNGSGOMHHEGALATGYLNDK-----GMOV--- 176  
OY 228 VAPGTTASNNVDFRT-----YDVERLSADTKTTTVN-----VESKDNCKTE 271  
DB 177 VAPGVATVTV--VNTGAGGDPDAENGDDIGVPRGDAVTTINKNGROIVREAGTANTTV 234  
OY 272 VIKGATSV-----IIEKGDKLVTKGSGKGENSSSTDEGEG 306  
DB 235 VVAGGQVYHGHADLTTLNGGYOYVANGSTADTVVNSGQWQIVKNG-GVAGATTVYNOG 293  
OY 307 LVTAKEVIDAVN--KAGRMKTTTANGOT-----GOADKFEVTSVGTKVTPA 351  
DB 294 RLOVDAGGATVNTLKGALVYSTAATVYTGINRLGAFSVESKADNV-VLENGGLDLVL 352

OY 352 SCNGTATVSKDDQNTITKYVDVNGDALNVNOLNOSGNLSDKAYAGSSGVISGNVSP 411  
DB 353 TGHATVNT-RVDDGGLDVR---NGSTATTVS-MGNGG-----VLLADSGAIVSSTRSD 401  
OY 412 SR-----GKMDETVNIAGNNIEITRNKNIDATSMPTQFSSVSIGADAPPTLSVDE 466  
DB 402 GRAFSTIGGQADALMLEKSSFTLNG-----DPATPTTVNGGLFTARGGTLAGTTLLNNG 457  
OY 467 GALNVGSKDANKPVRITVNAVPGYKEDVTINVAOLKGAONLNNRIDNVNGNARAGIAQAI 526  
DB 458 AITLISGKTVN-----NDLFTIREGD-----ALLQGSILTNQSVYK-SGSGTLTVSNNT 506  
OY 527 ATAGIVQALPLPKSMALIGGT-----YLGEAGYAICTVS-----SISAGNM 568  
DB 507 LTKQAVNL---NEGTLTNDSTVTTVDVIAORGTALKTGSTVLNGALIDPTNTVLLAGATW 563  
OY 569 IIKGTASGNS 578  
DB 564 NIPDNATVQS 573

RESULT 3  
ID OMPB\_RICCN STANDARD: PRT; 1655 AA.  
AC Q9KKA3; Q9KK98; Q9XC45;  
DT 16-OCT-2001 (Rel. 40; Created)  
DT 16-OCT-2001 (Rel. 40; Last sequence update)  
DT 01-MAR-2002 (Rel. 41; Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)  
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).  
DE OMPB OR RC1085.  
GN OMPB\_RICCN  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_Taxid=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RC MEDLINE=2142074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
RL Science 293:2093-2098(2001).  
RN [2]  
RP SEQUENCE OF 33-1649 FROM N.A.  
RC STRAIN=Indian tick typhus, and Malish 7;  
RC MEDLINE=20393643; PubMed=10939649;  
RA Roux V., Raoult D.;  
RT "Phylogenetic analysis of members of the genus Rickettsia using the  
RT gene coding the outer-membrane protein rOmpB (ompB).";  
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
RN [3]  
RP SEQUENCE OF 353-1655 FROM N.A.  
RC STRAIN=Malish 7;  
RC Stenos J., Walker D.;  
RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
RT australis, the most divergent rickettsia of the spotted fever group.";  
RL Submitted (May-1999) to the EMBL/GenBank/DBD databases.  
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
CC SIMILARITY).  
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
CC (BY SIMILARITY).  
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIE OMPA/OMPB FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AEO08659; AAL03623.1; -  
DR EMBL: AF123721; AAF34129.1; -  
DR EMBL: AF123726; AAF34129.1; -  
DR EMBL: AF149110; AAD39533.1; -  
DR InterPro: IPR003858; rompa\_rompb.  
DR Pfam: PF02708; rompa\_rompb.1.  
KW Antigen; S-layer; Cell wall; Complete proteome.  
FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1 1335 1655 32 KDA BETA PEPTIDE.  
FT VARIANT 61 65 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 413 413 I -> D (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).  
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
FT CONFLICT 353 354 KD -> GH (IN REF. 3).  
FT CONFLICT 776 776 F -> S (IN REF. 3).  
FT CONFLICT 1159 1159 E -> D (IN REF. 3).  
FT CONFLICT 1177 1177 G -> S (IN REF. 3).  
FT CONFLICT 1492 1492 H -> R (IN REF. 3).  
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 7.1%; Score 212; DB 1; Length 1655;  
Best Local Similarity 22.8%; Pred. No. 0.0042;  
Matches 139; Conservative 76; Mismatches 264; Indels 130; Gaps 29;

QY 45 ATVOANATDEDE---EELLESVQSVSGSIQASMEGSVELETISLMTSDKEFYDPY 99  
DB 261 AITFNGDGTGRLVLLSKNAADPENVTSIGLNLKGIIEFNVAVNGQ----- 310  
QY 100 IVVTLKADNLIKONTNENTNASSFTYSLKKDLTGLINVEKELSPANKKVNII SDT 159  
DB 311 -LKNANAGANAIVGTNNAGRAAGFVVSV-----NKKVATIDGOV 350  
QY 160 KGLNFAKETAAGNDPTV-HLNGIGSTLTDMLNTGATTNT-NDNV-TDEKKRASV- 215  
DB 351 YAKDNVIOASNAVGOVNRHIVDGTDTAPKTAASVAITONSFGTTPGMLAADI 410  
QY 216 ---KDLNAGNNIKGKPKDPTASDNVDFRTYD---TVEFLSADTKTTVN---VESKD 265  
DB 411 VPNTWLTNGNFTGSDASNGNTAG---VTFDANGTLASASADANVAVTNNITAFIEASG 465  
QY 266 NG-----KTEVKIGAKTSYIKEDGKLVYTK-----GKGENSSSTDEGGLVTA 310  
DB 466 AGVVOULSGTHAAELRLGNAGSVFKLADGTIVNGKNOTALVGGALAACTITLDGSATTG 525  
QY 311 KEVIDAVKAKGRMKTTANGOTGOADKFEYVT-----SGTKVFFASNGTTATVS 361  
DB 526 ----DIGNAG---AALOGITITLANDATKTLITLGGANIITGANGTINFGANGTIKLT 577  
QY 362 KDDOGNITVYKYDV-----NVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSG 414  
DB 578 -TQNNIVVDFDLAATDGTGVASSSLTNQOTLTLNGKIGVAGNNKNTLQGFNIGSSKPT 635  
QY 415 KM-DETVIN--AGNN--IETTRNGKNIDTATSWTPQ---FSSV-----SLGAGADAP 459  
DB 636 VLSDGDVAINELVIGNNGAVOFANHTYLTITRTNAGGOKIIFNFVNNNTTLATGTNIG 695  
QY 460 TLYVDEGALVWGSKDAKPRITNVAPRGEGDVTNVAOLKGVAONNNRIDVNG--NA 518  
DB 696 S-ATPLPLAINEFGSKGANVDTVLWVGKVM--YATNITTTDA---NGSGIFENGGTINI 750  
QY 519 RAGIAQAIATAGIYO-----AYLPGRSKMAIGGGTYLGEAGYAIIGYSSISAGGNWIIK 571

DB 751 VSG-----TVGGQGGKMFNTVALDNGTVMKFLGNATFNNGNTTIAN-STLQIGNGYTAD 803  
QY 572 GTAGNSRG 580  
DB 804 FVASADGTG 812

RESULT 4  
OMPA\_RICRI STANDARD; PRT; 2249 AA.  
ID OMPA\_RICRI  
AC P15921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (cell surface  
DE antigen) (rompa) (romp A).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_Taxid=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R.  
RA MEDLINE=90354033; PubMed=2117568;  
RX Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RT repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
RL -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC -1- S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PFM: GLYCOSYLATED (PROBABLE).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

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DR EMBL: M31227; AAA26380.1; -  
DR PIR: A41477; A41477.  
DR InterPro: IPR003858; rompa\_rompb.  
DR Pfam: PF02708; rompa\_rompb.1.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 212 286 A (TYPE I).  
FT REPEAT 287 358 B (TYPE II).  
FT REPEAT 359 430 C (TYPE II).  
FT REPEAT 431 505 D (TYPE II).  
FT REPEAT 506 577 E (TYPE II).  
FT REPEAT 578 652 F (TYPE I).  
FT REPEAT 653 724 G (TYPE II).  
FT REPEAT 725 799 H (TYPE I).  
FT REPEAT 800 874 I (TYPE I).  
FT REPEAT 875 949 J (TYPE I).  
FT REPEAT 950 1021 K (TYPE II).  
FT REPEAT 1022 1093 L (TYPE II).  
FT REPEAT 1094 1165 M (TYPE II).  
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).  
SQ SEQUENCE 2249 AA; 224333 MW; A9D646C089D087 CRC64;

Query Match 7.1%; Score 211.5; DB 1; Length 2249;  
Best Local Similarity 23.7%; Pred. No. 0.0065;  
Matches 144; Conservative 69; Mismatches 263; Indels 131; Gaps 28;

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OY 46 TVQANATDE-----DEEELESQVRVYSGIOASMEGSVELETISLSMTNDSKEFV 96
DB 91 TVTAAADIIKAINAVAGTTPVGLNTQNTVVGSI--ITKGLN-----131
OY 97 DRYIVVTKAGNLIKIKONTNENTNASSFTYSLKAD-LTGLINVEKISFGANG-----150
DB 132 ---LPTVLNAGKSLTLNGN---NAVAANHGFADPADNNTGLNIALG---CANALLIIQ 181
OY 151 ----KKVNIIS--DTRKGLNFAKETAGTNGDTVLHNGISLTLDMLNTGATTNTYNDV 204
DB 182 SAAPSKITLAGINDGGGLITVTDAAINGT-----IGNTALATVNVAGATATLIGAV 234
OY 205 ---TDDEKRAASVRDVNLNAGWNINIKVPCQTASDNVDFRYDYEFSLADTKT-----257
DB 235 IKATTTKLTLNASSVLTLTNANAVLTGALDNTGGDNVGVNLNAGLSQVTGDIQNTSLA 294
OY 238 TVNVESKD---NG---KTEVKIGAKTSYIKERKGLVYG---KKGENGSSJDEGEGL 307
DB 295 TTSVGAGTATLIGAVIKATTTKLTDAASAVKFTNPVYVVGALDNTGNANNGLVTFGNST 354
OY 308 VFAK----EVIDAVNKAGRMKTTTANGOTGADKEFVTSCTKYTFAGNGTATVSKD 363
DB 335 VTGNVGNLTALVTVNAGGLD---VQGGVVRKANTINLTDNASAVFT--NPVYVYTGALD 409
OY 364 DQGNIT---VKYDVN---VGDALNVNOLQNSGMNLSKRAVSSGKVGISGNVSPSKKMD 417
DB 410 NMGNANNGLVTTTGSSTYTGDIQNTNALTATVNVAGATATLIGAVIKATTTKLTNASSVLT 469
OY 418 ETVNINA--GNNIETTRNCKNIDAT-----SMTPOFSSVSLGAGADAPFTLSV 463
DB 470 LT--NANAVLTGALDNTGGDNVGVNLNAGLSQVTGNISNTSLATISVAG--TATLGG 526
OY 464 DDEGALNVSGRANPVRTTNAPGVKEGDVTNNVQKVAQNLNRRIDNVGNMARA----520
DB 522 AVIKATTTKLTDAASAVKFTN--PVYVYTGALDNTG-----NANGIYVTFGTGNSVTGD 577
OY 521 -GIAOAIATAGLVQAVLTPKRSMAAGG-----TYLGEAGYAGISSISAGGNWITIKGT 573
DB 578 IGTNTSLNTISV-----GAGTATLIGAVIKATTTKLTNASSVLTLTNANAVLTGALDNT 631
OY 574 ASGNSRG 580
DB 632 TCGDNVG 638

```

## RESULT 5

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OMP_RICRI STANDARD: PRT: 1654 AA.
ID OMP_RICRI 053047:
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiinae; Rickettsia.
OX NCBI_TaxId=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R:
RA MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RT Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN-R:

```

```

RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC or send an email to license@sib-sib.ch).
DR EMBL: X16353; CAA34403.1; -
DR InterPro: IPR003858; rOmpB_rOmpB.
DR Pfam: PF02708; rOmpB_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70EB7087F618 CRC64;

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Query Match 6.9%; Score 206.5; DB 1; Length 1654;  
 Best Local Similarity 22.6%; Pred. No. 0.0078;  
 Matches 152; Conservative 89; Mismatches 247; Indels 185; Gaps 37;

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OY 14 NAMAVASELFRNHTKRASATVKTAVLAT--LLEAT-----VQA-----NATDEDE 56
DB 218 NFIQVS-----NKSFAVKAINAIADGGIIFNTDANNANTLNQAGTTINFGTGD 270
OY 57 EEELESVQR-----SVGSGIOASMEGSVELETISLSMTNDSKEVDYIYVTLKAGN 109
DB 271 TGRVLVLSKHAATNENITGSLGKLVIERFVAV---DQ-----LTANAGAA 318
OY 110 LRIKQNTNENTNASSFTYSLKADLTGLINVEKISFGANGKVNIIPTKGLNFAKETA 169
DB 319 NAVIGTNAGARAGRVYVD-----NGKATYIDGOVYAKADMYIQSA 360
OY 170 GTNGDTTV--HLNGISLTLDMLNTGATTNTYNDN--VTDEKRAASVK--DVLNAGNN 224
DB 361 NATGOVNFPHIYDVGADGTAFKASKVLTITQDSNFGMTDGNLAAQIKVPRATLTGN 420
OY 225 IKG--VKPGTTASDNVDFRYTD--TYEFLSADTKTTTVN--VESKDN-----K 268
DB 421 FTGDASNPPNTAG-----VITPDANGTLESASADANAVATNNITALEAGAGVQLSGTH 475
OY 269 KTEVKIGAKTSYIKERKGLVYTG-----KKGENGSSJDEGEGLVFAKEVIDAVNKA 320
DB 476 AAEFLRGNAGSIFKLADGVYINKVQRTALVGCALAAAGTTTLDGSAITTIGD--IGNAGGA 533
OY 321 GWRMKTTTANGOTGADKEFVTSCTKYTFASNGT-----TATVSKDDQGN 368
DB 534 AALQRTITLAN-----DAKTTLLGGANLIGAGGCTIDQANGTFLKNT--QNNI 582
OY 369 TYKIDV-----NVGDALNVNOLQNSGMN-----LDSKAVA-----GSSGKVIS--GVV 409
DB 583 VYDFDLAINTDQTVGVDASLTNAQTLTNGIKTIGANNKTLTGQPNISGSKVIVLSNGAV 642
OY 410 SPSKGMDETVNINAG-----NNIETR-----NGKNI--DIASMTPOFSSVSLGAG 455
DB 643 A-----INLVIGNDGAVPADHYITLTITTTNAAAGGKILFNPVYVNGTTLAAGTWLGS- 696
OY 456 ADAPTLVDEGALNVSGRANPVRTTNAPGVKEGDVTNNVQKVAQNLNRRIDNVN 515
DB 697 -----ATNPLEINFGSGVNVDT--VLNVGECVNL--YATNITTTDA--NVGSEFVFNAG 745

```





FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MM; B83A12C8B53220EE CRC64;

## Query Match

Best local similarity 23.1%; Pred. No. 0.025;  
Matches 158; Conservative 88; Mismatches 239; Indels 198; Gaps 39;

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OY 55 DEEELESVORSVVGSIQASMEGSVELE-----TISLSTNDNSKEFY----- 96
DB 149 DKTEKTLITLIDSVF--TYTENADGTISLSDSGNRKATINLMQIDEANNTVALEGSADGAT 207
OY 97 -----DPYIVTLKAGDNLIKONTNENTNASSFTYSLKDLTGL-IN-----VETEK 143
DB 208 KWOYNHNGELVIT--GDNAIV--NNNGKTTVDS-----KDSGTETLNGNGKVIQDGD 256
OY 144 LSGGANGKVNIIISDT-----KG-----LNFAKETAGTNGDTTVH 178
DB 257 LDVSGGGHGDITGDSATVNDKGTMTVDPESMGIDGDKAIVNNGESTITNGTGTQ 316
OY 179 LNC-----IGSTLTMMLNTGATTVNDNTVD-----EKK 210
DB 317 INGDDATANNNGKTTVYKSKSTGEIENGNGKVIQDGDLDVSGGGHGDITGDSATVNDK 376
OY 211 RAASVKDVLNAGWNIKGVKPGTASDNVDFRYTVEFLSADTKTTTVNYESKONGKK- 269
DB 377 GTMTVTDPEISIGIYVDG--DQAVVNNEGESATNGTGTQINGDDATANNNGKTTVDDKDS 435
OY 270 --TEVKIGATSVIKERDGL-VTGKKG--ENGSTDEGGLVTAKE-----VIDA- 316
DB 436 TGEI--AGNNGKVI--ODGDLVSGGGHGDITGDSATVNDKGTMTVTDPEISIGIYVDG 492
OY 317 ---VNKAGWMTKTTTANGGQADKFEYVTSGTFTVFAAGTATATVSKD-----GNT 368
DB 493 QAIYVNEG--ESTITNGGTG-----TQINGNDAT--ANNSGKTTVDKDSGTGKIAGNI 542
OY 369 TVKYDVNVDGALANV-----NOLQNSGN--LDSE-----AVASSGKYISGNVSPSKMD 417
DB 543 GI-----VILDSGLVYTGAGHGENIGDNGTVNKKDIYVSDIGLNGGATVSNMGD 599
OY 418 ETVNINAGNNIETTRNGKNIDATSM--TPOSS--VSLGAGADAPTLVSD-----EGA 468
DB 600 VNVS--NEATGFSITNGSKVSLAGSMQVGDSTVDLNGNNSVTLAKDKVVGOKATG 658
OY 469 LNVGSKANKPVRTTNVAPVKEGDTNNVAQL---KGAQQLNRRIDNVNNGNARAGI--- 522
DB 659 INV--SGDAN--TVNITGVNLYDKDKTADNAAEYFPDPVSGIIVGSDNNVTLLDGLTVVSD 716
OY 523 -----AQAIVTAGIYQAVILPGKSMMAIGGTYLGE-----AGYA 556
DB 717 SEVTSRQSNLFDGSAEKTSGIV--VIGDGNVYNNMGLELIGERKALADGSGVTSLRGTGS 775
OY 557 I-----GYSSISAGNNMIIG 572
DB 776 YTSVIYVSGESSVYLNQDITISG 798

RESULT 9
OMP_B_RICJA STANDARD; PRT; 1656 AA.
AC 006653;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scab) (rOMP B)
DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=35790;
```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-YH.
RA Uchiyama T.;
RT "Sequencing of the gene encoding the protein rOMP B of Rickettsia
japonica."
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
SIMILARITY).
CC -! FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
(BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY.
CC -! SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.
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CC -----
DR EMBL: AB003681; BAA20138.1; -.
DR InterPro: IPR003858; rOMP_B_rompB.
DR Pfam: PF02708; rOMP_B_rompB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1338 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 528 533 32 KDA BETA PEPTIDE.
FT DOMAIN 528 533 POLY-GLY.
SQ SEQUENCE 1656 AA; 168097 MM; 3132A69CDD5999F CRC64;
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Query Match 6.6%; Score 197; DB 1; Length 1656;  
Best local similarity 20.8%; Pred. No. 0.022;  
Matches 166; Conservative 78; Mismatches 260; Indels 296; Gaps 36;

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OY 30 ASATVKTAVLATLTFAYOANATDE-----DEEELESVORSVVGSIQASMEGS 78
DB 20 STATIVASFGSAGAAIDQNRRTNGVATVDGVFOQYVALAAVAPNAVITANNNG 79
OY 79 VELET-----ISLSTNDNSKEFYVTVTLKAGDLKIKONTNENTNASSFTYSLK 131
DB 80 INLTPAGSENGGLPLSNAN-----LAVTSEDITLGINNANNANRPNLTLDAK 131
OY 132 DLT-----GLINVE----- 140
DB 132 TLTITGGITVQSAATHNQNIVAKFNGGAIAIANDLSGLTIDFGAASTLVFDLANP 191
OY 141 -TEKLSF-----GANG-----KKVNIISDTKGLNAKETAG 170
DB 192 TTKAPLILADNALIVGANGNTLVNTNGFIQVSDKSPATVAKIN-IDDGGQFMFTNATN 250
OY 171 TN-----GDTTVHLNGSGSLTDLMLN--TGATTVNTNDVTDDEKKRAASVKOVLANGW 223
DB 251 ANALLDQAGTTTFNFGDTGRLVLSKNGCAATDF--ANTG-----SLGG 294
OY 224 NIKGVKPGTASDNVDFRYTVEFLSADTKTTTVN-----VESKDNKTEV--K 273
DB 295 NLKGIITELNTVAINGQLIANNG-----PANNAVITNNGAGRAAGFVYVDGKATIDGQ 349
OY 274 IGATSVYKE-----KDKGLVYKKGKGEVSSSTDEEGGLVTA 310
DB 350 VYADAVNKAAGWNRKTTTANGQGOADKFEYVTSGTFTVFAAGTATATVSKDQGNITV 370
OY 311 KEVIDAVNKAAGWNRKTTTANGQGOADKFEYVTSGTFTVFAAGTATATVSKDQGNITV 370
DB 409 VTVPDITM-----TLGN--FTGDANN--PGNTAGV--ITFAA--NGTLASASAD--ANAV 454
OY 371 KYDVNVDGALVNDLQNSGNWILDSKAV--AGSSGKVIISGNVSPSKGMDET----- 420
```

DB 445 TNNITAEASGVVQVLSCTHTAELRLGNAGSVFKLADGT--INGKVNQVLVGGVLA 512  
OY 421 -----NINA-GNN 427  
DB 513 GAITLDGSAFTITGDI GGGGALOSTLANATYTLTLGANNIISANGCTINPOANGST 572  
OY 428 IETTRNGKNI-----DIATSMTPQFSSVSLGAGADAPTLSDVE-----GALANG 472  
DB 573 IKLTSTQNNIIVVDCDLALA-TDQGVDAASSLJTNQTLTISTGIGANNNTLGGFNG 631  
OY 473 SKDA---NKPAVITVAAGVKEGDV-----TNVAOLKVAQNLNRIDNVGNMARA 520  
DB 632 SKRTLLNGNVAINELVIG--NNGSVQFAHNTYLTTRTNAAGCKIIFNPVNNNTTLAA 690  
OY 521 GIAQAIATAGLVQAVLPCK-----SMMAIIGGCTVGEAGYA-----IGYSSISAGG 566  
DB 691 GTNLGSAANPLAEINFGSKGARADTVLVNGEGVNL---YAINITTTDANVGSFVFNAGG 746  
OY 567 NWIIRGTASGNSRGHFGASA 586  
DB 747 KIVSGTVGGGCGGNKFNTRYA 766

RESULT 10  
OMP\_RICTY STANDARD: PRT: 1645 AA.  
AC P69899:  
DB 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (Comp)  
DE (Comp B) (Contains: 120 kDa surface-exposed protein (Surface protein  
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).  
GN OMP OR SLP.  
OS Rickettsia typhi.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OX Rickettsiaceae; Rickettsiase; Rickettsia.  
OX NCBI\_TaxId=785;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WILMINGTON;  
RX MEDLINE=94040787; PubMed=8224886;  
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
RT "Cloning and sequence analysis of the gene encoding the crystalline  
RT surface layer protein of Rickettsia typhi.";  
RL Gene 133:129-133(1993).  
RN [2]  
RP PARTIAL SEQUENCE.  
RC STRAIN-WILMINGTON;  
RX MEDLINE=92114896; PubMed=1370573;  
RA Ching W.M., Carl M., Dasch G.A.;  
RT "Mapping of monoclonal antibody binding sites on CNBR fragments of  
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia  
RT prowazekii.";  
RL Mol. Immunol. 29:95-105(1992).  
RN [3]  
RP IDENTIFICATION OF CLEAVAGE SITE.  
RX MEDLINE=92104668; PubMed=1729180;  
RA Hackstadt T., Messer R., Cleplak W., Peacock M.G.;  
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
RT membrane protein of rickettsiae: identification of an avirulent  
RT mutant deficient in processing.";  
RL Infect. Immun. 60:159-165(1992).  
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
DR EMBL: L04661; AAB48987.1; -.  
DR InterPro: IPR003858; romPA\_romPB.  
DR Pfam: PF02708; romPA\_romPB; 1.  
KW Antigen; S-layer; Transmembrane; Cell wall.  
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
FT TRANSMEM 1354 1645 32 KDA BETA PEPTIDE.  
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
FT CONFLICT 657 657 H -> N (IN REF. 2).  
FT CONFLICT 842 842 V -> I (IN REF. 2).  
FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

Query Match 6.4%; Score 190; DB 1; Length 1645;  
Best Local Similarity 22.1%; Pred. No. 0.049;  
Matches 157; Conservative 78; Mismatches 258; Indels 218; Gaps 35;

OY 9 WNSALNAAWVAVSELTRNHTKRASATYKTAIVLATLLEFATVOAANTDEDEELESVQRSVY 68  
DB 123 FNFITGAGKSLTITGHCITAOQATTKS--NONVSKNAGCAINDND-----LSGV 172  
OY 69 GSIOASMEGSVELETISLMTNDSKEFVDPIYVTLKAGDNLKIKONTNENTNASSFTYS 128  
DB 173 GSIDFPAASV---LEFNLINPTTQ-----EAPLTLDNKKIVGANGILNITN---- 218  
OY 129 LKKDLTGLINETEKLSFGANKKVNIIISDTGKLNFAKETAGTN-----GDTTVLNGI 182  
DB 219 -----GFVKVSPDKTFA-----GIKTINIDNOGIMFNTTTPDANALNLGGGNTINFNGR 268  
OY 183 GSTLFDMLNTGATTVTNDVNTDDEKRAASKVDLVNMGNNIKG--KPGTTPA----- 224  
DB 269 DG--TGKLVVSKNGNATEPNTVG-----SLGNNLKVIEPDTTAAACKLIA 313  
OY 235 -----SDN-----VDFVETDYVEFLSADTKTTVNVESKD-----NGKKT- 270  
DB 314 NGGAANAIVGTDNAGARAAGFIYSVD-----NENATISGOVYAKXIVIQSANAAGOVTF 368  
OY 271 ----EYKIGAKTSVIEKDKGLVTKGKGNGS--STDEG-----EGLVTAKEVI 314  
DB 369 EHLVDVGLGKTN-FKTAADSKVII-----TENASFGSTDFGNLAVQIVVPNNKILTNFII 423  
OY 315 DAVNK---AGWRKKTTTAGQ--TGQADKFEFVTS-----CTKVTFAAG-----NG 355  
DB 424 DAKNNNGTAG--VTTFNAGTLLVSGMTDPVITNTKAIEVBAGIVQVSGIHGAELRUG 481  
OY 356 TTAATVSKDOGNTVYKVDVNVGDALNVNOLONGSMILDSKAAVSGSGKIVSNVSPSKG 415  
DB 482 NAGSTFKLADGIV-INGPNQNPVNNNALAAGSITLDDSAIT--TGDIT--GAGAVNAAL 536  
OY 416 MDET-----VNINAGNNIETTRNGKNI-----DIATSMT 444  
DB 537 ODITLANDASKILTLGANNIGANAGCAIHFQANGSTIQLTSTQNNIIVDFDIDVTDDGT 596  
OY 445 PQESSVSL-----GAGADAPTLSDVEDEGALVNGSK-----D 475  
DB 597 GAVDASSLTNNQTLTNGISITGATFKTL-----GRPNVSSKTTLLNAGDAVAINELVME 651  
OY 476 ANKPAVIT-NVAAGVKEGDVTVNAQLKVAQNLNRIDNVGNARAGIAQAIATAGLVYA 534  
DB 652 NCGSVHLTHTNTYIITITIANANGKIIIVAADPIINTFPALADGNTLGSASPSLNIHFARK 711  
OY 535 YLPKSMMAIGGCTVYGEAGYA-----IGYSSISAGNNIITKGTASG 576  
DB 712 AANGDSILHIGKGVNL---YANNITTTDANVGSILFRSGGTSISVSGTVGG 758







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Db 766 VGVILNGALSCVNTGNTGNTALATISVAGAKATLGAVIKATTTKLDNNAVFTNPV 765
Oy 288 LVTG---KGKNGSSTDEGEGLTAK---EVIDAVNKA-----GWRKTTTAN-- 330
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 766 VVTGALDNTGNANNGIATFTGTGTGNTGNTALATYVAGGLLRVOGCVKSMINTLT 825
Oy 331 -----GOTGOADK-FETVSGTKVTFASGN-GTATVTS----- 361
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 826 DNASAVFTNPVVTGALDNTGNANNGIATFTGTGTGNTGNTALATISVAGAKATLG 885
Oy 362 -----KDOGNTVTKYDVNVGDLNVNQLNSGWNDSKRAVAGSSKVIISGNVS 410
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 886 GAIKATTTKLTLDNNAVFTNPVVTGATID-----NTG-NANNGIVFTGTGTGNTG 939
Oy 411 PSKGMDETVINAGNNNEI--TRNGKNIDITSMTPQSSVSLGAGADAP-----TLSV 463
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 940 NTNAL-ATVNVAGVTLQAGSLDANNDIFGARSTLENGLDGGAGNAPIYFKGALAN 997
Oy 464 DDEGALNYGSK-----DANK-PVRLTN----- 484
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 998 GNNALLNNTKLTATYHLTGTVAEINIGAGNLFALIDSAGVYTLIMODIHFALDSAL 1057
Oy 485 -----VAPGVEGDV-----TNVAQLKGVAQNLNRRIDN 513
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1058 VLSNLTGVVNNIILADLVAGVDEGTVEFGVGNLIGSNVA---GAARN---IGD 1110
Oy 514 VNGNA-----RAGIAQATITAGLVQAYLPK-----SMAAIGGT-YLGEAGYAI--- 557
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1111 VGGNFENTLLIYNAVITDDVNLGIONVLNNNADFTSTAFNMGITOIDATYITIDAN 1170
Oy 558 -GYSSISAGS-----NMIIKTASGNSR 579
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1171 NGNLNPAGNIKFAHADQILLQNSSGNDR 1200

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RESULT 12
BIGA_SALTY STANDARD: PRF: 1953 AA.
1D BIGA_SALTY STANDARD: PRF: 1953 AA.
AC P25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein biga precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rbs homolog.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=L12 / SGSC1412 / ATCC 700720;
RA MEDLINE=21534948; PubMed=11677609;
RA McEldelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Malyaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L12.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN=L12;
RA MEDLINE=91100301; PubMed=1987123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysG plasmid to overcome limiting streptome

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RT cofactor";
RL J. Bacteriol. 173:325-333(1991).
Cc -1- CAUTION: Ref 3 sequence differs from that shown due to frameshifts
Cc in positions 414 and 732.
Cc -----
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Cc -----
DR EMBL; AF133696; AAD39458.1; -
DR EMBL; AE008859; AAL22340.1; -
DR EMBL; M64606; AAA27042.1; ALT_FRAME.
DR EMBL; M64606; AAA27043.1; ALT_FRAME.
DR PIR; C39200; C39200.
DR PIR; D39200; D39200.
DR Stygene; SG10437; biga.
DR Virulence; Repeat; Signal; Complete proteome.
KM SIGNAL 1 27
FT CHAIN 28 1953
FT FT 101 252
FT REPEAT 101 103
FT REPEAT 104 113
FT REPEAT 114 122
FT REPEAT 123 133
FT REPEAT 134 144
FT REPEAT 145 155
FT REPEAT 156 166
FT REPEAT 167 177
FT REPEAT 178 188
FT REPEAT 189 199
FT REPEAT 200 210
FT REPEAT 211 221
FT REPEAT 222 232
FT REPEAT 233 243
FT REPEAT 244 252
FT CONFLICT 207 207
FT CONFLICT 514 514
FT CONFLICT 1698 1698
FT CONFLICT 1795 1798
FT CONFLICT 1836 1837
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match 6.3%; Score 188; DB 1; Length 1953;
Best Local Similarity 23.6%; Pred. NO. 0.074; Mismatches 222; Indels 212; Gaps 42;
Matches 161; Conservative 87;
Oy 50 NATDEDEEELSVOR-----SVYGSIOASMEGSVELETISLMTNDSKEFVPIYV 101
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 288 NYSQDNQWQLTAPDCKTLNTVGMWDTANAAVIBETQE---NGLWKKDSR---GYLL 340
Oy 102 VTLKAGDNLIKONTNENTNASSFTYSLKKDLTGLI-----NVT-----EKLSPGANGK 152
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 341 I---ADNTTIVISGDOAHNSDRGMDISQDRGVIIISGDRVTNLTGDSVYDGTGW 397
Oy 153 V-----NIISD-----TKGL-----NFAKFTAGTNGDT-----T 176
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 398 ISGDDGTTNTISGSHVYDANATGALISGNGTTTNAGIAVSGGTALIIDGDNATIKNTGT 457
Oy 177 VHLNGIGSTLT-----DMLNTGAT-TVATNDVYTDDEKRAASVYKDLVNG 222
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 458 SDISGSGTGTVIDGNNAVNNDGDMTITDGGTGHITGDVYID-----NMG 505
Oy 223 WKIKGVKPGTTASDNVDVRYDYVEELSADTKTTTVNVEKDN-----GKTEVKICA 276
Cc :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 506 -----STVS-----GAD--ATATLYIEG-DNALVINEGNOT-ISGGA 538
Oy 277 KTSVIREKDKG-----LVTKGK-----KGENGSSTDEGEGLV--AKEVI--DAVVK 319

```



Db 560 VLGVDSVIADGQVIGDQNNIVIGLGSNDGIIYNATTVLVAGISTLNNGCYTLSCGVN 619  
 QY 478 KPVRTINAPGVKEDVDYVNAOLKGYAQNLRNIDVNGNARAGIAQAIATAGLYOAYLP 537  
 Db 620 TGTGYVGLGTIGAGSKFKQVT-----FTTDTYNNLGNITATNATNDGVTVTGTGIAIGFD 675  
 QY 538 GKSMAGIGGCTYLGEAGVAGISYSISAGNMIITKGTASNSNGHPCASASVG 589  
 Db 676 GK--ITLGSVNGNNGVRFADGLISNSTS--MIGTKANNGVTVYTLGNMFAVG 722

RESULT 14

SLAP\_CAME ID SLAP\_CAME STANDARD: PRT: 933 AA.  
 AC P35827.  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE S-layer protein (Surface array protein) (SAP).  
 GN SAP.  
 OS Campylobacter fetus.  
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
 OC Campylobacter.  
 OX NCBI\_TaxID=196;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
 RC STRAIN=84-32 / 23D;  
 RA MEDLINE=90354448; PubMed=2387868;  
 RA Blaser M.J., Gotschlich E.C.;  
 RT "Surface array protein of Campylobacter fetus. Cloning and gene  
 structure";  
 RT J. Biol. Chem. 265:14529-14535(1990).  
 RN [2]  
 RP ERRATUM.  
 RX MEDLINE=91035477; PubMed=2229082;  
 RA Blaser M.J., Gotschlich E.C.;  
 RL J. Biol. Chem. 265:19372-19372(1990).

CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
 OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
 CRITICAL FOR VIRULENCE.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL, J05577; AAA23032.1; -  
 KW Cell wall; S-layer.  
 CC -----  
 SQ SEQUENCE 933 AA: 96757 MW: F88C729B4BA5B1E9 CRC64;

Query Match 6.2%; Score 184; DB 1; Length 933;  
 Best Local Similarity 22.9%; Pred. No. 0.048;  
 Matches 134; Conservative 69; Mismatches 231; Indels 150; Gaps 23;

QY 51 AIDDEDEEELLESYQSRVSGISQASMEGSELEETISLS-MTNSKEVDYIYVTLKAGN 109  
 Db 309 AIDASSVNEVET--GTTAFTAAAGKVDVAGKISALTASRTSV-----N 354  
 QY 110 LKIKONTNENTVASSFT--YSLK---KDLTGLINVENTEKLSEFGANGKKNYISDTGLNF 164  
 Db 355 LKATNTDTITLGNMNTSVNLKORAKDAT-----ITSAMQCKYNNRRRIATITTSAT-- 407  
 QY 165 AKETAGTNGDVTYVHLNGISSTLTMLNTGA-----TTNTNDNVTDDEK---- 209  
 Db 408 AVENILTKVAKHATVNAALGMDKLTATVLDNAALTAIDIKSASTLNLINSVNGPKHLYSS 467

QY 210 -----KRAASYKDYVLNMGNNIKGVKPGTTASDNDVFRVTVDFEELSADTKTTVNV 262  
 Db 468 KRRYCKFKRAAA-----KVLNTTA-----ATDQTVLKAN 498  
 QY 263 SKDNGKRTVEKIGAKTSVIREKDKLVGTGKENGSSYDEGLVTAKEVIDAVKAGW 322  
 Db 499 ATDNSLEPDSATAKTTSVYASGSKTLVIKGA-----EVELTVN-----IDPTAF 543  
 QY 323 RAKTTTANGOTGADKF--EYVTSKTVFPASGNGTTATVSK--DDQGNITVYDVNVGD 378  
 Db 544 NALQSVFGRKTGGGKFSVKTGTGDKIEFV--GTTLEGSYLDAPGNDTLMKSAALT 600  
 QY 379 ALNVNOLNSGMNLDKAVAG---SSGVYISGVNSPSKGMDETVINMGNNIEIRNCK 435  
 Db 601 SANFTWIKNIENVVAISDAVATADLSSARKNSYITITKEADDTLITNKDQV----- 653  
 QY 436 NDIATSMTPPESSVSLGADAPTLVDDEGALNVGSKDANKPVRITVAPGVKEDVY 495  
 Db 654 NFTAADAGSVKLITVTLN--DVTALMIVYKIVLDAARD-----TIALGTAAADKA 703  
 QY 496 NVAOLKGYAQNLRNIDVNGNARAGIAQAIATAGLYOAYLPKSMALIG----- 546  
 Db 704 LV-----IDTGIETINITSLVKATSPETTANTVNMKLDVTSIITDGMQITLGHAG 754  
 QY 547 --GTYLG-----EAGVAGYSISAGNMWIKGTASGNS 578  
 Db 755 TACTDYSKVSMIDASALKAGLTFDASATITLGANATIKGSGADS 798

RESULT 15

HLA\_SERMA ID HLA\_SERMA STANDARD: PRT: 1608 AA.  
 AC P15320;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Hemolysin precursor.  
 GN SHLA.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
 RC STRAIN=SN8;  
 RX MEDLINE=88257037; PubMed=3290200;  
 RA Poole K., Schiebel E., Braun V.;  
 RT "Molecular characterization of the hemolysin determinant of Serratia  
 marcescens";  
 RT J. Bacteriol. 170:3177-3188(1988).  
 RL J. Bacteriol. 170:3177-3188(1988).  
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
 CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
 DEFINED.  
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
 ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
 REQUIRES SHLB FUNCTION.  
 CC -1- SUBCELLULAR LOCATION: Outer membrane.  
 CC -1- SIMILARITY: TO P-MIRABILIS HEMOLYSIN (HPMA).  
 CC -----  
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 CC EMBL, M22618; AAA50323.1; -  
 DR PIR: A28182; A28182.  
 KW Hemolysis; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 1608 HEMOLYSIN.  
 FT CHAIN 31 1608 HEMOLYSIN.  
 SQ SEQUENCE 1608 AA: 165078 MW: D669B476FE7DAD51 CRC64;

QY 210 -----KRAASYKDYVLNMGNNIKGVKPGTTASDNDVFRVTVDFEELSADTKTTVNV 262  
 Db 468 KRRYCKFKRAAA-----KVLNTTA-----ATDQTVLKAN 498  
 QY 263 SKDNGKRTVEKIGAKTSVIREKDKLVGTGKENGSSYDEGLVTAKEVIDAVKAGW 322  
 Db 499 ATDNSLEPDSATAKTTSVYASGSKTLVIKGA-----EVELTVN-----IDPTAF 543  
 QY 323 RAKTTTANGOTGADKF--EYVTSKTVFPASGNGTTATVSK--DDQGNITVYDVNVGD 378  
 Db 544 NALQSVFGRKTGGGKFSVKTGTGDKIEFV--GTTLEGSYLDAPGNDTLMKSAALT 600  
 QY 379 ALNVNOLNSGMNLDKAVAG---SSGVYISGVNSPSKGMDETVINMGNNIEIRNCK 435  
 Db 601 SANFTWIKNIENVVAISDAVATADLSSARKNSYITITKEADDTLITNKDQV----- 653  
 QY 436 NDIATSMTPPESSVSLGADAPTLVDDEGALNVGSKDANKPVRITVAPGVKEDVY 495  
 Db 654 NFTAADAGSVKLITVTLN--DVTALMIVYKIVLDAARD-----TIALGTAAADKA 703  
 QY 496 NVAOLKGYAQNLRNIDVNGNARAGIAQAIATAGLYOAYLPKSMALIG----- 546  
 Db 704 LV-----IDTGIETINITSLVKATSPETTANTVNMKLDVTSIITDGMQITLGHAG 754  
 QY 547 --GTYLG-----EAGVAGYSISAGNMWIKGTASGNS 578  
 Db 755 TACTDYSKVSMIDASALKAGLTFDASATITLGANATIKGSGADS 798



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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:37 ; Search time 168.02 Seconds  
(without alignments)  
609.529 Million cell updates/sec

Title: US-09-771-382-2

Perfect score: 2987  
Sequence: 1 MKKIRIINNSALNMAVAVS.....TASGNSRGHFGASASGYQM 592

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_19:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.protist:\*  
13: sp.virus:\*  
14: sp.unclassified:\*  
15: sp.rviro:\*  
16: sp.bacteriophage:\*  
17: sp.archaeal:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2987   | 100.0       | 592    | 2  | 093QY2             |
| 2          | 2942   | 98.5        | 592    | 2  | 09JPS9             |
| 3          | 2779   | 93.0        | 592    | 16 | 09JQW4             |
| 4          | 2699.5 | 90.4        | 599    | 2  | 09JPS8             |
| 5          | 2696   | 90.3        | 594    | 2  | 09JPI3             |
| 6          | 2692   | 90.1        | 594    | 2  | 09JPS2             |
| 7          | 2667   | 89.3        | 598    | 2  | 09JPS0             |
| 8          | 2664   | 89.2        | 594    | 2  | 09JPH7             |
| 9          | 2658   | 89.0        | 598    | 2  | 093QY5             |
| 10         | 2653   | 88.8        | 598    | 2  | 09JPS9             |
| 11         | 2645   | 88.6        | 590    | 2  | 09JPS3             |
| 12         | 2636   | 88.2        | 594    | 2  | 093QY4             |
| 13         | 2623   | 87.8        | 600    | 2  | 09JPS6             |
| 14         | 2573.5 | 86.2        | 591    | 16 | 09JRI8             |
| 15         | 2569.5 | 86.0        | 591    | 2  | 09JPS7             |
| 16         |        |             |        |    | 09JPS7 neisseria m |

|    |        |      |      |    |        |                    |
|----|--------|------|------|----|--------|--------------------|
| 17 | 2566   | 85.9 | 600  | 2  | 09JPS5 | 09JPS5 neisseria m |
| 18 | 2554.5 | 85.5 | 591  | 2  | 093QY3 | 093QY3 neisseria m |
| 19 | 2552   | 85.4 | 592  | 2  | 09AQF0 | 09AQF0 neisseria m |
| 20 | 2540.5 | 85.1 | 595  | 2  | 09JPH0 | 09JPH0 neisseria m |
| 21 | 2527.5 | 84.6 | 599  | 2  | 09JPS8 | 09JPS8 neisseria m |
| 22 | 2526   | 84.6 | 598  | 2  | 09JPS7 | 09JPS7 neisseria m |
| 23 | 2490.5 | 83.4 | 589  | 2  | 093QY1 | 093QY1 neisseria m |
| 24 | 2478.5 | 83.0 | 589  | 2  | 09JPI0 | 09JPI0 neisseria m |
| 25 | 2363.5 | 79.1 | 526  | 2  | 09JPS4 | 09JPS4 neisseria m |
| 26 | 2361.5 | 79.1 | 530  | 2  | 09JPS1 | 09JPS1 neisseria m |
| 27 | 1146   | 38.4 | 2353 | 2  | P71401 | P71401 haemophilus |
| 28 | 1014   | 33.9 | 1098 | 2  | 048152 | 048152 haemophilus |
| 29 | 416.5  | 13.9 | 1299 | 16 | 09F3X6 | 09F3X6 pasteurella |
| 30 | 392.5  | 13.1 | 2059 | 16 | 09PD50 | 09PD50 xylella fas |
| 31 | 373.5  | 12.5 | 1107 | 2  | 09F2D8 | 09F2D8 salmonella  |
| 32 | 371    | 12.4 | 1190 | 16 | 09PC04 | 09PC04 xylella fas |
| 33 | 345    | 11.6 | 2712 | 16 | 09F3X5 | 09F3X5 pasteurella |
| 34 | 271.5  | 9.1  | 1291 | 16 | 092K07 | 092K07 rhizobium m |
| 35 | 256    | 8.6  | 1004 | 16 | 09PD63 | 09PD63 xylella fas |
| 36 | 245.5  | 8.2  | 1953 | 16 | 098H72 | 098H72 rhizobium 1 |
| 37 | 235.5  | 7.9  | 1265 | 2  | 09FDA0 | 09FDA0 xanthomonas |
| 38 | 231    | 7.7  | 1536 | 2  | 048031 | 048031 haemophilus |
| 39 | 230.5  | 7.7  | 3930 | 16 | 098E20 | 098E20 rhizobium 1 |
| 40 | 229.5  | 7.7  | 2276 | 2  | 093T66 | 093T66 staphylococ |
| 41 | 228.5  | 7.6  | 989  | 2  | 09XD84 | 09XD84 escherichia |
| 42 | 227.5  | 7.6  | 1112 | 2  | 052781 | 052781 campylobact |
| 43 | 225    | 7.5  | 1109 | 2  | 053505 | 053505 campylobact |
| 44 | 223.5  | 7.5  | 1557 | 2  | 09RN12 | 09RN12 haemophilus |
| 45 | 223.5  | 7.5  | 4919 | 2  | 09ZHL0 | 09ZHL0 haemophilus |

#### ALIGNMENTS

RESULT 1  
ID 093QY2 PRELIMINARY: PRT: 592 AA.  
AC 093QY2.  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
CN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H41;  
RA Peak 1.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157609; AAK68870.1; -  
SQ SEQUENCE 592 AA: 61869 MW: P9403A0BA18FEAF CRC64:

Query Match 100.0%; Score 2987; DB 2; Length 592;  
Best Local Similarity 100.0%; Pred. No. 6.1e-115;  
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| QY | 1   | MKKIRIINNSALNMAVAVSELTRNHTRKASATVKTAVLATVLLFATVQANATDEDEEEL   | 60  |
| DB | 1   | MKKIRIINNSALNMAVAVSELTRNHTRKASATVKTAVLATVLLFATVQANATDEDEEEL   | 60  |
| QY | 61  | ESVQSVVGSIOASMEGSVELETTISLMTNDSEKVPYIVVTLKAGDNLTKQNTNMT       | 120 |
| DB | 61  | ESVQSVVGSIOASMEGSVELETTISLMTNDSEKVPYIVVTLKAGDNLTKQNTNMT       | 120 |
| QY | 121 | NASSFTYSLKQDLTGTLINVEETKLSFGANGKKVNIISPTKGLNFAKETAGTGGDTTVHLN | 180 |
| DB | 121 | NASSFTYSLKQDLTGTLINVEETKLSFGANGKKVNIISPTKGLNFAKETAGTGGDTTVHLN | 180 |

QY 181 GIGSTLTDLMLNTGATTNTVNDVTDDEKRAASVSKDVLNAGWNKGVKPGTTASDNVDF 240  
| | | | |  
DB 181 GIGSTLTDLMLNTGATTNTVNDVTDDEKRAASVSKDVLNAGWNKGVKPGTTASDNVDF 240  
QY 241 VRRYDVEFLSADTKTTTAVESKDNCKTEVKIGATSVYIKEDGKLVYKKGKGENSS 300  
| | | | |  
DB 241 VRRYDVEFLSADTKTTTAVESKDNCKTEVKIGATSVYIKEDGKLVYKKGKGENSS 300  
QY 301 TDEEGELVTAKEVIDAVNKKAGWRKTTTANGOTGOADKFEVTSVSGTVTFASGNGTATV 360  
| | | | |  
DB 301 TDEEGELVTAKEVIDAVNKKAGWRKTTTANGOTGOADKFEVTSVSGTVTFASGNGTATV 360  
QY 361 SKDDQGNITVYKDVNVDALNVNQLQNSGWNLDKAAVAGSSGKVIISGNVSPSKGMDTV 420  
| | | | |  
DB 361 SKDDQGNITVYKDVNVDALNVNQLQNSGWNLDKAAVAGSSGKVIISGNVSPSKGMDTV 420  
QY 421 NINAGNNIETTRNGKNIDITSMTPPFSSVSLGAGADAPLTSVDDGALNVGSKDANKPV 480  
| | | | |  
DB 421 NINAGNNIETTRNGKNIDITSMTPPFSSVSLGAGADAPLTSVDDGALNVGSKDANKPV 480  
QY 481 RITNVAPGVEGDVTNVAQLKGVANLNRIIDNVNGNARAGIAQAITAGLVQAYLPKGS 540  
| | | | |  
DB 481 RITNVAPGVEGDVTNVAQLKGVANLNRIIDNVNGNARAGIAQAITAGLVQAYLPKGS 540  
QY 541 MMAIGGTTYGEAGYAGYSSISAGNMIIKGTASGNSRGHFGASASVGYOM 592  
| | | | |  
DB 541 MMAIGGTTYGEAGYAGYSSISAGNMIIKGTASGNSRGHFGASASVGYOM 592

RESULT 2  
QJUP59 PRELIMINARY; PRT; 592 AA.  
ID QJUP59  
AC QJUP59;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=860800;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Masiagnan V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Ratelli C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratelli G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappunoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226361; AAF42510.1; -;  
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 98.5%; Score 2942; DB 2; Length 592;  
Best Local Similarity 98.6%; Pred. No. 4.2e-113;  
Matches 584; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MNKYRITMSALNAAVAASELTPNHRKRSATVKTAVLATILFATVQANATDEDEBEL 60  
| | | | |  
DB 1 MNKYRITMSALNAAVAASELTPNHRKRSATVKTAVLATILFATVQANATDEDEBEL 60  
QY 61 ESYORSYVSGISQASMEGSELETISLMTNDSKEFVDPYIVTLTKAGDNLIKONTMENT 120  
| | | | |  
DB 61 ESYORSYVSGISQASMEGSELETISLMTNDSKEFVDPYIVTLTKAGDNLIKONTMENT 120  
QY 121 NASSFTYSLKDLTGLINVTETKISFGANGKKNVVISDTYGLNFAKTAGNGDTTYHLN 180  
| | | | |

DB 121 NASSFTYSLKDLTGLINVTETKISFGANGKKNVVISDTYGLNFAKTAGNGDTTYHLN 180  
| | | | |  
QY 181 GIGSTLTDLMLNTGATTNTVNDVTDDEKRAASVSKDVLNAGWNKGVKPGTTASDNVDF 240  
| | | | |  
DB 181 GIGSTLTDLMLNTGATTNTVNDVTDDEKRAASVSKDVLNAGWNKGVKPGTTASDNVDF 240  
QY 241 VRRYDVEFLSADTKTTTAVESKDNCKTEVKIGATSVYIKEDGKLVYKKGKGENSS 300  
| | | | |  
DB 241 VRRYDVEFLSADTKTTTAVESKDNCKTEVKIGATSVYIKEDGKLVYKKGKGENSS 300  
QY 301 TDEEGELVTAKEVIDAVNKKAGWRKTTTANGOTGOADKFEVTSVSGTVTFASGNGTATV 360  
| | | | |  
DB 301 TDEEGELVTAKEVIDAVNKKAGWRKTTTANGOTGOADKFEVTSVSGTVTFASGNGTATV 360  
QY 361 SKDDQGNITVYKDVNVDALNVNQLQNSGWNLDKAAVAGSSGKVIISGNVSPSKGMDTV 420  
| | | | |  
DB 361 SKDDQGNITVYKDVNVDALNVNQLQNSGWNLDKAAVAGSSGKVIISGNVSPSKGMDTV 420  
QY 421 NINAGNNIETTRNGKNIDITSMTPPFSSVSLGAGADAPLTSVDDGALNVGSKDANKPV 480  
| | | | |  
DB 421 NINAGNNIETTRNGKNIDITSMTPPFSSVSLGAGADAPLTSVDDGALNVGSKDANKPV 480  
QY 481 RITNVAPGVEGDVTNVAQLKGVANLNRIIDNVNGNARAGIAQAITAGLVQAYLPKGS 540  
| | | | |  
DB 481 RITNVAPGVEGDVTNVAQLKGVANLNRIIDNVNGNARAGIAQAITAGLVQAYLPKGS 540  
QY 541 MMAIGGTTYGEAGYAGYSSISAGNMIIKGTASGNSRGHFGASASVGYOM 592  
| | | | |  
DB 541 MMAIGGTTYGEAGYAGYSSISAGNMIIKGTASGNSRGHFGASASVGYOM 592

RESULT 3  
QJUM4 PRELIMINARY; PRT; 592 AA.  
ID QJUM4  
AC QJUM4;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE POTATIVE SURFACE FLIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).  
GN NMA1200 OR GNA992.  
OS Neisseria meningitidis (serogroup A), and  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699, 487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE=20222556; PubMed=10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
Davies K.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,  
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,  
Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
Whitehead S., Spratt B.G., Bartell B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria  
meningitidis 22491.";  
RL Nature 404:502-506(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=205900, B2133, F6124, AND 22491;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Masiagnan V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Ratelli C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratelli G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappunoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AL162755; CAB84461.1; -;  
EMBL: AF226357; AAF42506.1; -;

DR EMBL: AF226365; AAF42514.1; -  
 DR EMBL: AF226373; AAF42522.1; -  
 DR EMBL: AF226386; AAF42535.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EBF8754 CRC64;

Query Match 93.0%; Score 2779; DB 16; Length 592;  
 Best Local Similarity 93.9%; Pred. No. 1.9e-106;  
 Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

OY 1 MNKIRIINNSALNMAVAASELNRHHTKRASATVKTAVLATLILFATVQANATDEDEEEL 60  
 DB 1 MNKIRIINNSALNMAVAASELNRHHTKRASATVKTAVLATLILFATVQANATDEDEEEL 60  
 OY 61 ESVQSVSGSIQASMEGSELETTISLMTNDSKEFVDPYIVTTLKAGDLKIKONTNMT 120  
 DB 61 ESVQSVSGSIQASMEGSELETTISLMTNDSKEFVDPYIVTTLKAGDLKIKONTNMT 120  
 OY 121 NASSFTYSLKRDLTGLINVEETKLSFGANGKRVNIISDTKGLNPAKETAGTNGDTVHLN 180  
 DB 121 NASSFTYSLKRDLTGLINVEETKLSFGANGKRVNIISDTKGLNPAKETAGTNGDTVHLN 180  
 OY 181 GIGSTLTDLMTGATTVNTNDVTDDKKRAASYKVDLNAQMNKIGVPGTTA--SDNV 238  
 DB 181 GIGSTLTDLMTGATTVNTNDVTDDKKRAASYKVDLNAQMNKIGVPGTTA--SDNV 238  
 OY 239 DEVRITDYVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKENG 298  
 DB 239 DEVRITDYVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKENG 298  
 OY 299 SSTDEGEGLVTAKEVIDAIVKAGMRKTTTANGOTGQADKEFTVSGVNTVTSASGCTTA 358  
 DB 299 SSTDEGEGLVTAKEVIDAIVKAGMRKTTTANGOTGQADKEFTVSGVNTVTSASGCTTA 358  
 OY 359 TVSKDQGNITVYDVNVGDALNVNOLNSGWNLDLSKAVAGSSGKVISGNVSPSKGMD 418  
 DB 359 TVSKDQGNITVYDVNVGDALNVNOLNSGWNLDLSKAVAGSSGKVISGNVSPSKGMD 418  
 OY 419 TVNINAGNNEIETRNKKNIDTATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANK 478  
 DB 419 TVNINAGNNEIETRNKKNIDTATSMTPQFSSVSLGAGADAPLTVDDGALNVGSKDANK 478  
 OY 479 PVRITNVAPGVKESDVTNAOLKGYAQNINNRIDNVNNGARAGINQATITAGLYQAYLPG 538  
 DB 479 PVRITNVAPGVKESDVTNAOLKGYAQNINNRIDNVNNGARAGINQATITAGLYQAYLPG 538  
 OY 539 KSMMAIGGTYLGEAGYAGYSSISAGSNMIIKGTASGNSRGHFGASASVGYOM 592  
 DB 539 KSMMAIGGTYLGEAGYAGYSSISAGSNMIIKGTASGNSRGHFGASASVGYOM 592

## RESULT 4

O9JPR8 PRELIMINARY; PRT: 599 AA.  
 AC O9JPR8:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA992 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGH38;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizsa M., Scalapato V., Massignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jemmings G.T., Baldi U., Bartolini E., Capeccchi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti R., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H38;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jemmings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF226383; AAF42532.1; -  
 DR EMBL: AF157608; AAK68869.1; -  
 SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 90.4%; Score 2699.5; DB 2; Length 599;  
 Best Local Similarity 91.2%; Pred. No. 3.4e-103;  
 Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

OY 1 MNKIRIINNSALNMAVAASELNRHHTKRASATVKTAVLATLILFATVQANATDEDEEEL 60  
 DB 1 MNKIRIINNSALNMAVAASELNRHHTKRASATVKTAVLATLILFATVQANATDEDEEEL 60  
 OY 61 ESVQSVSGSIQASMEGSELETTISLMTNDSKEFVDPYIVTTLKAGDLKIKONTNMT 114  
 DB 61 ESVQSVSGSIQASMEGSELETTISLMTNDSKEFVDPYIVTTLKAGDLKIKONTNMT 114  
 OY 115 --NTNENTVASSFTYSLKRDLTGLINVEETKLSFGANGKRVNIISDTKGLNPAKETAGTN 172  
 DB 115 --NTNENTVASSFTYSLKRDLTGLINVEETKLSFGANGKRVNIISDTKGLNPAKETAGTN 172  
 OY 173 GPTVHLNIGSTLTDMLNTGATTVNTNDVTDDKKRAASYKVDLNAQMNKIGVPGT 232  
 DB 173 GPTVHLNIGSTLTDMLNTGATTVNTNDVTDDKKRAASYKVDLNAQMNKIGVPGT 232  
 OY 233 TASDNDVFRITDYVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKG 292  
 DB 233 TASDNDVFRITDYVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKG 292  
 OY 299 SSTDEGEGLVTAKEVIDAIVKAGMRKTTTANGOTGQADKEFTVSGVNTVTSASGCTTA 352  
 DB 299 SSTDEGEGLVTAKEVIDAIVKAGMRKTTTANGOTGQADKEFTVSGVNTVTSASGCTTA 352  
 OY 359 TVSKDQGNITVYDVNVGDALNVNOLNSGWNLDLSKAVAGSSGKVISGNVSPSKGMD 412  
 DB 359 TVSKDQGNITVYDVNVGDALNVNOLNSGWNLDLSKAVAGSSGKVISGNVSPSKGMD 412  
 OY 413 KGMDETIVNINAGNNEIETRNKKNIDTATSMTPQFSSVSLGAGADAPLTVDDGALNVG 472  
 DB 413 KGMDETIVNINAGNNEIETRNKKNIDTATSMTPQFSSVSLGAGADAPLTVDDGALNVG 472  
 OY 479 PVRITNVAPGVKESDVTNAOLKGYAQNINNRIDNVNNGARAGINQATITAGLYQAYLPG 532  
 DB 479 PVRITNVAPGVKESDVTNAOLKGYAQNINNRIDNVNNGARAGINQATITAGLYQAYLPG 532  
 OY 533 QAYLPKSMMAIGGTYLGEAGYAGYSSISAGSNMIIKGTASGNSRGHFGASASVGYOM 592  
 DB 533 QAYLPKSMMAIGGTYLGEAGYAGYSSISAGSNMIIKGTASGNSRGHFGASASVGYOM 592

## RESULT 5

O9JPR8 PRELIMINARY; PRT: 594 AA.  
 AC O9JPR8:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

NCBI\_TaxID=487;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND B2332;  
RC MEDLINE=20175756; PubMed=10710308;  
RA Pliza M., Scariato V., Maignan V., Giuliani M.M., Arico' B.,  
R Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
R Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
R Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
R Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
R Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
R Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -;  
DR EMBL: AF226379; AAF42528.1; -;  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;

Query Match 90.3%; Score 2696; DB 2; Length 594;

Best Local Similarity 91.2%; Pred. No. 4.7e-103;  
Matches 547; Conservative 11; Mismatches 28; Indels 14; Gaps 4;

```
QY 1 MNKIYRIIMNSALNAAWVAVSELTFRNHTKRASATVATLTLFATVOANATDEDEEEL 60
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 1 MNKIYRIIMNSALNAAWVAVSELTFRNHTKRASATVATLTLFATVOASTTD-DDDLYL 59
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 61 ESVORSY-VGSIOASMGSEVLETLISMTNDS-----KEFDPYIVYTLKAGDNLKI 112
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 60 EPVORTAPVLSFHADSEGTGEKE-----VTEDSMWGVYFPKKGVLTAAGTTLKAGDNLKI 114
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 113 KONENMTNASSFTYSLKQDLTGLINETEKLSPGANGKKNITSDPKGLNFAKETAGTN 172
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 115 KONIDENTNASSFTYSLKQDLTGLINETEKLSPGANGKKNITSDPKGLNFAKETAGTN 174
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 173 GDTTVHLNGIGSTLLDMLNTGATTNTNDVYDDEKRRASVYKDVNLNAGNINIGVRPGT 232
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 175 GDTTVHLNGIGSTLLDMLNTGATTNTNDVYDDEKRRASVYKDVNLNAGNINIGVRPGT 234
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 233 TASDNVDFVRYDVEFLSADTKTTTYNVESKDKGKTEYKIGAKTSYIKKDKLVTGK 292
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 235 TASDNVDFVRYDVEFLSADTKTTTYNVESKDKGKTEYKIGAKTSYIKKDKLVTGK 294
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 293 GKGENGSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGAQDKFETVSGTKVTFAS 352
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 295 DKGENGSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGAQDKFETVSGTKVTFAS 354
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 353 GNGTTATVSKDQGNITVKKYDVNVDALNVQNLONGSNWIDSKAVAGSSGKVIISGNVSPS 412
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 355 GNGTTATVSKDQGNITVKKYDVNVDALNVQNLONGSNWIDSKAVAGSSGKVIISGNVSPS 414
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 413 KGKDEVTNINAGNIIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSDDEGALNVG 472
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 415 KGKDEVTNINAGNIIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSDDEGALNVG 474
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 473 SKDANKPVRITNVAPGVKEGVTNVAAQLKGYAQNILNRIIDVNVGNARAGIAQAIATAGLV 532
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 475 SKDANKPVRITNVAPGVKEGVTNVAAQLKGYAQNILNRIIDVNVGNARAGIAQAIATAGLV 534
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 533 QAYLPKSKMAIIGGTYLGEAGVAIGYSSISAGGNNIITKTASGNSRCHFGASASVGYOW 592
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 535 QAYLPKSKMAIIGGTYLGEAGVAIGYSSISAGGNNIITKTASGNSRCHFGASASVGYOW 594
    |||.....|.....|.....|.....|.....|.....|.....|.....|
```

RESULT 6

Q9JPS2 ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE OUTER MEMBRANE PROTEIN GNA992.

GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RC MEDLINE=20175756; PubMed=10710308;  
RA Pliza M., Scariato V., Maignan V., Giuliani M.M., Arico' B.,  
R Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
R Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
R Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
R Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
R Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
R Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -;  
DR EMBL: AF226376; AAF42525.1; -;  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 90.1%; Score 2692; DB 2; Length 594;

Best Local Similarity 91.0%; Pred. No. 6.9e-103;  
Matches 546; Conservative 11; Mismatches 29; Indels 14; Gaps 4;

```
QY 1 MNKIYRIIMNSALNAAWVAVSELTFRNHTKRASATVATLTLFATVOANATDEDEEEL 60
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 1 MNKIYRIIMNSALNAAWVAVSELTFRNHTKRASATVATLTLFATVOASTTD-DDDLYL 59
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 61 ESVORSY-VGSIOASMGSEVLETLISMTNDS-----KEFDPYIVYTLKAGDNLKI 112
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 60 EPVORTAPVLSFHADSEGTGEKE-----VTEDSMWGVYFPKKGVLTAAGTTLKAGDNLKI 114
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 113 KONENMTNASSFTYSLKQDLTGLINETEKLSPGANGKKNITSDPKGLNFAKETAGTN 172
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 115 KONIDENTNASSFTYSLKQDLTGLINETEKLSPGANGKKNITSDPKGLNFAKETAGTN 174
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 173 GDTTVHLNGIGSTLLDMLNTGATTNTNDVYDDEKRRASVYKDVNLNAGNINIGVRPGT 232
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 175 GDTTVHLNGIGSTLLDMLNTGATTNTNDVYDDEKRRASVYKDVNLNAGNINIGVRPGT 234
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 233 TASDNVDFVRYDVEFLSADTKTTTYNVESKDKGKTEYKIGAKTSYIKKDKLVTGK 292
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 235 TASDNVDFVRYDVEFLSADTKTTTYNVESKDKGKTEYKIGAKTSYIKKDKLVTGK 294
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 293 GKGENGSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGAQDKFETVSGTKVTFAS 352
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 295 DKGENGSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGAQDKFETVSGTKVTFAS 354
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 353 GNGTTATVSKDQGNITVKKYDVNVDALNVQNLONGSNWIDSKAVAGSSGKVIISGNVSPS 412
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 355 GNGTTATVSKDQGNITVKKYDVNVDALNVQNLONGSNWIDSKAVAGSSGKVIISGNVSPS 414
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 413 KGKDEVTNINAGNIIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSDDEGALNVG 472
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 415 KGKDEVTNINAGNIIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLVSDDEGALNVG 474
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 473 SKDANKPVRITNVAPGVKEGVTNVAAQLKGYAQNILNRIIDVNVGNARAGIAQAIATAGLV 532
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 475 SKDANKPVRITNVAPGVKEGVTNVAAQLKGYAQNILNRIIDVNVGNARAGIAQAIATAGLV 534
    |||.....|.....|.....|.....|.....|.....|.....|.....|

QY 533 QAYLPKSKMAIIGGTYLGEAGVAIGYSSISAGGNNIITKTASGNSRCHFGASASVGYOW 592
    |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 535 QAYLPKSKMAIIGGTYLGEAGVAIGYSSISAGGNNIITKTASGNSRCHFGASASVGYOW 594
    |||.....|.....|.....|.....|.....|.....|.....|.....|
```

RESULT 7

Q9JPT0 ID Q9JPT0 PRELIMINARY; PRT; 598 AA.

AC Q9JPT0;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)



DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2996;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226359; AAF42508.1; -  
 SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 89.3%; Score 2667; DB 2; Length 598;  
 Best Local Similarity 89.6%; Pred. No. 7.3e-102;  
 Matches 543; Conservative 11; Mismatches 30; Indels 22; Gaps 6;

OY 1 MNKRIIINNSALNANAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANATDEDEEEL 60  
 DB 1 MNKRIIINNSALNANAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANATD-DDDLYL 59  
 OY 61 ESYVR-SVYGSIOASMEGSVELETTISLMTNDSKEVPYI-----VTLKAGDNL 110  
 DB 60 EPVQRTAVVLSFRSDKEGTEGEGE-----TEDSNMAY--YFDEKRYLKAGATILKAGDNL 112  
 OY 111 KIKQNTNENTNA-----SFTYSLKDKDTGLINYTEKLSFGANGKRYNIISDRLGKLNFAK 166  
 DB 113 KIKQNTNENTNENTNDSSTFYSLKDKDTGLINYTEKLSFGANGKRYNIISDRLGKLNFAK 172  
 OY 167 ETAGTNGDTVHLNGIGSTLTDLMLNTGATTNTVNDVTDDEKKRAASVADVLNAGMNK 226  
 DB 173 ETAGTNGDPTVHLNGIGSTLTDLMLNTGATTNTVNDVTDDEKKRAASVADVLNAGMNK 232  
 OY 227 GVKPGTTASNDVDFVRYTDFVEFLSADTKTTTVNVESKNGKTEYKIGAKTSVIKEKDQ 286  
 DB 223 GVKPGTTASNDVDFVRYTDFVEFLSADTKTTTVNVESKNGKTEYKIGAKTSVIKEKDQ 292  
 OY 287 KLVGTGKGKENGSSDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKEFTVTSGT 346  
 DB 293 KLVGTGKGKENGSSDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKEFTVTSGT 352  
 OY 347 KYTFASGNGTTATVSKDDGQNTITVKYDVNVGDALNVNOLNSGMNLSKRAVASSGKVIS 406  
 DB 353 KYTFASGNGTTATVSKDDGQNTITVKYDVNVGDALNVNOLNSGMNLSKRAVASSGKVIS 412  
 OY 407 GNVSPSKGKMDDEVNINAGNNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLVSVD 466  
 DB 413 GNVSPSKGKMDDEVNINAGNNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLVSVD 472  
 OY 467 GALNVSCKANKPVRITTNVAPGVKEGDVTNVVQALKGVAQNLNRINDVNGNAGIAQAI 526  
 DB 473 GALNVSCKANKPVRITTNVAPGVKEGDVTNVVQALKGVAQNLNRINDVNGNAGIAQAI 532  
 OY 527 ATAGLVAQVLPCKSMMAIGGGTYLGEAGYAIGVSSISAGQNMILIKTASGNSRGHGASA 586  
 DB 533 ATAGLVAQVLPCKSMMAIGGGTYRGEAGYAIGVSSISDGMNVIKGTASGNSRGHGTS 592  
 OY 587 SVGYQW 592  
 DB 593 SVGYQW 598

RESULT 8  
 ID 09JPS0 PRELIMINARY; PRI: 598 AA.  
 AC 09JPS0;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA992 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGH15;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226359; AAF42508.1; -  
 DR EMBL: AF157607; AAK68868.1; -  
 SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 89.3%; Score 2667; DB 2; Length 598;  
 Best Local Similarity 89.8%; Pred. No. 7.3e-102;  
 Matches 544; Conservative 10; Mismatches 30; Indels 22; Gaps 6;

OY 1 MNKRIIINNSALNANAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANATDEDEEEL 60  
 DB 1 MNKRIIINNSALNANAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANATD-DDDLYL 59  
 OY 61 ESYVR-SVYGSIOASMEGSVELETTISLMTNDSKEVPYI-----VTLKAGDNL 110  
 DB 60 EPVQRTAVVLSFRSDKEGTEGEGE-----TEDSNMAY--YFDEKRYLKAGATILKAGDNL 112  
 OY 111 KIKQNTNENTNA-----SFTYSLKDKDTGLINYTEKLSFGANGKRYNIISDRLGKLNFAK 166  
 DB 113 KIKQNTNENTNENTNDSSTFYSLKDKDTGLINYTEKLSFGANGKRYNIISDRLGKLNFAK 172  
 OY 167 ETAGTNGDTVHLNGIGSTLTDLMLNTGATTNTVNDVTDDEKKRAASVADVLNAGMNK 226  
 DB 173 ETAGTNGDPTVHLNGIGSTLTDLMLNTGATTNTVNDVTDDEKKRAASVADVLNAGMNK 232  
 OY 227 GVKPGTTASNDVDFVRYTDFVEFLSADTKTTTVNVESKNGKTEYKIGAKTSVIKEKDQ 286  
 DB 223 GVKPGTTASNDVDFVRYTDFVEFLSADTKTTTVNVESKNGKTEYKIGAKTSVIKEKDQ 292  
 OY 287 KLVGTGKGKENGSSDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKEFTVTSGT 346  
 DB 293 KLVGTGKGKENGSSDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGOADKEFTVTSGT 352  
 OY 347 KYTFASGNGTTATVSKDDGQNTITVKYDVNVGDALNVNOLNSGMNLSKRAVASSGKVIS 406  
 DB 353 KYTFASGNGTTATVSKDDGQNTITVKYDVNVGDALNVNOLNSGMNLSKRAVASSGKVIS 412  
 OY 407 GNVSPSKGKMDDEVNINAGNNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLVSVD 466  
 DB 413 GNVSPSKGKMDDEVNINAGNNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPTLVSVD 472

| QY     | 467                                                                   | GALVNGSKDANKPVITVAVPCREKGDYTNVQQLGVGQNLNNRIDNVGNMRAAGIAQAI                   | 526          |
|--------|-----------------------------------------------------------------------|------------------------------------------------------------------------------|--------------|
|        |                                                                       |                                                                              |              |
| Db     | 473                                                                   | GALVNGSKDANKPVITVAVPCREKGDYTNVQQLGVGQNLNNRIDNVGNMRAAGIAQAI <td>532</td>      | 532          |
| QY     | 527                                                                   | ATAGLVQALYLPGRKSMMAIGGTYTLGEAGYALGYGSSISAGNNIINGTASGNSRGHGASA <td>586</td>   | 586          |
|        |                                                                       |                                                                              |              |
| Db     | 533                                                                   | ATAGLVQALYLPGRKSMMAIGGTYTLGEAGYALGYGSSISDPTGNMVIKGTASGNSRGHGASA <td>592</td> | 592          |
| QY     | 587                                                                   | SVGYQW 592 <td></td>                                                         |              |
|        |                                                                       |                                                                              |              |
| Db     | 593                                                                   | SVGYQW 598 <td></td>                                                         |              |
| RESULT | 9                                                                     |                                                                              |              |
| Q9JPH7 |                                                                       |                                                                              |              |
| AC     | Q9JPH7                                                                | PRELIMINARY:                                                                 | PRF: 594 AA. |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Created)                                  |                                                                              |              |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                     |                                                                              |              |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                   |                                                                              |              |
| OS     | OUTER MEMBRANE PROTEIN GMA992 (NMHA OUTER MEMBRANE PROTEIN).          |                                                                              |              |
| GN     | GMA992 OR NMHA.                                                       |                                                                              |              |
| OS     | Neisseria meningitidis.                                               |                                                                              |              |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |                                                                              |              |
| OX     | NCBI_TaxID=487;                                                       |                                                                              |              |
| RN     | [1]                                                                   |                                                                              |              |
| RP     | SEQUENCE FROM N.A.                                                    |                                                                              |              |
| RC     | STRAIN=B2198. AND 297-0;                                              |                                                                              |              |
| RX     | MEDLINE=20175756; PubMed=10710308;                                    |                                                                              |              |
| RA     | Pizza M., Scariello V., Masignani V., Giuliani M.M., Arico' B.,       |                                                                              |              |
| RA     | Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,   |                                                                              |              |
| RA     | Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  |                                                                              |              |
| RA     | Ratti G., Santili L., Savino S., Scarselli M., Storni E., Zuo P.,     |                                                                              |              |
| RA     | Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tietelin H.,     |                                                                              |              |
| RA     | Hood D.W., Jeffries A.C., Sanders N.J., Granoff D.M., Venter C.,      |                                                                              |              |
| RA     | Moxon E.R., Grandi G., Rappuoli R.;                                   |                                                                              |              |
| RT     | "Identification of Vaccine Candidates Against Serogroup B             |                                                                              |              |
| RT     | Meningococcus by Whole-Genome Sequencing.";                           |                                                                              |              |
| RL     | -Science 287:1816-1820(2000).                                         |                                                                              |              |
| RN     | [2]                                                                   |                                                                              |              |
| RP     | SEQUENCE FROM N.A.                                                    |                                                                              |              |
| RC     | STRAIN=B2198.                                                         |                                                                              |              |
| RA     | Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;    |                                                                              |              |
| RT     | "Identification and characterization of a gene encoding a novel outer |                                                                              |              |
| RT     | membrane protein of Neisseria meningitidis.";                         |                                                                              |              |
| RL     | Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.               |                                                                              |              |
| DR     | EMBL: AF226368; AAF42517.1; -                                         |                                                                              |              |
| DR     | EMBL: AF226368; AAF42507.1; -                                         |                                                                              |              |
| DR     | EMBL: AF157604; AAK68865.1; -                                         |                                                                              |              |
| SO     | SEQUENCE 594 AA; 62361 MW; 436BDDDED68263C5C CRC64;                   |                                                                              |              |

|    |                                                                    |              |                    |                |            |        |
|----|--------------------------------------------------------------------|--------------|--------------------|----------------|------------|--------|
|    | Query Match                                                        | 89.2%        | Score 2664         | DB 21          | Length 594 |        |
|    | Best Local Similarity                                              | 90.0%        | Pred. No. 9.6e-102 |                |            |        |
|    | Matches 542:                                                       | Conservative | 9;                 | Mismatches 33; | Indels 18; | Gaps 5 |
| QY | 1 MNKTYRIIMNSALNMAWVSELTRNHTRASATVKTAVLATLTLFATVCANATDEDEEEL       | :            | :                  | :              | :          | :      |
| Dd | 1 MNKYIRIIMNSALNMAWVVSELTNRHTRKRASATVATVLATLLPFTQVANND-DDDLXL      | :            | :                  | :              | :          | :      |
| QY | 61 ESVQR-SVVGSIQASMESVELETTSLSMNTDSKEFYVDYT-----VYLKAGDNL          | :            | :                  | :              | :          | :      |
| Dd | 60 EPVORTAVLVLSFRSKESTGEKEG-----TEDSNAAV-YEPDEKRVLKAGATITLLAAGDNL  | :            | :                  | :              | :          | :      |
| QY | 111 KIKONTNENTASSPTYSGLKKDGLINVERPEKLSFGANGKKVNIIISDTKGINFPAKETAG  | :            | :                  | :              | :          | :      |
| Dd | 113 KIKONTNENTDSSFTTSLKRDLDLTIVSETETPKLSFGANGKNVNTSDTKGINFAKETAG   | :            | :                  | :              | :          | :      |
| QY | 171 TNGDTTVALLNGIGSLTIDMLLNTGATVTWTDNNNVDDDEKKRAASVKDYVLNAGMNIKGVP | :            | :                  | :              | :          | :      |
| Dd | 173 TNGDPYVALNGIGSLTIDTLTNTGATTNTVINDNVTDDEKKRAASVKDYVLNAGMNIKGVAP | :            | :                  | :              | :          | :      |

|    |      |                                                                 |     |
|----|------|-----------------------------------------------------------------|-----|
| Qy | 2.21 | GTTSADNVDFRKYDVEEPLSADKKTITTVANESKDNGKTEVKGAKTSYIKKEDGLVY       | 290 |
| Db | 2.23 | GTTSADNVDFRKYDVEEPLSADKKTITTVANESKDNGKTEVKGAKTSYIKKEDGLVY       | 292 |
| Qy | 2.91 | GKGGANGENSSTDEEGEGLVYAKVEIDAVNKAQWRKKTITTAAGQOQADKFEFTVYSGTKVTF | 350 |
| Db | 2.93 | GKGGANGENSSTDEEGEGLVYAKVEIDAVNKAQWRKKTITTAAGQOQADKFEFTVYSGTKVTF | 352 |
| Qy | 3.51 | ASGKGTATYVSKDDOGNITTYKYDVYVNGDALNVNOLONGSNHLSKAVAGSSGKVISGNVS   | 410 |
| Db | 3.53 | ASGKGTATYVSKDDOGNITTYKYDVYVNGDALNVNOLONGSNHLSKAVAGSSGKVISGNVS   | 412 |
| Qy | 4.11 | PSKGMDETVINAGNNIEITRNKKNIDATSYMPORSSVSLAGADAPLTVSDDEGALN        | 470 |
| Db | 4.13 | PSKGMDETVINAGNNIEITRNKKNIDATSHAPORSSVSLAGADAPLTVSDDEGALN        | 472 |
| Qy | 4.71 | VGSKDANKPVATITNVAVGVKRGDVTNVAOLKGYAQNUNNRIDVNVNGNARAGIAQATATAG  | 530 |
| Db | 4.73 | VGSKDANKPVATITNVAVGVKRGDVTNVAOLKGYAQNUNNRIDVNVNGNARAGIAQATATAG  | 532 |
| Qy | 5.31 | LVQAYLPEKSMMAITGGCTTYGEGAGYATGYSSISAGCMMITIKTASGNSRKHFGASASVGY  | 590 |
| Db | 5.33 | LVQAYLPEKSMMAITGGCTTYGEGAGYATGYSSISDGGMWITIKTASGNSRKHFGASASVGY  | 592 |
| Qy | 5.91 | QW 592                                                          |     |
| Db | 5.93 | QW 594                                                          |     |

| RESULT                                                                | ID              | PRELIMINARY;            | PRT; | 598 AA. |
|-----------------------------------------------------------------------|-----------------|-------------------------|------|---------|
| 0930Y5                                                                | AC              |                         |      |         |
| 0930Y5                                                                | AC              |                         |      |         |
| 0930Y5                                                                | AC              |                         |      |         |
| 01-DEC-2001                                                           | (TREMblrel. 19, | Created)                |      |         |
| 01-DEC-2001                                                           | (TREMblrel. 19, | Last sequence update)   |      |         |
| 01-DEC-2001                                                           | (TREMblrel. 19, | Last annotation update) |      |         |
| NHHA OUTER MEMBRANE PROTEIN.                                          |                 |                         |      |         |
| NHHA.                                                                 |                 |                         |      |         |
| Neisseria meningitidis.                                               |                 |                         |      |         |
| Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |                 |                         |      |         |
| NCCL_TaxID=487;                                                       |                 |                         |      |         |
| [1]                                                                   |                 |                         |      |         |
| SEQUENCE FROM N.A.                                                    |                 |                         |      |         |
| STRAIN=B210;                                                          |                 |                         |      |         |
| Peak I.R., Sitkhantha Y., Dieckelman M., Moxon R., Jennings M.P.;     |                 |                         |      |         |
| "Identification and characterization of a gene encoding a novel outer |                 |                         |      |         |
| membrane protein of Neisseria meningitidis".                          |                 |                         |      |         |
| Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.               |                 |                         |      |         |
| EMBL: AF157603; AAK68864.1; .                                         |                 |                         |      |         |
| SEQUENCE 598 AA: 62687 MW: 18CFEFE6410A15DF CRC64;                    |                 |                         |      |         |

|    | Query Match           | 89.0%;                                                        | Score        | 2658;         | DB         | 2;  | Length | 598; |
|----|-----------------------|---------------------------------------------------------------|--------------|---------------|------------|-----|--------|------|
|    | Best Local Similarity | 89.4%;                                                        | Pred.        | No. 1.7e-101; |            |     |        |      |
|    | Matches               | 542;                                                          | Conservative | 11;           | Mismatches | 31; | Indels | 22;  |
|    |                       |                                                               |              |               |            |     | Gaps   | 6;   |
| QY | 1                     | MNKYIRIINWSALNMAVAVSELTRNHTKRASTVKTAVLATITLPTVQANATDEDEEEL    |              |               |            |     |        | 60   |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| Db | 1                     | MNKISRIIINWSALNMAVYVSELTRNHTKRASTVKTAVLATITLPTVQANATD-DDDLVL  |              |               |            |     |        | 59   |
|    |                       |                                                               |              |               |            |     |        |      |
| QY | 61                    | ESVOR-SVYGSIOASMEGSVELLETSLSMTNRSKFEVPYI-----VYTLKAGDVL       |              |               |            |     |        | 110  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| Db | 60                    | EPVQGTAVVLSFRSDKEBTGEKEG-----TEBSNNAV--YFPEKRVLKAGATITLKAQDVL |              |               |            |     |        | 112  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| QY | 111                   | KIKQNTNNTNA---SSFTYSLKDLTGLINVEFEKLSFGANGKKVNIISPTKGLNFAK     |              |               |            |     |        | 166  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| Db | 113                   | KIKQNTNNTNNTNNTNDSFTYSLKDLTDLTVSETEKLSFGANGKKVNIISPTKGLNFAK   |              |               |            |     |        | 172  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| QY | 167                   | ETAGNCGTPTVHLNIGSTLTDMLNTGATVVTNDYNTDDEKRAASAKVDVLNAGMNK      |              |               |            |     |        | 226  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| Db | 173                   | ETAGNCGPTVHLNIGSTLTDLTDLNTGATTVVTNDYNTDDEKRRRAASAKVDVLNAGMNK  |              |               |            |     |        | 232  |
|    |                       |                                                               |              |               |            |     |        |      |
|    |                       |                                                               |              |               |            |     |        |      |
| QY | 227                   | GAKPGTTASDNVDFVRIYDFVEELSDTRKTTTVNVESSKONGKTEKIGAKTSVIREKDG   |              |               |            |     |        | 286  |

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|||||
Db 233 GYKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNVESKDNKRGTEVIGAKTSVIREKDG 292
OY 287 KLVYTGKGEKNGSSDTEGEGLVYAKEVDAVNAKGRMKTTPANNGTGGADKFEYVTSGT 346
Db 293 KLVYTGKGEKNGSSDTEGEGLVYAKEVDAVNAKGRMKTTPANNGTGGADKFEYVTSGT 352
OY 347 KYTFASGNGTATVSKDDGNTTVKDYVNVGDALNVNOLNSGWNLSRAVAGSSGKVLIS 406
Db 353 KYTFASGNGTATVSKDDGNTTVKDYVNVGDALNVNOLNSGWNLSRAVAGSSGKVLIS 412
OY 407 GNVSPSKGMDETVNNAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDE 466
Db 413 GNVSPSKGMDETVNNAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDE 472
OY 467 GALNVGSKRANKPVRTTNVAPGVKEGDDVTNVQOLKGVNOLNRRIDNVNGNARAGIAQAI 526
Db 473 GALNVGSKRANKPVRTTNVAPGVKEGDDVTNVQOLKGVNOLNRRIDNVNGNARAGIAQAI 532
OY 527 ATAGLVQAVLPKGSMAIGGTYLGEAGYALIGSSISAGNNIITKGTASGNSGHEGASA 586
Db 533 ATAGLVQAVLPKGSMAIGGTYLGEAGYALIGSSISAGNNIITKGTASGNSGHEGASA 592
OY 587 SVGYQM 592
Db 593 SVGYQM 598
```

## RESULT 11

```
O9JPS9 PRELIMINARY: PRT: 598 AA.
AC O9JPS9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1;
SQ SEQUENCE 598 AA: 62718 MW: 9095f8e31ad7c76d CRC64;
```

Query Match 88.8%; Score 2653; DB 2; Length 598;  
Best Local Similarity 89.4%; Pred. No. 2.7e-101;  
Matches 542; Conservative 9; Mismatches 33; Indels 22; Gaps 6;

```
OY 1 MNKIYRIINNSALNMAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANADEDEEEL 60
Db 1 MNKIYRIINNSALNMAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANADEDEEEL 59
OY 61 ESVQR-SVYGSIOASMEGSVELETISLSMTNDSKEFVDYI-----VTLKAGDWL 110
Db 60 EYVQRRAVAVLSFRSDKEGEGKEG-----TEDSNNAV--YFDEKRYLKAGATITLKAGDWL 112
OY 111 KIKONTNENTNA---SFTYSLKDKDGLINVEETKLSFGANGKKVNIISDTKGLNFAK 166
Db 113 KIKONTNENTNENTNDSFTYSLKDKDGLINVEETKLSFGANGKKVNIISDTKGLNFAK 172
```

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OY 167 ETAGNGDTVHLNGIGSTLIDMLNTGATTNTVNDVTDDEKKRAASYKDVNLNAGNNIK 226
Db 173 ETAGNGDTPVHLNGIGSTLIDTLNTGATTNTVNDVTDDEKKRAASYKDVNLNAGNNIK 232
OY 227 GYKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNVESKDNKRGTEVIGAKTSVIREKDG 286
Db 233 GYKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNVESKDNKRGTEVIGAKTSVIREKDG 292
OY 287 KLVYTGKGEKNGSSDTEGEGLVYAKEVDAVNAKGRMKTTPANNGTGGADKFEYVTSGT 346
Db 293 KLVYTGKGEKNGSSDTEGEGLVYAKEVDAVNAKGRMKTTPANNGTGGADKFEYVTSGT 352
OY 347 KYTFASGNGTATVSKDDGNTTVKDYVNVGDALNVNOLNSGWNLSRAVAGSSGKVLIS 406
Db 353 KYTFASGNGTATVSKDDGNTTVKDYVNVGDALNVNOLNSGWNLSRAVAGSSGKVLIS 412
OY 407 GNVSPSKGMDETVNNAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDE 466
Db 413 GNVSPSKGMDETVNNAGNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDE 472
OY 467 GALNVGSKRANKPVRTTNVAPGVKEGDDVTNVQOLKGVNOLNRRIDNVNGNARAGIAQAI 526
Db 473 GALNVGSKRANKPVRTTNVAPGVKEGDDVTNVQOLKGVNOLNRRIDNVNGNARAGIAQAI 532
OY 527 ATAGLVQAVLPKGSMAIGGTYLGEAGYALIGSSISAGNNIITKGTASGNSGHEGASA 586
Db 533 ATAGLVQAVLPKGSMAIGGTYLGEAGYALIGSSISAGNNIITKGTASGNSGHEGASA 592
OY 587 SVGYQM 592
Db 593 SVGYQM 598
```

## RESULT 12

```
O9JPS3 PRELIMINARY: PRT: 590 AA.
AC O9JPS3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Rati G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1;
SQ SEQUENCE 590 AA: 61661 MW: 8AA476AC300D80C8 CRC64;
```

Query Match 88.6%; Score 2645; DB 2; Length 590;  
Best Local Similarity 89.3%; Pred. No. 5.7e-101;  
Matches 533; Conservative 21; Mismatches 31; Indels 12; Gaps 4;

```
OY 1 MNKIYRIINNSALNMAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANADEDEEEL 60
Db 1 MNKIYRIINNSALNMAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANADEDEEEL 60
OY 61 ESVQR-SVYGSIOASMEGSVELETISLSMTNDSKEFVDYI-----VTLKAGDWL 115
```

|    |     |                                                                |     |
|----|-----|----------------------------------------------------------------|-----|
| Db | 61  | DPVQRTVAVLVNSDKDGGTGKEKVE--ENSDMAYFNEKGVLTAGTITLKAGDLKTKQ-     | 118 |
| Qy | 116 | TNEHTNASSFTYSLKKDLTGLINETERKESFGANGKVVNIISDTKGLNPAKETAGTNGDT   | 175 |
| Db | 119 | -----NGTNFYSLSKKDLTDLTSVGETEKLSPSANGKVNVTISDTKGLNPAKETAGTNGDT  | 173 |
| Qy | 176 | TVHLNGIGSTLTDMLNLTNGATTNTNINVTNDDEKKRAASVDYLNAAQWNIKGVKPGTTAS  | 235 |
| Db | 174 | TVHLNGIGSTLTDLTLNLTNGATTNTNINVTNDDEKKRAASVDYLNAAQWNIKGVKPGTTAS | 233 |
| Qy | 236 | DNVDFVRYDYVEFLSADTKTTTVNVESSKONGKKEVIAKTSVIEKDKGLVYTGKGG       | 295 |
| Db | 234 | DNVDFVRYDYVEFLSADTKTTTVNVESSKONGKRTVIAKTSVIEKDKGLVYTGKGG       | 293 |
| Qy | 296 | ENGSTDEGEGLVYAKVEYIDAVNKAQRMTTTTANGOTGADKFEYVTSCTNVTFASGNG     | 355 |
| Db | 294 | ENGSTDEGEGLVYAKVEYIDAVNKAQRMTTTTANGOTGADKFEYVTSCTNVTFASGNG     | 353 |
| Qy | 356 | TTATVYSKDDGNIITVKKDYVNVGDLANNOLNONGSMWNLDSKRAVSGSKVTSGNVSPSKG  | 415 |
| Db | 354 | TTATVYSKDDGNIITVKKDYVNVGDLANNOLNONGSMWNLDSRAVSSGKVTSGNVSPSKG   | 413 |
| Qy | 416 | MDETVINIAGNNIEITRNGKNIDTATSMTPQSFSSVSGAGADAPTLSEVDDDEGALNVSSKD | 475 |
| Db | 414 | MDETVINIAGNNIEITRNGKNIDTATSMTPQSFSSVSGAGADAPTLSEVDDDEGALNVSSKD | 473 |
| Qy | 476 | ANKPVRTITNVA PGVEGDVTNVAOLKGYAQNLRNIDVNGMAFAGIAQAIATAGLVQAY    | 535 |
| Db | 474 | ANKPVRTITNVA PGVEGDVTNVAOLKGYAQNLRNIDVNGMAFAGIAQAIATAGLVQAY    | 533 |
| Qy | 536 | LPKGSMAAIGGGTGLGEGVAYIGVSSISAGGNMTIKCTASGNSGHHGASASVGYOM       | 592 |
| Db | 534 | LPKGSMAAIGGGTGLGEGVAYIGVSSISDGNMTIKCTASGNSGHHGASASVGYOM        | 590 |

|    |     |                                                                  |     |
|----|-----|------------------------------------------------------------------|-----|
| Dd | 115 | KONTNENTMASSFFIYSLUKKDLDTLDSVGETKLSFSSANSNMVNITSDTKGLNPAKKAETAEN | 174 |
| Oy | 173 | GDTVHLNGIGSTFLTDMLLNTGATTVNTNDNVTDDEKKRAASVYKDVINAGMINIKVAPGT    | 232 |
| Dd | 175 | GDTPVHLNGISSTFLDTLLNTGATTVNTNDNVTDDEKKRAASVYKDVINAGMINIKVAPGT    | 234 |
| Oy | 233 | TASNDNVFRTYDYVEELISADTKTTTYNVBSKONGKTEYKIGAKTSVIEKDGKLVTK        | 292 |
| Dd | 235 | TASDNDVDFRTYDYVEELISADTKTTTYNVBSKONGKTEYKIGAKTSVIEKDGKLVTK       | 294 |
| Oy | 293 | KGKENGSTDEGEGLYTAKEYIDAVNKNAGMKTTTTANGOTGADKREYTSIGTYTFAS        | 352 |
| Dd | 295 | DKGENDSSTDEGEGLYTAKEYIDAVNKNAGMKTTTTANGOTGADKREYTSIGTYTFAS       | 354 |
| Oy | 353 | GNCTATYVSKDOGNITYKYVYVNGDALNVQNLONGSMNLDKRAVAGSSSKRYISGANSPTS    | 412 |
| Dd | 355 | GKGTATYVSKDOGNITYKYVYVNGDALNVQNLONGSMNLDKRAVAGSSSKRYISGANSPTS    | 414 |
| Oy | 413 | KGKDEFTYVINAAGNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLTVSDDEGALNVG     | 472 |
| Dd | 415 | KGKDEFTYVINAAGNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLTVSDDEGALNVG     | 474 |
| Oy | 473 | SKDANKPVRITNVAPGVESGVTVNAOLKGAQOLNLRINRVNGNARAGIAQALATAGLV       | 532 |
| Dd | 475 | SKDANKPVRITNVAPGVESGVTVNAOLKGAQOLNLRINRVNGNARAGIAQALATAGLV       | 534 |
| Oy | 533 | QAYLPKGSMAIIGGTYLGEAGVYAIAGSSISAGCNWIIKGTASGNSRGHGASASVYQW       | 592 |
| Dd | 535 | QAYLPKGSMAIIGGTYLGEAGVYAIAGSSISDGCMWIIKGTASGNSRGHGASASVYQW       | 594 |

|        |                                                                       |              |              |
|--------|-----------------------------------------------------------------------|--------------|--------------|
| 0930Y4 | 13                                                                    |              |              |
| ID     | 0930Y4                                                                | PRELIMINARY; | PRT; 594 AA. |
| AC     | 0930Y4;                                                               |              |              |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Created)                                  |              |              |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                     |              |              |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                   |              |              |
| DE     | NHHA OUTER MEMBRANE PROTEIN.                                          |              |              |
| GN     | NHHA.                                                                 |              |              |
| OS     | Neisseria meningitidis.                                               |              |              |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |              |              |
| OX     | NCBI_TaxID=487;                                                       |              |              |
| RN     | [1]                                                                   |              |              |
| RP     | SEQUENCE FROM N.A.                                                    |              |              |
| RC     | STRAIN=EG327.                                                         |              |              |
| RA     | Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.V., Jennings M.P.;    |              |              |
| RT     | "Identification and characterization of a gene encoding a novel outer |              |              |
| RL     | membrane protein of Neisseria meningitidis.";                         |              |              |
| RQ     | Submitted (JUN-1999) to the EMBL/GenBank/DBD databases.               |              |              |
| SE     | EMBL; AF157605; AAK68866.1; -.                                        |              |              |
| SQL    | SEQUENCE 594 AA; 62297 MW; 9DD048B04B3A8EA2 CRC64;                    |              |              |

| Q9JPS6 | 14                                                                    | Q9JPS6 | PRELIMINARY; | PRT; | 600 AA. |
|--------|-----------------------------------------------------------------------|--------|--------------|------|---------|
| ID     | Q9JPS6                                                                |        | PRELIMINARY; | PRT; | 600 AA. |
| AC     | Q9JPS6;                                                               |        |              |      |         |
| DT     | 01-OCT-2000 (TREMblrel, 15, Created)                                  |        |              |      |         |
| DT     | 01-OCT-2000 (TREMblrel, 15, Last sequence update)                     |        |              |      |         |
| DT     | 01-MAR-2001 (TREMblrel, 15, Last annotation update)                   |        |              |      |         |
| DE     | OUTER MEMBRANE PROTEIN GNA92.                                         |        |              |      |         |
| GN     | GNA92.                                                                |        |              |      |         |
| OS     | Neisseria meningitidis.                                               |        |              |      |         |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |        |              |      |         |
| OX     | NCHI_TaxID=487;                                                       |        |              |      |         |
| RN     | [1]                                                                   |        |              |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |        |              |      |         |
| RC     | STRAIN=E26;                                                           |        |              |      |         |
| RX     | MEDLINE=20175756; PubMed=10710308;                                    |        |              |      |         |
| RA     | Pizza M., Scarlato V., Masiiani V., Giuliani M.M., Arico' B.,         |        |              |      |         |
| RA     | Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,     |        |              |      |         |
| RA     | Gattioli C.L., Luzi E., Manetti R., Marchetti E., Mora M., Nuti S.,   |        |              |      |         |
| RA     | Ratti G., Santilli L., Savino S., Scarselli M., Storni E., Zuo P.,    |        |              |      |         |
| RA     | Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,      |        |              |      |         |
| RA     | Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,     |        |              |      |         |
| RA     | Moxon E.R., Grandi G., Rappuoli R.;                                   |        |              |      |         |
| RT     | "Identification of Vaccine Candidates Against Serogroup B             |        |              |      |         |
| RT     | Meningococcus by Whole-Genome Sequencing."                            |        |              |      |         |
| RL     | Science 287:1816-1820(2000).                                          |        |              |      |         |
| DR     | EMBL, AF226371, AAF42520.1; -                                         |        |              |      |         |
| SO     | SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;                    |        |              |      |         |

|    | Query Match                                                       | 88.2%            | Score 2636;         | DB 2;      | Length 594; |
|----|-------------------------------------------------------------------|------------------|---------------------|------------|-------------|
|    | Best Local Similarity                                             | 89.3%;           | Pred. No. 1.3e-100; |            |             |
|    | Matches 536;                                                      | Conservative 15; | Mismatches 35;      | Indels 14; | Gaps        |
| QY | 1 MNKRIIRIWNALAAWAAYSELTRNHRKRASATKTAVLATLLFATVQAANATDEDEEEL      | 60               |                     |            |             |
|    |                                                                   |                  |                     |            |             |
| Db | 1 MNKRIIRIWNALAAWAAYSELTNRHKKRASATVATVLAITLFLFATVQAOSTTD-DDDLYL   | 59               |                     |            |             |
|    |                                                                   |                  |                     |            |             |
| QY | 61 ESYOR-SYVGSIQASMGEVFLETSIMNDSDS-----KEFDYPIYVTTLAKGDLKI        | 112              |                     |            |             |
|    | :       :       :       :       :       :       :       :       : |                  |                     |            |             |
| Db | 60 EPVORTAAYLFESRDKDGSTGEKE-----VTEDSMMGVYPFKKGVLTAAGTTTLAKGDLKI  | 114              |                     |            |             |
|    |                                                                   |                  |                     |            |             |
| QY | 113 KQNENNTNASSPFYSLEKLDTGLINETEKLSFGANGKRVNIISPTRGILNFAKETAGTN   | 172              |                     |            |             |
|    |                                                                   |                  |                     |            |             |

|             |                       |             |            |                    |
|-------------|-----------------------|-------------|------------|--------------------|
|             | 87.8%;                | Score 2623; | DB 2:      | Length 600;        |
| Query Match | Best Local Similarity | 88.7%;      | Pred. No.  | 4.6e-100;          |
| Matches     | Conservative          | 14;         | Mismatches | Indels 14; Gaps 5; |

  

|    |    |                                                               |     |
|----|----|---------------------------------------------------------------|-----|
| Oy | 1  | NNKIYRIIINSLNMAVAVSELRHHTRKASATVTCAVLATLLFATVQANA-----TDE     | 54  |
| Dd | 1  | NNKIYRIIINSLNMAVVVSSELRRHTRKASATVETAVLATLLEFAVQASADNVQASADN   | 60  |
| Oy | 55 | DEEELLESVRSV--GGSIQASMESGVLETITSLSMNTNSKEPVDPYIV---VTLKKAGD   | 109 |
| Dd | 61 | EEEELEPVPVKAPPLASTYSDAEDTGEEKV--TEENTNMGIYFDKGNGAKGITTLTKAGDN | 118 |

QY 110 LKIKONTNENTNASSFFYSLSKDLTGLINVEETKLSFGANGKVNIIISDTKGLNFAKET 169  
 DB 119 LKIKONTNENTNASSFFYSLSKDLTGLINVEETKLSFGANGKVNIIISDTKGLNFAKET 178  
 QY 170 GNGGTTVHLNIGSTLDMMLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMINKGV 229  
 DB 179 GNGGTTVHLNIGSTLDMMLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMINKGV 238  
 QY 230 PGTTSADVNFRTDYVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVKEKDKGLV 289  
 DB 239 PGTTSADVNFRTDYVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVKEKDKGLV 298  
 QY 290 TKGKGENGSTDEGEGLTAKVIDAVNKAQMRKTTTANGOTQADKFEETVSTGTYT 349  
 DB 299 TKGKGENGSTDEGEGLTAKVIDAVNKAQMRKTTTANGOTQADKFEETVSTGTYT 358  
 QY 350 PASGNGTATVSKDDGNTTVKYDVNVGDALNVNOLNSGMNLSKRAVAGSSGKVIYGNV 409  
 DB 359 PASGNGTATVSKDDGNTTVKYDVNVGDALNVNOLNSGMNLSKRAVAGSSGKVIYGNV 418  
 QY 410 SPSKGMDETVINNAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADPTLSVDGAL 469  
 DB 419 SPSKGMDETVINNAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADPTLSVDGAL 477  
 QY 470 NGSKDANKPRITNAPGVKEGDTNVAQLKGVANLNRRIDNVNAGNAGIAQAIATA 529  
 DB 478 NGSKDANKPRITNAPGVKEGDTNVAQLKGVANLNRRIDNVNAGNAGIAQAIATA 537  
 QY 530 GLVQAYLPKSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVY 589  
 DB 538 GLVQAYLPKSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVY 597  
 QY 590 YOW 592  
 DB 598 YOW 600

RESULT 15  
 Q9JR18 PRELIMINARY: PRT: 591 AA.  
 AC 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA992 OR NMB0992 OR NHHA.  
 OS Neisseria meningitidis, and  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_Taxid=487, 491;  
 RA SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capocchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nulì S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brooker M., Hündt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
 RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B;  
 RX MEDLINE=20175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,  
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Yamatevian J.,  
 RA Gill J., Scarlato V., Masignani V., Piza M., Grandi G., Sun L.,  
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,  
 RA "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";  
 RT Science 287:1809-1815(2000).  
 RL [3]  
 RN RP SEQUENCE FROM N.A.  
 RC SPECIES=N.meningitidis; STRAIN=PMC21;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF226375; AAF42524.1; -;  
 DR EMBL: AE002450; AAF41395.1; -;  
 DR EMBL: AF226367; AAF42516.1; -;  
 DR EMBL: AF226370; AAF42519.1; -;  
 DR EMBL: AF226374; AAF42523.1; -;  
 DR EMBL: AF157611; AAK68872.1; -;  
 DR TIGR: NMB0992; -;  
 KM Complete proteome.  
 SQ SEQUENCE 591 AA: 62112 MW: 7C22F3CAE7F73EC6 CRC64;

Query Match 86.2%; Score 2573.5; DB 16; Length 591;  
 Best Local Similarity 87.5%; Pred. No. 4.7e-98;  
 Matches 524; Conservative 23; Mismatches 37; Indels 15; Gaps 6;  
 QY 1 MKRIYRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATLLFATVQANATDEDEER- 59  
 DB 1 MKRIYRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATLLFATVQANATDEDEER 60  
 QY 60 -LESVQRSY-VGSIQASMGSVLETLISLMTNDSKEFDPIYV---VTLAKGNLKLK 113  
 DB 61 YDPPVQRTVAVLIVNSDKGTEGEKEVE-ENSDWAYFENEKGLVLAARETLTLAGDLKLK 119  
 QY 114 ONTENTNASSFFYSLSKDLTGLINVEETKLSFGANGKVNIIISDTKGLNFAKETAGTG 173  
 DB 120 Q-----KGTNTTYSLSKDLTGLTDLTSGTEKLSFGANGKVNIIISDTKGLNFAKETAGTG 173  
 QY 174 DTTVHLNIGSTLDMMLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMINKGVPGTT 233  
 DB 174 DTTVHLNIGSTLDMMLNTGATNTVNDVNTDDEKKRAASVYKDVNLGNMINKGVPGTT 233  
 QY 234 ASDNDVFNRTDYVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVKEKDKLVTGKG 293  
 DB 234 ASDNDVFNRTDYVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVKEKDKLVTGKG 293  
 QY 294 KGENGSTDEGEGLTAKVIDAVNKAQMRKTTTANGOTQADKFEETVSTGKTVFASG 353  
 DB 294 KGENGSTDEGEGLTAKVIDAVNKAQMRKTTTANGOTQADKFEETVSTGKTVFASG 353  
 QY 354 NCTTATVSKDDGNTTVKYDVNVGDALNVNOLNSGMNLSKRAVAGSSGKVIYGNVSPK 413  
 DB 354 NCTTATVSKDDGNTTVKYDVNVGDALNVNOLNSGMNLSKRAVAGSSGKVIYGNVSPK 413  
 QY 414 GKMDDEVINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADPTLSVDGALNVGS 473  
 DB 414 GKMDDEVINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADPTLSVDGALNVGS 472  
 QY 474 KQANKPRITNAPGVKEGDTNVAQLKGVANLNRRIDNVNAGNAGIAQAIATAGLVO 533  
 DB 473 KQANKPRITNAPGVKEGDTNVAQLKGVANLNRRIDNVNAGNAGIAQAIATAGLVO 532  
 QY 534 AYLPGKSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVYOW 592  
 DB 533 AYLPGKSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVYOW 591

Search completed: July 3, 2002, 08:28:39  
 Job time: 1160 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:03 ; Search time 168.6 Seconds

(without alignments)  
388.034 Million cell updates/sec

Title: US-09-771-382-3

Perfect score: 2994

Sequence: 1 MNKXRIINWSALNAWVVS.....TASGNRGHFGTSASVGYQW 589

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 2994   | 100.0       | 589    | 20    | AAV23745    |
| 2          | 2994   | 100.0       | 589    | 22    | AAU06173    |
| 3          | 2694   | 90.0        | 599    | 20    | AAV23743    |
| 4          | 2694   | 90.0        | 599    | 22    | AAU06176    |
| 5          | 2626.5 | 87.7        | 592    | 20    | AAU06180    |
| 6          | 2616.5 | 87.4        | 598    | 22    | AAV23738    |
| 7          | 2616.5 | 87.4        | 598    | 22    | AAU06178    |
| 8          | 2610.5 | 87.2        | 598    | 20    | AAV23742    |
| 9          | 2610.5 | 87.2        | 598    | 22    | AAU06177    |
| 10         | 2580.5 | 86.2        | 592    | 20    | AAV27203    |
| 11         | 2573.5 | 86.0        | 594    | 20    | AAV23739    |

|    |        |      |      |    |          |
|----|--------|------|------|----|----------|
| 12 | 2573.5 | 86.0 | 594  | 22 | AAU06179 |
| 13 | 2516.5 | 84.1 | 594  | 20 | AAV23740 |
| 14 | 2516.5 | 84.1 | 594  | 20 | AAV57044 |
| 15 | 2516.5 | 84.1 | 594  | 22 | AAU06174 |
| 16 | 2490.5 | 83.2 | 592  | 20 | AAV23744 |
| 17 | 2490.5 | 83.2 | 592  | 22 | AAU06172 |
| 18 | 2486   | 83.0 | 591  | 21 | AAV57045 |
| 19 | 2479   | 82.8 | 591  | 20 | AAV27202 |
| 20 | 2479   | 82.8 | 591  | 20 | AAV23746 |
| 21 | 2479   | 82.8 | 591  | 20 | AAU06171 |
| 22 | 2467   | 82.4 | 591  | 20 | AAV23741 |
| 23 | 2467   | 82.4 | 591  | 22 | AAU06175 |
| 24 | 2462.5 | 82.2 | 592  | 20 | AAV23737 |
| 25 | 2317.5 | 77.4 | 502  | 22 | AAU06186 |
| 26 | 2314   | 77.3 | 513  | 22 | AAU06183 |
| 27 | 2254.5 | 75.3 | 512  | 22 | AAU06182 |
| 28 | 2231.5 | 74.5 | 604  | 22 | AAU06181 |
| 29 | 1964   | 65.6 | 433  | 22 | AAU06185 |
| 30 | 1848   | 61.7 | 407  | 22 | AAU06184 |
| 31 | 1179.5 | 39.4 | 2353 | 17 | AAV27201 |
| 32 | 1177.5 | 39.3 | 2411 | 21 | AAV23860 |
| 33 | 1169.5 | 39.1 | 1098 | 17 | AAV23857 |
| 34 | 1064   | 35.5 | 679  | 17 | AAV23856 |
| 35 | 1064   | 35.5 | 679  | 21 | AAV23855 |
| 36 | 1001.5 | 33.5 | 1094 | 21 | AAV23858 |
| 37 | 803.5  | 26.8 | 245  | 20 | AAV27201 |
| 38 | 774.5  | 25.9 | 1004 | 21 | AAV23857 |
| 39 | 771.5  | 25.8 | 1002 | 21 | AAV23854 |
| 40 | 708.5  | 23.7 | 1104 | 21 | AAV23856 |
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| 42 | 571    | 13.0 | 116  | 21 | AAV23832 |
| 43 | 389    | 12.9 | 2123 | 22 | AAV27201 |
| 44 | 387    | 12.9 | 2123 | 22 | AAV27201 |
| 45 | 384    | 12.8 | 1992 | 17 | AAV27201 |

#### ALIGNMENTS

|          |                                                                |
|----------|----------------------------------------------------------------|
| RESULT   | 1                                                              |
| AAV23745 |                                                                |
| ID       | AAV23745 standard; Protein: 589 AA.                            |
| XX       |                                                                |
| AC       | AAV23745;                                                      |
| XX       |                                                                |
| DT       | 08-SEP-1999 (first entry)                                      |
| XX       |                                                                |
| DE       | A surface protein of Neisseria meningitidis.                   |
| XX       |                                                                |
| KW       | Surface protein; surface glycoprotein; infection; vaccine;     |
| KW       | Immunoreactive peptide.                                        |
| XX       |                                                                |
| OS       | Neisseria meningitidis.                                        |
| XX       |                                                                |
| PN       | W0931132-AL.                                                   |
| XX       |                                                                |
| PD       | 24-JUN-1999.                                                   |
| XX       |                                                                |
| PF       | 14-DEC-1998; 98WO-AU01031.                                     |
| XX       |                                                                |
| PR       | 12-DEC-1997; 97GB-0026398.                                     |
| XX       |                                                                |
| PA       | (ISIS-) ISIS INNOVATION LTD.                                   |
| PA       | (UTOU) UNIV QUEENSLAND.                                        |
| XX       |                                                                |
| PI       | Jennings MP, Moxon ER, Peak IRA;                               |
| XX       |                                                                |
| DR       | WPI: 1999-418754/35.                                           |
| XX       |                                                                |
| PT       | N-PSDB: AAX85797.                                              |
| XX       |                                                                |
| PT       | Neisseria meningitidis surface proteins useful for treating N. |
| XX       | meningitidis infections                                        |





|          |                                                                |                                                                  |     |
|----------|----------------------------------------------------------------|------------------------------------------------------------------|-----|
| OY       | 1                                                              | MNKYIRIIMNLSALNAWVYSLTJTNHRRKRSATVATVLTLLSATVQAATPDDEEEL         | 60  |
| Db       | 1                                                              | mkyirilmnsalanaawwvsseltjtnhrrksatvatvltllsatvqaatpdddeee        | 60  |
| OY       | 61                                                             | ESVARSAVLVLOFMIDKEGNGEIESTGDIIGMSIYYDDHNTLHGATVTLKAGDNLIKOSGK    | 120 |
| Db       | 61                                                             | esvarsalvlvlfmidekengneiestgdiigwsiyyddhnlhगतvtlkagdnlikqsgk     | 120 |
| OY       | 121                                                            | DFTYSLKLEKDLTSTETEKISFGANGKNYNTSDIKGLNPAKETAGTNGDPVYHLNGIG       | 180 |
| Db       | 121                                                            | dftyslkklekdltsteteksifgngknlyntsdikglnfaketag tngdprcvhlnig     | 180 |
| OY       | 181                                                            | STLDTLTLGSSASHVDKNGONSTHTTRAASITKDYVNAACMWNLKGYVGTSGTGOSENVDPVRT | 240 |
| Db       | 181                                                            | stldtcltlgssashvdkngsthttraasikdyvlnaagwnlkgyvtgstlgsgenvdvt     | 240 |
| OY       | 241                                                            | YDVEFLSADTKTTTNNVESKDNKRFREVIIGAKTSYIKERDGLVYKGGKGENGSSTDE       | 300 |
| Db       | 241                                                            | ydtveflsadtkttnnnveskdngkrfevrigaktstykergdglvygkkgngsgstde      | 300 |
| OY       | 301                                                            | GEGVLVTAKEVIDAVNKKAGMRKTTTANGQTOADKEFTVTSGTKVTFASGNGTTATVSKD     | 360 |
| Db       | 301                                                            | gegvlvtakevldavnkagmrktttlangtqgqadkeftvsgtkvtfasngttatvskd      | 360 |
| OY       | 361                                                            | DOGNITATKYDVNVDGDLNVLNVOLNOSGNLDSKAVAGSSGKVISGNVSPSKGMDYEYIN     | 420 |
| Db       | 361                                                            | dognitatkdyvndvgdlnvnlvnlolnsgnldskavagssgkvisgnvspkghmdetvnl    | 420 |
| OY       | 421                                                            | AGNNIETTRNGKNIDITMSMTPOFSSVSLGADAPTLISVDDDEGALNVGSKDNANKPVRT     | 480 |
| Db       | 421                                                            | agnniettrngkniditmsmtprfssvslgagadaprlstvddegalnvgskdnankpyrt    | 480 |
| OY       | 481                                                            | NVAPEKVEGDVTNVAQLKGYAQNLENNRIDVNVGNARAGIAQAIATAGIAQAYLPGKSMA     | 540 |
| Db       | 481                                                            | nvapekvegdtvnvaqlkgyaqnlennridvngnaraglaqalataaglaqaylpgkemma    | 540 |
| OY       | 541                                                            | IGGFTVYIGEAGYATGAYSSISPTGGMWYIKGTASGNSRHFSTASVGYQW               | 589 |
| Db       | 541                                                            | iggftvyigeagyalgysisidtgmmwlykgtasgnsrghfstsasvgyqw              | 589 |
| RESULT 3 |                                                                |                                                                  |     |
| AAV23743 |                                                                |                                                                  |     |
| ID       | AAV23743 standard; Protein: 599 AA.                            |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| AC       | AAV23743:                                                      |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| DT       | 08-SEP-1999 (first entry)                                      |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| DE       | A surface protein of Neisseria meningitidis.                   |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| KM       | Surface protein; surface glycoprotein; infection; vaccine;     |                                                                  |     |
| KM       | immunoreactive peptide.                                        |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| OS       | Neisseria meningitidis.                                        |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PN       | W09931132-A1.                                                  |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PD       | 24-JUN-1999.                                                   |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PF       | 14-DEC-1998: 98WO-A001031.                                     |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PR       | 12-DEC-1997: 97GB-0026398.                                     |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PA       | (ISIS-) ISIS INNOVATION LTD.                                   |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PA       | (UYOU) UNIV QUEENSLAND.                                        |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| FI       | Jennings MP, Moxon ER, Peak RA;                                |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| DR       | WPI: 1999-418754/35.                                           |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| DR       | N-PSDB: AAX85795.                                              |                                                                  |     |
| XX       |                                                                |                                                                  |     |
| PT       | Neisseria meningitidis surface proteins useful for treating N. |                                                                  |     |

|          |                                                                           |  |
|----------|---------------------------------------------------------------------------|--|
| PT       | meningitidis infections                                                   |  |
| XX       |                                                                           |  |
| PS       | Claim 1; Page 114-115; 132pp; English.                                    |  |
| XX       |                                                                           |  |
| CC       | The present sequence represents a surface protein of <i>Neisseria</i>     |  |
| CC       | meningitidis which is approximately 62 kDa. The <i>N. meningitidis</i>    |  |
| CC       | surface glycoproteins, nucleic acids, the primers and optionally          |  |
| CC       | a thermostable polymerase, or antibodies are useful in a kit for          |  |
| CC       | the detection or diagnosis of <i>N. meningitidis</i> infection in humans. |  |
| CC       | The <i>N. meningitidis</i> surface glycoproteins can also be used to      |  |
| CC       | prevent or treat <i>N. meningitidis</i> infection in humans, especially   |  |
| CC       | in the form of vaccines. The proteins and antibodies can also             |  |
| CC       | be used to identify immunoreactive peptides.                              |  |
| XX       |                                                                           |  |
| SO       | Sequence 599 AA;                                                          |  |
|          |                                                                           |  |
|          | Query Match 90.0%; Score 2694; DB 20; Length 599;                         |  |
|          | Best Local Similarity 89.7%; Pred. No. 5.3e-148;                          |  |
|          | Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;           |  |
| QY       | 1 MNKIRIIMNSALNMAVVVSELTNRHNRKASATVATAVLATLTSATVOANATDDEDEL 60            |  |
| DB       | 1 mkkYIRIImSnalnMAwvseLtnrhkRaastvtKtaVtlacllftatqanacdeeeel 60           |  |
| QY       | 61 ESVARSALVLOPMDKEGNGEIESTGDIQWSIYYDDHNTLHCAITVTLKAGDMLKIKO--- 117       |  |
| DB       | 61 epvrvaIsvIqlfmdIkEgnEgEsgnIqswIsYdnhnlbgaTvtlKagDhIkIkqtn 120          |  |
| QY       | 118 -----SGKDETVSLKKELKDLTSVEFEKISFEFGANGKVNVTISPTDKGINFAKETAGTNG 170     |  |
| DB       | 121 knntentdsstLySikKdlcltalvatefekIsfgangnvnmltsdKgnlntakeagtnng 180     |  |
| .QY      | 171 DPTVHLNGIGSTLPDITLKGSSASHDAGNQSY--HYTTRASIKDVLNMGWNIKGVKTGST 228      |  |
| DB       | 181 dltvhlngIgstlcltcltlntgatntvndnyrdckkkkRaasvKdvlInagwnIkgyKpgrt 240   |  |
| QY       | 229 TGSQSENVDPVRTYDVEFLSADTKTITYVNESKDNKGKRTVEKIGAKTSYIAKRDGKLVTG 288     |  |
| DB       | 241 a--sdnvhfvhtydlvefIsadtkclttnveskDngkrteVkiGaktsvIkEkdgklvtg 298      |  |
| QY       | 289 KKGKNGSGSTDEGELVNAKEVYIDAVNKGAGMKTTTANQGTGADKPEFTVSGTKVTPFA 348       |  |
| DB       | 299 kkgEgngsstdegeglvtaKEvIdavnKagvTmklttlangcTgqadkfeIvtsqtnvtfa 358     |  |
| QY       | 349 SGNGTATVNSKDDQNIYKYDYVNVGDAALNVNQLNSGNMLDSKAVVAGSSGKVIISGNVSP 408     |  |
| DB       | 359 sgkgtlaIvskddggnltvKydvnnvgdaInvgdlngsnGmlsdKvagsgKvIsignvsp 418      |  |
| QY       | 409 SKGMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDDEGALNV 468         |  |
| DB       | 419 skgmdeIvnlagnnieltRngkNIdatSmtpqfssvslgaGadaprlsvsdDkgalnv 478        |  |
| QY       | 469 GSKDANKVYRTTNVAPGVKESGDTVVAQOLKGAOVLNNNDVNNNDVNNANRAGIDQALATGL 528    |  |
| DB       | 479 gskdankvYrtltnvApGVKegdtvvaqLkyaqoLnnldvndgnatagIdaqataIagI 538       |  |
| QY       | 529 AQAIVPGKSMALIGGATVLGEAGVYAIIGVSSISDTONMVKITAGSGNSRGHFTSASVQGO 588     |  |
| DB       | 539 vqayIvpgKsmmaIggatvLygeagvayIygsIsdGgnwlkgtlaSgnsrghfIgaasvgyq 598    |  |
| QY       | 589 W 589                                                                 |  |
| DB       | 599 W 599                                                                 |  |
| RESULT 4 |                                                                           |  |
| AA006176 | AA006176                                                                  |  |
| ID       | AA006176 standard; Protein: 599 AA.                                       |  |
| XX       | AA006176;                                                                 |  |
| XX       |                                                                           |  |
| DT       | 24-OCT-2001 (first entry)                                                 |  |

|    |          |                                                                         |
|----|----------|-------------------------------------------------------------------------|
| XX | DE       | N. meningitidis H38 surface antigen NhhA polypeptide sequence.          |
| XX | KM       | Surface antigen NhhA; meningococcal disease; meningitis vaccine.        |
| XX | OS       | Neisseria meningitidis strain H38.                                      |
| XX | XX       |                                                                         |
| XX | Key      | Location/Qualifiers                                                     |
| XX | FT       | Region                                                                  |
| XX | FT       | /label= C1                                                              |
| XX | FT       | /note= "Conserved region 1"                                             |
| XX | FT       | Region                                                                  |
| XX | FT       | 51..105                                                                 |
| XX | FT       | /label= V1                                                              |
| XX | FT       | /note= "Variable region 1"                                              |
| XX | FT       | Region                                                                  |
| XX | FT       | 106..117                                                                |
| XX | FT       | /label= C2                                                              |
| XX | FT       | /note= "Conserved region 2"                                             |
| XX | FT       | Region                                                                  |
| XX | FT       | 118..131                                                                |
| XX | FT       | /label= V2                                                              |
| XX | FT       | /note= "Variable region 2"                                              |
| XX | FT       | Region                                                                  |
| XX | FT       | 132..195                                                                |
| XX | FT       | /label= C3                                                              |
| XX | FT       | /note= "Conserved region 3"                                             |
| XX | FT       | Region                                                                  |
| XX | FT       | 196..217                                                                |
| XX | FT       | /label= V3                                                              |
| XX | FT       | /note= "Variable region 3"                                              |
| XX | FT       | Region                                                                  |
| XX | FT       | 218..236                                                                |
| XX | FT       | /label= C4                                                              |
| XX | FT       | /note= "Conserved region 4"                                             |
| XX | FT       | Region                                                                  |
| XX | FT       | 237..243                                                                |
| XX | FT       | /label= V4                                                              |
| XX | FT       | /note= "Variable region 4"                                              |
| XX | FT       | Region                                                                  |
| XX | FT       | 244..599                                                                |
| XX | FT       | /label= C5                                                              |
| XX | FT       | /note= "Conserved region 5"                                             |
| XX | XX       |                                                                         |
| XX | PN       | WO200155182-A1.                                                         |
| XX | XX       |                                                                         |
| XX | PD       | 02-AUG-2001.                                                            |
| XX | XX       |                                                                         |
| XX | PF       | 25-JAN-2001; 2001WO-AU00659.                                            |
| XX | XX       |                                                                         |
| XX | PR       | 25-JAN-2000; 2000US-0177917.                                            |
| XX | XX       |                                                                         |
| XX | PA       | (UYOU ) UNIV QUEENSLAND.                                                |
| XX | XX       |                                                                         |
| XX | P1       | Peak IRA, Jennings MP;                                                  |
| XX | PI       | WPI; 2001-488774/53.                                                    |
| XX | DR       | N-PSDB; AAS09166.                                                       |
| XX | XX       |                                                                         |
| XX | XX       |                                                                         |
| XX | PT       | New NhhA surface antigen polypeptides and polynucleotides from          |
| XX | PT       | Neisseria meningitidis, useful in producing vaccines for treating or    |
| XX | PT       | preventing broad spectrum of Neisseria meningitidis -                   |
| XX | PS       |                                                                         |
| XX | PS       | Claim 9; Fig 1; 91pp; English.                                          |
| XX | XX       |                                                                         |
| XX | CC       | The present invention relates to the isolation of novel Neisseria       |
| XX | CC       | meningitidis mutant polypeptides of the surface antigen NhhA            |
| XX | CC       | (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are       |
| XX | CC       | characterised by deletions of non-conserved amino acids, particularly   |
| XX | CC       | the deletion of variable regions. The deletion mutants are useful in    |
| XX | CC       | diagnostics, therapeutic and prophylactic vaccines against a broader    |
| XX | CC       | spectrum of N. meningitidis, and in designing and/or screening of       |
| XX | CC       | medicaments. The mutant proteins when used as a vaccine can effectively |
| XX | CC       | immunise against a broader spectrum of N. meningitidis strains than     |
| XX | CC       | would be expected from a corresponding wild-type surface antigen.       |
| XX | CC       | The present sequence representing the wild type surface antigen NhhA    |
| XX | CC       | from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences   |
| XX | CC       | (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  |
| XX | CC       | the present invention.                                                  |
| XX | XX       |                                                                         |
| XX | Sequence | 599 AA;                                                                 |
| XX | XX       |                                                                         |

| Query Match                                                                 | 90.0%: Score 2694; DB 22; Length 599; |
|-----------------------------------------------------------------------------|---------------------------------------|
| Best Local Similarity                                                       | 89.7%: Pred. No. 5.3e-148;            |
| Matches 539: Conservative 14; Mismatches 34; Indels 14; Gaps 3;             |                                       |
| QY 1 MNKIRIRIINWSALNMAVYVSELTNRNHTKRASATVATAVLATLLSATVOANATDDEDEL 60        |                                       |
| Db 1 mkiyrlimnalsalnavawsseltrnhltkraasvltavlatllfatvganatedeeseel 60       |                                       |
| QY 61 ESVARSAVLVOPMIDKEONGEIEEGSDIGMSIYYDHDHMLHCATYTLKAGDMLKIKQ--- 117      |                                       |
| Db 61 epvrsalvlvfmldkegnenesgnlqwslyghnltlghatvcllkagdnllkqntn 120          |                                       |
| QY 118 -----SGKFTTYSLKKEKLDLTSVERTEKLSFGANGKRVNTSDTKGLNFAKEATAGTNG 170      |                                       |
| Db 121 knntentudssftyslkkdclcldeseteleklsfgangnkvnltastklgnfaketaing 180    |                                       |
| QY 171 DPTVHLNGISGLTDLTLGASSASHVDAGNOST--HYTAASTIKDVLNAGMWIKYKTKGST 228     |                                       |
| Db 181 dltvhlngisgltlcltlntgtatvtnvtdkdkkkkraasvkdvlinaqwnllkgykpgtl 240    |                                       |
| QY 229 TGOSENVDFVRHYDVEFLSADTKTNTVNVESKDKGRPEYKIGAKTSVIREKDGKLVTG 288       |                                       |
| Db 241 a--sonvafvnlhycltvelisadtkcltynveskngkrilevligaktsvllkekdgklytg 298  |                                       |
| QY 289 KKGGENSGSTEGEGELVYAKEVIDAVNKAQWRMKTTTANQGTGQADKEFETVYSGTRVTEFA 348   |                                       |
| Db 299 kkggensgstdegeglvleakevidavnkagwrmtcttanqgtgqadkletvsgtnvfta 358     |                                       |
| QY 349 SGNQGTATVASKDDQGNITVYKDYNNQDLNVLNQLNSGWNLDKSKAVASSSGKAVISGNNSP 408   |                                       |
| Db 359 sgkgtlatvaskddqgnltvkvdyvnygdalnvynqlnqswmldskavasssgkvlisgnvsp 418  |                                       |
| QY 409 SKGKMDDEVNTINAGNINIEITRNKKNIDTATSMTPQFSSVSICAGADAPTLSDVDEGALNV 468   |                                       |
| Db 419 skgkmddevntinagmnielttrngkhiidatmtcpqfssvsigagadapltlsvddkgaln 478   |                                       |
| QY 469 GSKDANKPVRTTNAAPGVKESGDVTNVAOLKGYAQNLLNRIDVNGNABAGIAQAATATAGL 528    |                                       |
| Db 479 gskdankpvriltvnvpykgegdvtrvvaqlkygaqnlmrtdvndvgnaraglaqatalagl 538   |                                       |
| QY 529 AQAATVPGKSMAIIGCGTATLGEAGVATIGVSSISDPDGNWYIKAGASGNSRGHFGTSSAVGYO 588 |                                       |
| Db 539 vqaylpgksmmailgggtlyrgeagyaligyslsddgnwllkgtlaasgnstgthgasasvgyq 598 |                                       |
| QY 589 W 589                                                                |                                       |
| Db 599 W 599                                                                |                                       |
| RESULT 5                                                                    |                                       |
| AA06180                                                                     |                                       |
| ID AA06180 standard; Protein: 592 AA.                                       |                                       |
| XX AA06180;                                                                 |                                       |
| XX AC                                                                       |                                       |
| XX DT 24-OCT-2001 (first entry)                                             |                                       |
| XX XX                                                                       |                                       |
| XX XX                                                                       |                                       |
| XX XX                                                                       |                                       |
| DE N. meningitidis Z2491 surface antigen Nhha polypeptide sequence.         |                                       |
| XX XX                                                                       |                                       |
| KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.         |                                       |
| XX XX                                                                       |                                       |
| OS Neisseria meningitidis strain Z2491.                                     |                                       |
| XX XX                                                                       |                                       |
| FH Key Location/Qualifiers                                                  |                                       |
| FT 1..50                                                                    |                                       |
| FT Region /label= C1                                                        |                                       |
| FT /note= "Conserved region 1"                                              |                                       |
| FT 51..102                                                                  |                                       |
| FT Region /label= V1                                                        |                                       |
| FT /note= "Variable region 1"                                               |                                       |
| FT 103..114                                                                 |                                       |
| FT Region                                                                   |                                       |

|    |                                                                         |
|----|-------------------------------------------------------------------------|
| FT | /label- C2                                                              |
| FT | /note= "Conserved region 2"                                             |
| FT | 113..124                                                                |
| FT | /label- V2                                                              |
| FT | /note= "Variable region 2"                                              |
| FT | 125..188                                                                |
| FT | /label- C3                                                              |
| FT | /note= "Conserved region 3"                                             |
| FT | 189..208                                                                |
| FT | /label- V3                                                              |
| FT | /note= "Variable region 3"                                              |
| FT | 209..227                                                                |
| FT | /label- C4                                                              |
| FT | /note= "Conserved region 4"                                             |
| FT | 228..236                                                                |
| FT | /label- V4                                                              |
| FT | /note= "Variable region 4"                                              |
| FT | 237..592                                                                |
| FT | /label- C5                                                              |
| FT | /note= "Conserved region 5"                                             |
| PN | WO200155182-A1.                                                         |
| XX |                                                                         |
| XX |                                                                         |
| PD | 02-AUG-2001.                                                            |
| XX |                                                                         |
| PF | 25-JAN-2001; 2001WO-AU00069.                                            |
| XX |                                                                         |
| PR | 25-JAN-2000; 2000US-O177917.                                            |
| XX |                                                                         |
| PA | (UYOU ) UNIV QUEENSLAND.                                                |
| XX |                                                                         |
| PI | Peak IRA., Jennings MP;                                                 |
| XX |                                                                         |
| DR | WPI; 2001-488774/53.                                                    |
| DR | N-PSDB; AAS09170.                                                       |
| XX |                                                                         |
| PT | New Nhba surface antigen polypeptides and polynucleotides from          |
| PT | Neisseria meningitidis, useful in producing vaccines for treating or    |
| PT | preventing broad spectrum of Neisseria meningitidis -                   |
| XX |                                                                         |
| PS | Claim 9; Fig 1; 91pp; English.                                          |
| XX |                                                                         |
| CC | The present invention relates to the isolation of novel Neisseria       |
| CC | meningitidis mutant polypeptides of the surface antigen Nhba            |
| CC | (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are       |
| CC | characterised by deletions of non-conserved amino acids, particularly   |
| CC | the deletion of variable regions. The deletion mutants are useful in    |
| CC | diagnostics, therapeutic and prophylactic vaccines against a broader    |
| CC | spectrum of N. meningitidis, and in designing and/or screening of       |
| CC | medicaments. The mutant proteins when used as a vaccine can effectively |
| CC | immunise against a broader spectrum of N. meningitidis strains than     |
| CC | would be expected from a corresponding wild-type surface antigen.       |
| CC | The present sequence representing the wild type surface antigen Nhba    |
| CC | from N. meningitidis strain Z2491 is 1 of 10 Nhba polypeptide sequences |
| CC | (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  |
| CC | the present invention.                                                  |
| XX |                                                                         |
| XQ | Sequence 592 AA;                                                        |

|    |     |                                                                |     |
|----|-----|----------------------------------------------------------------|-----|
| Dd | 117 | hentnaasfelyskkdlqglmveteklsitgankkwnllsdcyklmfaetacgtngdtc    | 176 |
| Qy | 174 | vhlnngisgtltdtLAGSSASHVDHGDNSTHYTRAASJIKDVLNMGWNIKYKGTSTTGQSE  | 233 |
| Dd | 177 | vhlngisgtltdtLAGSSASHVDHGDNSTHYTRAASJIKDVLNMGWNIKYKGTSTTGQSE   | 236 |
| Qy | 234 | NVDYFRITYDIWEFLSADTKTTTVAVESKDNKGRPEVAKITAKTSYIKKDKDLVTGKGKCE  | 293 |
| Dd | 237 | nvdfritydveflsadtktttvveskdngrkrevrfgaktsvikegdqklvtgkykge     | 296 |
| Qy | 294 | NGSSDDEEGIVTAKEVDAVNKAGWMMKTTTANCGOGADKPEPTVYSGKKVMPASNGCT     | 353 |
| Dd | 297 | ngssddeegivtlakevadvankagwmmktttancgogadqktfevysglnvftaasqkyl  | 356 |
| Qy | 354 | TATVSKSDOGCNIYTKYDVNWDALANVQLOLNSGWNILDSKAVAGSSGCVISGANSPSKGM  | 413 |
| Dd | 357 | tatvskdodgcnlitykdyvnwddalnvqlolnsgwnildskevagsqkylsgnvspskglm | 416 |
| Qy | 414 | DETVMINAGNNIEITRNGKNIDITSMTPOFSSVSLAGADAPTLVSDDEGALNVGSKDA     | 473 |
| Dd | 417 | detvminagnnieitrngkniditatsmapqfssvslagadaptlvsddegalnvgskda   | 476 |
| Qy | 474 | NKPVRITVAVGVEEGDVTYNVQLOKGYAQNUNNRIDVNVGNARAGTQOALATAGLAQAYL   | 533 |
| Dd | 477 | nkpvriltvavgveegdvtynvqlokygaqnunnrldvvnvgnaragtaglaqataglayl  | 536 |
| Qy | 534 | PGKSMMAIAGGTGYEGAGYALGYSSTIDTCMMWVKGNFASNSRGHETSASVGYOM        | 589 |
| Dd | 537 | pgksmmaiaggttyegagyalgysstidtcmmwvkgnfasnsrghetassvgyow        | 592 |

| Query Match           | 87.7%            | Score 2626.5;                                                 | DB 22;     | Length 592; |
|-----------------------|------------------|---------------------------------------------------------------|------------|-------------|
| Best Local Similarity | 89.1%            | Pred. No. 42e-14;                                             |            |             |
| Matches 531;          | Conservative 13; | Mismatches 14;                                                | Indels 11; | Gaps 4;     |
| Oy                    | 1                | NNKIRIITNSALNMMVYSELTRNHTKRASATVTAVALATLLSATVQANATDTEDEEL     | 60         |             |
| Db                    | 1                | mkfyrilmselinafwavseltrnhktraasatxatvalatlffatvgaaacdeedeel   | 60         |             |
| Oy                    | 61               | ESVARSALVLFQIMDKEGNGEIESTGDIQMSIYYDDHNTLHG-AVYTLKAGNLKIKI--   | 117        |             |
| Db                    | 61               | esvgrs-vvgsiqasmeqgetel---islntundsketvdrpyivvtlkagandlkikqnt | 116        |             |
| Oy                    | 118              | ----SGKPTYSKKELKDLQTSVETEKLSFGANGKNVNTSDTKGLNFAKETAAGTNGDPT   | 173        |             |

|         |                                                                              |
|---------|------------------------------------------------------------------------------|
| RESULT  | 6                                                                            |
| AA23738 |                                                                              |
| ID      | AA23738 standard; Protein: 598 AA.                                           |
| XX      |                                                                              |
| XX      |                                                                              |
| AC      | AA23738;                                                                     |
| XX      |                                                                              |
| DT      | 08-SEP-1999 (first entry)                                                    |
| DE      | A surface protein of <i>Neisseria meningitidis</i> .                         |
| XX      |                                                                              |
| KW      | Surface protein; surface glycoprotein; infection; vaccine;                   |
| KW      | immunoreactive peptide.                                                      |
| XX      |                                                                              |
| OS      | <i>Neisseria meningitidis</i> .                                              |
| XX      |                                                                              |
| PN      | W09931132-A1.                                                                |
| XX      |                                                                              |
| PD      | 24-JUN-1999.                                                                 |
| XX      |                                                                              |
| PF      | 14-DEC-1998; 98WO-AU01031.                                                   |
| XX      |                                                                              |
| PR      | 12-DEC-1997; 97GB-0026398.                                                   |
| XX      |                                                                              |
| PA      | (ISIS-) ISIS INNOVATION LTD.                                                 |
| XX      | (UYOU ) UNIV QUEENSLAND.                                                     |
| PI      | Jennings MP, Moxon ER, Peak IRA;                                             |
| XX      |                                                                              |
| DR      | WPI; 1999-418754/35.                                                         |
| XX      |                                                                              |
| DR      | N-PSDB; AAX85790.                                                            |
| XX      |                                                                              |
| PT      | <i>Neisseria meningitidis</i> surface proteins useful for treating <i>N.</i> |
| XX      | <i>meningitidis</i> infections                                               |
| XX      |                                                                              |
| PS      | Claim 1; Page 91-93; 132pp; English.                                         |
| XX      |                                                                              |

The present sequence represents a surface protein of *Neisseria meningitidis* which is approximately 62 kDa. The *N. meningitidis* surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of *N. meningitidis* infection in humans

CC The N. meningitidis surface glycoproteins can also be used to  
 CC prevent or treat N. meningitidis infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

SO Sequence 598 AA:

Query Match 87.4%; Score 2616.5; DB 20; Length 598;  
 Best Local Similarity 87.7%; Pred. No. 1.6e-143;  
 Matches 527; Conservative 18; Mismatches 41; Indels 15; Gaps 4;

QY 1 MNKIRIITNSALNANWVVSSELTNRHTRKASATATATLTSATVOANATDDEDEL 60  
 DB 1 mskisrlimnalsnawvvselttrnhktrasatavatlalilfatvqanad-dddlyl 59  
 QY 61 ESVARSALVLOPMIDKEGNEIESTGDIQMSIYDDHNTLHGATVTLKAGDNLKTKOSGK 120  
 DB 60 epvgrtavlvsfrsdkegeledsnwavyidekrvlkagallkagdnlkkgntn 119  
 QY 121 D-----FTYSIKKELKDLTSVETKLSFGANGKRNVTSDTKGLNFAKETAGTNG 170  
 DB 120 entnentndssftyslkkldlcltsveteklsifangnkvhltsdtkylnfakelagtn 179  
 QY 171 DPTVHLNGISGTLDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGWNIKGVKTGST 228  
 DB 180 dptvhlngisgltldtlntgatlnvtdndekkraasvkdvlmagwnlkgykpgtt 239  
 QY 229 TGOSENDPFRVTPVFEFLSADTKTTPVNESKNGKTEKIKAKTSVTEKXGKIVTG 288  
 DB 240 a--sdnvdfrtlytvelslsadtcltlvnveskngkrtlekvikaktsvlkekkgkltvg 297  
 QY 289 KKGEGSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGOADKFEVTSKTVFA 348  
 DB 298 kkgengsstdegeglvakevidavnkagrmktttangotgqadkfevtsgtkvfa 357  
 QY 349 SGNGTATVSKDDOGNTTKTDVNVGALNVNQLONGSMNIDSKAVAGSSKRVISGNVSP 408  
 DB 358 sgngtatlavskddggnltvktdvvnvgdelnvnglqnsqwnidskavagssgkvlisgnvsp 417  
 QY 409 SKGMDEVTNINAGNNTIEITRNGKNIDTATSMTPQSFVSIGAGADAPTLSVDEGALNV 468  
 DB 418 skgmdevtvnnagnnlelttrngknidatmtcpfssvsiqagadapclisvdegaln 477  
 QY 469 GSKDANKFVRTTNVAPGKEGDVTVNAOLKGAONLNNRINDNVGNARAGIAQAIATAGL 528  
 DB 478 gskdankfvrtlnvapgkegdvtnvaqlkvaqnlmrridnvgnaragiatagtl 537  
 QY 529 AQAATLPGKSMMAIGGTYLGEAGTAIGTSSISDTGNMVIKGTASGNSRHFQTSASVQ 588  
 DB 538 aqaylpgksmmaiggytlyrgeaaylaigyssisdtnvwlkgtasgnsrghfqtasvgyq 597  
 QY 589 W 589  
 DB 598 W 598

RESULT 7  
 AAU06178  
 ID AAU06178 standard; Protein: 598 AA.

AC AAU06178;  
 AC 24-OCT-2001 (first entry)  
 DT XX  
 DE N. meningitidis B210 surface antigen Noha polypeptide sequence.  
 XX  
 KW Surface antigen Noha; meningococcal disease; meningitis vaccine.  
 OS Neisseria meningitidis strain B210.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..50

FT /label= C1  
 FT /note= "Conserved region 1"  
 FT Region  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT 105..116  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT 117..130  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT 131..194  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT 195..216  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT 217..235  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT 236..242  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT 243..598  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 PN W020015182-A1.  
 PD 02-AUG-2001.  
 PP 25-JAN-2001; 2001WO-AU00069.  
 PR 25-JAN-2000; 2000US-01177917.  
 PA (UYOU ) UNIV QUEENSLAND.  
 PI Peak IRA, Jennings MP.  
 PI WPI: 2001-48874/53.  
 DR N-PSDB; AAS09168.  
 DR New Noha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX Claim 9; Fig 1; 91pp; English.  
 PS The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Noha  
 CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Noha  
 CC from N. meningitidis strain B210 is 1 of 10 Noha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 CC  
 CC  
 SO Sequence 598 AA:

Query Match 87.4%; Score 2616.5; DB 22; Length 598;  
 Best Local Similarity 87.7%; Pred. No. 1.6e-143;  
 Matches 527; Conservative 18; Mismatches 41; Indels 15; Gaps 4;  
 QY 1 MNKIRIITNSALNANWVVSSELTNRHTRKASATATATLTSATVOANATDDEDEL 60  
 DB 1 mskisrlimnalsnawvvselttrnhktrasatavatlalilfatvqanad-dddlyl 59



|    |                                                                         |                             |
|----|-------------------------------------------------------------------------|-----------------------------|
| DT | 24-OCT-2001                                                             | (first entry)               |
| XX |                                                                         |                             |
| DE | N. meningitidis H15 surface antigen Nhma polypeptide sequence.          |                             |
| XX |                                                                         |                             |
| KW | Surface antigen Nhma: meningococcal disease; meningitis vaccine.        |                             |
| XX |                                                                         |                             |
| OS | Neisseria meningitidis strain H15.                                      |                             |
| XX |                                                                         |                             |
| FT | Key                                                                     | Location/Qualifiers         |
| FT | Region                                                                  | 1..50                       |
| FT |                                                                         | /label= C1                  |
| FT |                                                                         | /note= "Conserved region 1" |
| FT | Region                                                                  | 51..104                     |
| FT |                                                                         | /label= V1                  |
| FT |                                                                         | /note= "Variable region 1"  |
| FT | Region                                                                  | 105..116                    |
| FT |                                                                         | /label= C2                  |
| FT |                                                                         | /note= "Conserved region 2" |
| FT | Region                                                                  | 117..130                    |
| FT |                                                                         | /label= V2                  |
| FT |                                                                         | /note= "Variable region 2"  |
| FT | Region                                                                  | 131..194                    |
| FT |                                                                         | /label= C3                  |
| FT |                                                                         | /note= "Conserved region 3" |
| FT | Region                                                                  | 195..216                    |
| FT |                                                                         | /label= V3                  |
| FT |                                                                         | /note= "Variable region 3"  |
| FT | Region                                                                  | 217..235                    |
| FT |                                                                         | /label= C4                  |
| FT |                                                                         | /note= "Conserved region 4" |
| FT | Region                                                                  | 236..242                    |
| FT |                                                                         | /label= V4                  |
| FT |                                                                         | /note= "Variable region 4"  |
| FT | Region                                                                  | 243..598                    |
| FT |                                                                         | /label= C5                  |
| FT |                                                                         | /note= "Conserved region 5" |
| XX |                                                                         |                             |
| PM | W0200155182-A1.                                                         |                             |
| XX |                                                                         |                             |
| PD | 02-AUG-2001.                                                            |                             |
| XX |                                                                         |                             |
| PE | 25-JAN-2001; 2001WO-AU00069.                                            |                             |
| XX |                                                                         |                             |
| PR | 25-JAN-2000; 2000US-0177917.                                            |                             |
| XX |                                                                         |                             |
| PA | (UYOU ) UNIV QUEENSLAND.                                                |                             |
| XX |                                                                         |                             |
| PI | Peak IRA, Jennings MP;                                                  |                             |
| XX |                                                                         |                             |
| DR | WPI; 2001-488774/53.                                                    |                             |
| DR | N-PSDB; AAS09167.                                                       |                             |
| XX |                                                                         |                             |
| PT | New Nhma surface antigen polypeptides and polynucleotides from          |                             |
| PT | Neisseria meningitidis, useful in producing vaccines for treating or    |                             |
| XX | preventing broad spectrum of Neisseria meningitidis -                   |                             |
| PS | Claim 9; Fig 1; 91pp; English.                                          |                             |
| XX |                                                                         |                             |
| CC | The present invention relates to the isolation of novel Neisseria       |                             |
| CC | meningitidis mutant polypeptides of the surface antigen Nhma            |                             |
| CC | (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are       |                             |
| CC | characterised by deletions of non-conserved amino acids, particularly   |                             |
| CC | the deletion of variable regions. The deletion mutants are useful in    |                             |
| CC | diagnostics, therapeutic and prophylactic vaccines against a broader    |                             |
| CC | spectrum of N. meningitidis, and in designing and/or screening of       |                             |
| CC | medicaments. The mutant proteins when used as a vaccine can effectively |                             |
| CC | immunise against a broader spectrum of N. meningitidis strains than     |                             |
| CC | would be expected from a corresponding wild-type surface antigen.       |                             |
| CC | The present sequence representing the wild type surface antigen Nhma    |                             |
| CC | from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences   |                             |
| CC | (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  |                             |
| XX | the present invention.                                                  |                             |

| Seq                                                             | Sequence                                                                 | 598 AA: |
|-----------------------------------------------------------------|--------------------------------------------------------------------------|---------|
| Query Match                                                     | 87.2%; Score 2610.5; DB 22; Length 598;                                  |         |
| Best Local Similarity                                           | 87.4%; Pred. No. 3.5e-143;                                               |         |
| Matches 525; Conservative 19; Mismatches 42; Indels 15; Gaps 4; |                                                                          |         |
| QY                                                              | 1 MKKIRITINNSALNMMVYVSELTNRHTKRASTVATAVLATITLSATVQANARDTDEDELT 60        |         |
| DB                                                              | 1 mkkirritinnsalnmmvvyvseltnrhtkrasvatavatavlatilfatvqanard-dddyl 59     |         |
| QY                                                              | 61 ESVASALVLOQMIMKEGNGEIESTGDIQMSIYYDDHMTLHGATVTLKAGDMLIKIOSGK 120       |         |
| DB                                                              | 60 epyqtlavvlstfsckegtekegednsawayifiekrylkgagatlkkagdlkkkqntn 119       |         |
| QY                                                              | 121 D-----FTYSLKRELKDLTSVETEKLSEFGANGKMNITSDPKGLNFAKETAGTNG 170          |         |
| DB                                                              | 120 entnentndstfcljkkdltidltsveteklsfgangkvnltstclglnfaketeagntg 179     |         |
| QY                                                              | 171 DPTVHLNGIGSLDPTLAGSSASHVDAGNQST--HYTRAASIKDYLVNAGMNIKGYKTGST 228     |         |
| DB                                                              | 180 dptvhlnglgscltdlclintgatlntvndnyddeekkraasvkdvltnagwnlkgykpglt 239   |         |
| QY                                                              | 229 TGGSNVDFVRHYDVFELISADTKTNTYVNESKONGKREYVIGAKTSYIRKKGDKLVYTG 288      |         |
| DB                                                              | 240 a--sdnvdvtrtydveflisadtkcltynveskdngkklevkigaktsyikkdgklytq 297      |         |
| QY                                                              | 289 KKGKNGSSTDEGLVLAKEVYIDAVNKGAMKMTTANTGQTGQADKFEYVNSGTRKVTFA 348       |         |
| DB                                                              | 298 kykgdngssidegeglvtrakevidavnkagvmtktntangqgqgdktetvsgtkvtfa 357      |         |
| QY                                                              | 349 SGNGTTFATVSKDDGNTYKKYDVNVNGDALNVNQLONGSMNLDSKAVAGSSGKVIIGNVSP 408    |         |
| DB                                                              | 358 snggtlatvskddggnltvkydvnygdalnvnqlngsqwnldskavagssgkviignvsp 417     |         |
| QY                                                              | 409 SSGKMDERTVNIAGNIETFRNGKNIIDATSMTPQFSSVSGAGADAPTLISVDDGALNV 468       |         |
| DB                                                              | 418 ssgkmdertvniagmnieltfrngknidiatstmpqfssvslgagadaptlisvddgala 477     |         |
| QY                                                              | 469 GSKDNKNEPVRIINVAAPGKEGDPVTWVAOLKGYAONMLNRRIDVWNGNARAGIAQAATATAGL 528 |         |
| DB                                                              | 478 gskdnknepvriinvaapgykegdvtnvaqlkygaqnlmnrdivdgnaratagiatatagl 537    |         |
| QY                                                              | 539 AQAYLPGKSMMAIGGCTYLGEAGYAIIGVSSISDTGNMWYIKGTASGNSRCHFGTSAVGYQ 588    |         |
| DB                                                              | 538 aqaylpgksmmaiggctylgeagyaigyssisdctgnwylkgtasgnsrghfgasavgyq 597     |         |
| QY                                                              | 589 W 589                                                                |         |
| DB                                                              | 598 W 598                                                                |         |
| RESULT 10.                                                      |                                                                          |         |
| XX                                                              | AAV27203                                                                 |         |
| XX                                                              | AAV27203 standard; Protein; 592 AA.                                      |         |
| XX                                                              | AAV27203:                                                                |         |
| DT                                                              | 24-SEP-1999 (first entry)                                                |         |
| XX                                                              | Amino acid sequence of N. meningitidis protein ORP40a.                   |         |
| DE                                                              |                                                                          |         |
| XX                                                              | Neisseria meningitidis protein: pharmaceutical; vaccine; diagnosis;      |         |
| KW                                                              | bacterial infection; treatment.                                          |         |
| OS                                                              | Neisseria meningitidis.                                                  |         |
| PN                                                              | W09936544-A2.                                                            |         |
| XX                                                              |                                                                          |         |
| PD                                                              | 22-JUL-1999.                                                             |         |
| XX                                                              |                                                                          |         |
| PF                                                              | 14-JAN-1999; 99WO-IB00103.                                               |         |
| XX                                                              |                                                                          |         |

PR 09-OCT-1998: 98GB-0022143.  
PR 14-JAN-1998: 98GB-0000760.  
PR 01-SEP-1998: 98GB-0019015.  
XX  
XX (CHIR-) CHIRON SPA.  
XX  
XX Grandi G, Maignani V, Pizze M, Rappuoli R, Scarlato V;  
XX  
DR WPI: 1999-444400/37.  
DR N-PSDB: AAX99125.  
XX  
XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX  
XX  
PS Claim 1: Page 63; 123pp: English.  
XX  
XX The invention provides proteins (AA27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisseria  
CC bacteria, especially Neisseria meningitidis.  
XX  
XX  
SQ Sequence 592 AA:  
  
Query Match 86.2%; Score 2580.5; DB 20; Length 592;  
Best Local Similarity 87.9%; Pred. No. 1.9e-141;  
Matches 524; Conservative 13; Mismatches 48; Indels 11; Gaps 4;  
  
QY 1 MKKIYRIINNSALNMAVWVSELTRNHTKRASATVATVATLISATVQANATDDEEL 60  
DB 1 mkiyriiwnsalnawvseltrnhtkrasatvavtatlifavqanadedeeel 60  
QY 61 ESVARSAVLQFMIDKEGSEIESTGDIWSIYDDHNTLHG-ATVTLKAGNLKIKQ-- 117  
DB 61 esvqrs-vvgsiqasmegselet--islmsndskfvdpyivvcllagnlklkqnt 116  
QY 118 ---SGKDETVSLKRELKDLTVETEKLSFGANGKNVNTSDPTGLNFAKETAGTNGDPT 173  
DB 117 neotnassftlylkkdlglinvteklstfgangkvnlstdkgnlfaketagntgdt 176  
QY 174 VILNGIGSTLDTPLAGSSASHVDAGNOSTHYTPRASIKDVLNAGNLIKVGKSTTGQSE 233  
DB 177 vlnngisftldtllagssashvdagntxsthytraasikdvlagnwlikgvkxsttgse 236  
QY 234 NVDFRTYTVTEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVIREKKGKLVTKGKGE 293  
DB 237 nvdfvrtvteflsadtktttvnveskdngrktevkiqaktsvirekkgkltvgkge 296  
QY 294 NCSSTDEGEGLTAKELVIDAVNKAQRMAKTTTANGOTGOADRFETVSGTKYTFASGNGT 353  
DB 297 ngsstdegeglvtakevidavnkagrwmtktctangtgqadkfetrtsuntvfaagkbt 356  
QY 354 TATVSKDDOGNITVYKDVAVGALNVLNOLNSGWNLSRAVAGSGSKVTSGNVSPSKGM 413  
DB 357 tatsvskddogniltvmydvavgalnvnglqnswnlidskavagssgkvtlsnvspkkgm 416  
QY 414 DEFTVNTNAGNNTETIRPNKGNIDTATSMTPQFSVSLGAGADAPTLSVDEGALNVSSKA 473  
DB 417 deftvntnagnntetirpnlkgnidatstmapqfsvslgagadapltlsvdegalnvska 476  
QY 474 NRPVTRITNAPVKEGVDYVNVQALNKAQNLNLRINNVANGNARAGIAQAIATAGLQAAVL 533  
DB 477 nrpvtritnapvkegvdynvqalnkagvnlmrininvngnaraaglaqataglaqlqayl 536  
QY 534 PGKSMWATGGGTYLGRAGYAIGYSSISDPTGNVNTKGTASGNSRHFGTASAVGYQM 589  
DB 537 pgksmwaiggytylgragyaigyssisdgpnwllkgtasgnsrghftgasasvgyqm 592

RESULT 11  
AAX23739  
ID AAX23739 standard: Protein; 594 AA.  
XX  
XX AAX23739;  
XX  
XX AC  
XX  
XX AC  
XX  
XX DT 08-SEP-1999 (first entry)  
XX  
XX DE A surface protein of Neisseria meningitidis.  
XX  
XX KW Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
XX OS Neisseria meningitidis.  
XX  
XX PN WO9931132-A1.  
XX  
XX PD 24-JUN-1999.  
XX  
XX PF 14-DEC-1998; 98MO-AU01031.  
XX  
XX PR 12-DEC-1997; 97GB-0026398.  
XX  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX (UYOU) UNIT QUEENSLAND.  
XX  
XX PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX DR WPI: 1999-418754/35.  
XX N-PSDB: AAX85791.  
XX  
XX PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX  
XX PS Claim 1: Page 95-97; 132pp: English.  
XX  
XX CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX  
SQ Sequence 594 AA:  
  
Query Match 86.0%; Score 2573.5; DB 20; Length 594;  
Best Local Similarity 86.6%; Pred. No. 4.8e-141;  
Matches 517; Conservative 20; Mismatches 49; Indels 11; Gaps 4;  
  
QY 1 MKKIYRIINNSALNMAVWVSELTRNHTKRASATVATVATLISATVQANATDDEEL 60  
DB 1 mkiyriiwnsalnawvseltrnhtkrasatvavtatlifavqanadedddlyl 59  
QY 61 ESVARSAVLQFMIDKEGSEIESTGDIWSIYDDHNTLHGATVTLKAGNLKIKQSK 120  
DB 60 epvgrtaavlsfrsdegekegedswnwayfdekrvllkagatllkagdnllkqntn 119  
QY 121 D-----FTYSLKELKDLTVETEKLSFGANGKNVNTSDPTGLNFAKETAGTNDPTV 174  
DB 120 entndsfstyslkkdltdltstveklstfgangknvntsdptglnfaketagtgdpv 179  
QY 175 HLNGIGSTLDTPLAGSSASHVDAGNOST--HYTPRASIKDVLNAGNLIKVGKSTTGQSS 232  
DB 180 hlngisftldtllngatlnvndvtdckkrasvkdvlagnwllkgvnpqta--s 237  
QY 233 ENVDFRTYTVTEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVIREKKGKLVTKGKGE 292  
DB 238 envdfvrtvteflsadtktttvnveskdngrktevkiqaktsvirekkgkltvgkge 297





RESULT 13  
AAV23740  
ID AAY23740 standard; Protein: 594 AA.  
XX  
XX AAY23740;  
AC  
XX  
XX 08-SEP-1999 (first entry)  
DE A surface protein of Neisseria meningitidis.  
XX  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
XX WO9931132-A1.  
XX  
XX 24-JUN-1999.  
XX  
XX 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (OYU) UNIT QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
XX  
XX MPI: 1999-418754/35.  
DR N-PSDB: AAX85792.  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX  
PS Claim 1; Page 100-101; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX  
XX Sequence 594 AA;  
SQ

Query Match 84.1%; Score 2516.5; DB 20; Length 594;  
Best Local Similarity 85.3%; Pred. No. 9.6e-138;  
Matches 509; Conservative 19; Mismatches 58; Indels 11; Gaps 4;

OY 1 MWKIRITIMNSALNWVYSEIFRHHTRKASATVATVATLTLSTVQANADTDEDEL 60  
DB 1 mkiYrIImnsalnWvseIfrHhTrkAsatvAtvAtLtlStVqANADtDEdEL 59  
OY 61 ESVASALVLOPFMIDKENGSEIESTGDIQMSIYYDQHTLHGATVTLKAGDNLKIKO-- 117  
DB 60 epvqtlavnlfrsdekgtegevedsnwyrfdkkyltgatltlkagdnlkikgn 119  
OY 118 ---SGKDFYSLIKELKDLTSVETELKSPFGANGKRVNTSDTKGLNFAKETAGTNGDPTV 174  
DB 120 entnasfityslkdltdltsvgtelkspfsangknvntsdtkglnfakktaelngdtv 179  
OY 175 HUNGSGTLTDTLASSASHVDAGNSF--HYTRAASIKDVAANAMNIKGVATGSGTSGS 232  
DB 180 hngsgstltdtllntgatltnvndnvddekkraasvkdvnagwnlkgyvpgtla--s 237  
OY 233 ENVDVARTDYVEFLSADTKTTTAVNESKNGKRFTEVKIGAKTSYIKEDGKLTVGKKG 292  
:|||||

DB 238 dnvdfvrydlveflsadtktcttnveskdngkrtevkigaktvylkekdgklvctkdg 297  
OY 293 ENGSSDDEBEGIVTFAKEVIDAVNKAQWRKTTTANGQTGAQAKFEYVSGTVTRASGNG 352  
DB 298 endsstdkgeglvtakevldavnkagwrmtktlangqtgqadkfeyvsgtvtrastgng 357  
OY 353 TPATVSKDDQGNITVAKYDVNVGDALNVNOLONGSNMNLDSKAVASGSGKYSGNVSPSKK 412  
DB 358 ttatvskddqgnitlvmydvngdalinvglnqsgnmldskavagssgkysgnvspksk 417  
OY 413 MDETVINAGNNIEITRNGKNIDIASMTPOFSVSLGAGADAPTLVSDDEGALNVGSKD 472  
DB 418 mdevtniagnmleltrngknidiatmtpfssvslgagadapltlvsddegalnvgskd 477  
OY 473 ANKPVRITNVAGVKEGDVTNVAQLKVAQNLNNKIDNVNNGARAGIAQALITAGLAQAY 532  
DB 478 ankpvrilnvapgvkegdvtnvagqlkyaqnlnnhldvngnaraglaqalaaglvqay 537  
OY 533 LPKGMMAVIGGTYLGEAGYATGYSISDPTGNWVIRKGTASGSRGHFGTSASVQW 589  
DB 538 lpgkmmavlggtylgeagyaigysisdpgnwlkgtasgnsrghfgsasvgyqw 594

RESULT 14  
AAV57044  
ID AAY57044 standard; Protein: 594 AA.  
XX  
XX AAY57044;  
AC  
XX  
XX 21-FEB-2000 (first entry)  
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
XX BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
XX  
OS Neisseria meningitidis.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 104  
FT :/note="Encoded by AATC"  
XX  
XX  
XX MO9958683-A2.  
PD 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-EP03255.  
PF  
XX  
XX 13-MAY-1998; 98GB-0010276.  
PR  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA  
XX  
XX Ruelle J;  
PI  
XX  
XX MPI: 2000-053103/04.  
DR N-PSDB: AAZ39864.  
XX  
XX  
XX New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal  
XX  
XX  
XX Claim 4; Fig 2; 74pp; English.  
XX  
XX This is the Nisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
CC polypeptide sequences (AAV57044-V57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of



```

Db      1 mkiyrlwnsalnawavseltrnhlkrasatavlacllfatvgastcd-dddlyl 59
QY      61 ESVARSAVLQFMIDKEGCEIESTGDIWMSTIYYDDHNTLHGATVTLKAGDNLIKIQ--- 117
Db      60 epvqtrlaavlsfrsdkegveledsnmyyfdkkyvltagltllkagdnllkqnln 119
QY      118 ---SGKDFPYSLKKEKELKDTSVETEKLSFGANGKNVITSPTKGLNFAKETAGTNGDPYV 174
Db      120 entnassfyslkkdldtlsvgleklfsaansknlsdtkglnfakktaelngdtcv 179
QY      175 HUNGIGSTLTDPLAGSSASHVDAGNOST--HYTRAASIKDVLNAGWNIKGVKTGSTTGOS 232
Db      180 hlnglgsstltdcllnfgatlnvndhvtdekkraasvkdvlmagynlkvypgtta--s 237
QY      233 ENVDYFRITDYEFELSAQRTTTVNYESKDNKRTVEKIGAKTSVIREKDGKLYTGKGG 292
Db      238 dnvdfvryldvleflsadcltlnveskdngrtevkigaktsvirkedgklytgkdkg 297
QY      293 ENGSSSTDEGEGLVTAKVIDAVNKAQRMTTANGCOTGOADKFTVTSQTKVTFASGNG 352
Db      298 endssldkgeglvtakevidavnkagwrnktltangqltgqadkfetvsglnvtfasgk 357
QY      353 TTAATVSKDDQGNITVKKYDVNVGDALNVNQLQNSGMNLDKRAVAGSSGKYISGNVSPSKG 412
Db      358 ttatvskdqgnltvmydvrvgdalnvnqllqnsqwnldskavagsqkvlsqnvpskqk 417
QY      413 MDETVINANGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNVGSKD 472
Db      418 mdelvlnagmnlrltrngknldlatsmcpqltsvslgagadapltlsvdegalnvskd 477
QY      473 ANKPVRITNVAPGVKEGDTNVNAQLKGVAQNLNRRIDNTNNGNARAGIAQAIAATAGLAQAY 532
Db      478 ankpvriltvnapgvkegdvtnvaqlkgvaqnlmnhidnvdgnaraglaqaiaataglvqay 537
QY      533 LPEKSMALIGGTTYLGAGAYALGYSSISDPTGMWYIKGTASGNSRGHFGTASAVGYOW 589
Db      538 lpgksmmaiggytgygeagyaigyssisdqgnwllkgytasgnsrghfgasasvgyqw 594

```

Search completed: July 3, 2002, 08:09:05  
 Job time: 491 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:14 ; Search time 64.11 Seconds  
(without alignments)  
224.406 Million cell updates/sec

Title: US-09-771-382-3  
Perfect score: 2994  
Sequence: 1 MNKIYRIINNSALNAMYVS.....TASGNSRGHFGTSASVGYQW 589

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID               | Description       |
|------------|--------|-------------|--------|------------------|-------------------|
| 1          | 2994   | 100.0       | 589    | US-09-377-155-19 | Sequence 19, Appl |
| 2          | 2994   | 100.0       | 589    | US-09-669-974-19 | Sequence 19, Appl |
| 3          | 2694   | 90.0        | 599    | US-09-377-155-15 | Sequence 15, Appl |
| 4          | 2694   | 90.0        | 599    | US-09-669-974-15 | Sequence 15, Appl |
| 5          | 2616.5 | 87.4        | 598    | US-09-377-155-5  | Sequence 5, Appl  |
| 6          | 2616.5 | 87.4        | 598    | US-09-669-974-5  | Sequence 5, Appl  |
| 7          | 2610.5 | 87.2        | 598    | US-09-377-155-13 | Sequence 13, Appl |
| 8          | 2610.5 | 87.2        | 598    | US-09-669-974-13 | Sequence 13, Appl |
| 9          | 2573.5 | 86.0        | 594    | US-09-377-155-7  | Sequence 7, Appl  |
| 10         | 2573.5 | 86.0        | 594    | US-09-669-974-7  | Sequence 7, Appl  |
| 11         | 2516.5 | 84.1        | 594    | US-09-377-155-9  | Sequence 9, Appl  |
| 12         | 2516.5 | 84.1        | 594    | US-09-669-974-9  | Sequence 9, Appl  |
| 13         | 2490.5 | 83.2        | 592    | US-09-377-155-17 | Sequence 17, Appl |
| 14         | 2490.5 | 83.2        | 592    | US-09-669-974-17 | Sequence 17, Appl |
| 15         | 2479   | 82.8        | 591    | US-09-377-155-21 | Sequence 21, Appl |
| 16         | 2479   | 82.8        | 591    | US-09-669-974-21 | Sequence 21, Appl |
| 17         | 2467   | 82.4        | 591    | US-09-377-155-11 | Sequence 11, Appl |
| 18         | 2467   | 82.4        | 591    | US-09-669-974-11 | Sequence 11, Appl |
| 19         | 2462.5 | 82.2        | 592    | US-09-377-155-2  | Sequence 2, Appl  |
| 20         | 2462.5 | 82.2        | 592    | US-09-669-974-2  | Sequence 2, Appl  |
| 21         | 1179.5 | 39.4        | 2353   | US-09-377-155-33 | Sequence 33, Appl |
| 22         | 1179.5 | 39.4        | 2353   | US-08-913-942-4  | Sequence 4, Appl  |
| 23         | 1179.5 | 39.4        | 2353   | US-09-669-974-33 | Sequence 33, Appl |
| 24         | 1178.5 | 39.4        | 2354   | US-09-268-347-47 | Sequence 47, Appl |
| 25         | 1177.5 | 39.3        | 2411   | US-09-268-347-36 | Sequence 36, Appl |
| 26         | 1169.5 | 39.1        | 1098   | US-08-409-995-2  | Sequence 2, Appl  |
| 27         | 1169.5 | 39.1        | 1098   | US-08-685-467-2  | Sequence 2, Appl  |

|    |        |      |      |                  |                   |
|----|--------|------|------|------------------|-------------------|
| 28 | 1169.5 | 39.1 | 1098 | US-09-377-155-32 | Sequence 32, Appl |
| 29 | 1169.5 | 39.1 | 1098 | US-08-913-942-2  | Sequence 2, Appl  |
| 30 | 1169.5 | 39.1 | 1098 | US-09-669-974-32 | Sequence 32, Appl |
| 31 | 1169.5 | 39.1 | 1098 | US-09-268-347-44 | Sequence 44, Appl |
| 32 | 1158.5 | 38.7 | 658  | US-08-409-995-5  | Sequence 5, Appl  |
| 33 | 1158.5 | 38.7 | 658  | US-08-685-467-5  | Sequence 5, Appl  |
| 34 | 1158.5 | 38.7 | 658  | US-08-913-942-5  | Sequence 5, Appl  |
| 35 | 1121   | 37.4 | 607  | US-08-409-995-6  | Sequence 6, Appl  |
| 36 | 1121   | 37.4 | 607  | US-08-685-467-6  | Sequence 6, Appl  |
| 37 | 1121   | 37.4 | 607  | US-08-913-942-6  | Sequence 6, Appl  |
| 38 | 1121   | 37.4 | 1912 | US-08-409-995-4  | Sequence 4, Appl  |
| 39 | 1121   | 37.4 | 1912 | US-08-685-467-4  | Sequence 4, Appl  |
| 40 | 1064   | 35.5 | 679  | US-08-913-942-15 | Sequence 15, Appl |
| 41 | 1064   | 35.5 | 679  | US-09-268-347-26 | Sequence 26, Appl |
| 42 | 1001.5 | 33.5 | 1094 | US-09-268-347-32 | Sequence 32, Appl |
| 43 | 774.5  | 25.9 | 1004 | US-09-268-347-30 | Sequence 30, Appl |
| 44 | 771.5  | 25.8 | 1002 | US-09-268-347-24 | Sequence 24, Appl |
| 45 | 708.5  | 23.7 | 1104 | US-09-268-347-28 | Sequence 28, Appl |

ALIGNMENTS

|                                                                    |                          |                                 |
|--------------------------------------------------------------------|--------------------------|---------------------------------|
| RESULT 1                                                           | US-09-377-155-19         | Application US/09377155         |
| Sequence 19, Appl                                                  | 6197312                  |                                 |
| GENERAL INFORMATION:                                               |                          |                                 |
| APPLICANT:                                                         | PEAR, Ian Richard Anselm |                                 |
| APPLICANT:                                                         | JENNINGS, Michael Paul   |                                 |
| APPLICANT:                                                         | MOXON, E. Richard        |                                 |
| TITLE OF INVENTION:                                                | NOVEL SURFACE ANTIGEN    |                                 |
| FILE REFERENCE:                                                    | 065064/0128              |                                 |
| CURRENT APPLICATION NUMBER:                                        | US/09/377, 155           |                                 |
| CURRENT FILING DATE:                                               | 1999-08-19               |                                 |
| PRIOR APPLICATION NUMBER:                                          | PCT/AU98/01031           |                                 |
| PRIOR FILING DATE:                                                 | 1998-12-14               |                                 |
| PRIOR APPLICATION NUMBER:                                          | GB 9726398.2             |                                 |
| NUMBER OF SEQ ID NOS:                                              | 33                       |                                 |
| SOFTWARE:                                                          | Patentia Ver. 2.0        |                                 |
| SEQ ID NO 19                                                       |                          |                                 |
| LENGTH:                                                            | 589                      |                                 |
| TYPE:                                                              | PR                       |                                 |
| ORGANISM:                                                          | Neisseria meningitidis   |                                 |
| US-09-377-155-19                                                   |                          |                                 |
| Query Match                                                        | 100.0%                   | Score 2994; DB 4; Length 589;   |
| Best Local Similarity                                              | 100.0%                   | Pred. No. 2.9e-212;             |
| Matches 589; Conservative                                          | 0;                       | Mismatches 0; Indels 0; Gaps 0; |
| 1 MNKIYRIINNSALNAMYVSELNRHTRKASATVATVATLTLISATVQANATDTDEDEL 60     |                          |                                 |
| 1 MNKIYRIINNSALNAMYVSELNRHTRKASATVATVATLTLISATVQANATDTDEDEL 60     |                          |                                 |
| 61 ESVARALVQFMIDKEGKEISITGDSIYYDDHNTLHGTVTLKAGDNKIKQSK 120         |                          |                                 |
| 61 ESVARALVQFMIDKEGKEISITGDSIYYDDHNTLHGTVTLKAGDNKIKQSK 120         |                          |                                 |
| 61 ESVARALVQFMIDKEGKEISITGDSIYYDDHNTLHGTVTLKAGDNKIKQSK 120         |                          |                                 |
| 121 DFTYSKKEKLDLTSVETKELSGANGKNVNTSDTKGLNFAETAGTNDPPVHLNGIC 180    |                          |                                 |
| 121 DFTYSKKEKLDLTSVETKELSGANGKNVNTSDTKGLNFAETAGTNDPPVHLNGIC 180    |                          |                                 |
| 121 DFTYSKKEKLDLTSVETKELSGANGKNVNTSDTKGLNFAETAGTNDPPVHLNGIC 180    |                          |                                 |
| 181 STLTDLAASSASHVAGNOSTHYTRAASIKDVLNAGWNITKVGKSTGQSENVDVVRT 240   |                          |                                 |
| 181 STLTDLAASSASHVAGNOSTHYTRAASIKDVLNAGWNITKVGKSTGQSENVDVVRT 240   |                          |                                 |
| 181 STLTDLAASSASHVAGNOSTHYTRAASIKDVLNAGWNITKVGKSTGQSENVDVVRT 240   |                          |                                 |
| 241 YDVEELSLADTKTYTVNVSCKNGKRTVEYKIGKTSYIKEDKLVYGGKGGSGSTDE 300    |                          |                                 |
| 241 YDVEELSLADTKTYTVNVSCKNGKRTVEYKIGKTSYIKEDKLVYGGKGGSGSTDE 300    |                          |                                 |
| 241 YDVEELSLADTKTYTVNVSCKNGKRTVEYKIGKTSYIKEDKLVYGGKGGSGSTDE 300    |                          |                                 |
| 301 GSELVTAKEVLDVKNKAGNMKTTTANGGTGQADKFEYVTSKTKVTFASGNGTATVSKD 360 |                          |                                 |

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Db 301 GEGLTAAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTAFASGNGTATVSKD 360
Qy 361 DOGNTTAAVDVAVGALVAVNOLONSGWNLDKAVAGSSGKVTSGVNSPSKGMDETVNIN 420
Db 361 DOGNTTAAVDVAVGALVAVNOLONSGWNLDKAVAGSSGKVTSGVNSPSKGMDETVNIN 420
Qy 421 AGNNIEITRNGKNIDIAISMTPEQSSVSLGAGADAPTLSDVDEGALNYSKANKPVRT 480
Db 421 AGNNIEITRNGKNIDIAISMTPEQSSVSLGAGADAPTLSDVDEGALNYSKANKPVRT 480
Qy 481 NVAPGVKEGADVTVNVAQLKGVAVOENLNRRIDNVGNARAGIAQAIAATAGLAQAAYLPKSKMA 540
Db 481 NVAPGVKEGADVTVNVAQLKGVAVOENLNRRIDNVGNARAGIAQAIAATAGLAQAAYLPKSKMA 540
Qy 541 IGGGTYLGEAGYAIIGYSSISDTGNMVIKGTASGNSRGHGTASVGYOW 589
Db 541 IGGGTYLGEAGYAIIGYSSISDTGNMVIKGTASGNSRGHGTASVGYOW 589
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## RESULT 2

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US-09-669-974-19
; Sequence 19, Application US/0966974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-19
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Query Match 100.0%; Score 2994; DB 4; Length 589;
Best Local Similarity 100.0%; Pred. No. 2,9e-212;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MNKIRIITNSALNMAVYVSELTRNHTKRASATVATVATLTLSTVQANATDDEDEEL 60
Qy 61 ESVARSALVLOPMDIKEGNGEIESTGDIQWSIYYDDHNTLHGATVYTLKAGDMLKIKOSGK 120
Db 61 ESVARSALVLOPMDIKEGNGEIESTGDIQWSIYYDDHNTLHGATVYTLKAGDMLKIKOSGK 120
Qy 121 DFTYSLKELDLTISVETEKLSFGANGKNVNTSDTKGINFAKETAGTNGDPTVHLNGIG 180
Db 121 DFTYSLKELDLTISVETEKLSFGANGKNVNTSDTKGINFAKETAGTNGDPTVHLNGIG 180
Qy 181 STLDITLGGSSASHVDAGNOSTHYTRASIKDVLNAGWNKIKVKTGSTGSENDPVRT 240
Db 181 STLDITLGGSSASHVDAGNOSTHYTRASIKDVLNAGWNKIKVKTGSTGSENDPVRT 240
Qy 241 YDVEEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIEKEDKLVTKGKENGSSSTDE 300
Db 241 YDVEEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIEKEDKLVTKGKENGSSSTDE 300
Qy 301 GEGLTAAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTAFASGNGTATVSKD 360
Db 301 GEGLTAAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTAFASGNGTATVSKD 360
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Db 301 GEGLTAAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTAFASGNGTATVSKD 360
Qy 361 DOGNTTAAVDVAVGALVAVNOLONSGWNLDKAVAGSSGKVTSGVNSPSKGMDETVNIN 420
Db 361 DOGNTTAAVDVAVGALVAVNOLONSGWNLDKAVAGSSGKVTSGVNSPSKGMDETVNIN 420
Qy 421 AGNNIEITRNGKNIDIAISMTPEQSSVSLGAGADAPTLSDVDEGALNYSKANKPVRT 480
Db 421 AGNNIEITRNGKNIDIAISMTPEQSSVSLGAGADAPTLSDVDEGALNYSKANKPVRT 480
Qy 481 NVAPGVKEGADVTVNVAQLKGVAVOENLNRRIDNVGNARAGIAQAIAATAGLAQAAYLPKSKMA 540
Db 481 NVAPGVKEGADVTVNVAQLKGVAVOENLNRRIDNVGNARAGIAQAIAATAGLAQAAYLPKSKMA 540
Qy 541 IGGGTYLGEAGYAIIGYSSISDTGNMVIKGTASGNSRGHGTASVGYOW 589
Db 541 IGGGTYLGEAGYAIIGYSSISDTGNMVIKGTASGNSRGHGTASVGYOW 589
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## RESULT 3

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US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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Query Match 90.0%; Score 2694; DB 4; Length 599;
Best Local Similarity 89.7%; Pred. No. 3.4e-190;
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;
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Qy 1 MNKIRIITNSALNMAVYVSELTRNHTKRASATVATVATLTLSTVQANATDDEDEEL 60
Db 1 MNKIRIITNSALNMAVYVSELTRNHTKRASATVATVATLTLSTVQANATDDEDEEL 60
Qy 61 ESVARSALVLOPMDIKEGNGEIESTGDIQWSIYYDDHNTLHGATVYTLKAGDMLKIKO--- 117
Db 61 ESVARSALVLOPMDIKEGNGEIESTGDIQWSIYYDDHNTLHGATVYTLKAGDMLKIKO--- 117
Qy 118 -----SGKDFYSLKELDLTISVETEKLSFGANGKNVNTSDTKGINFAKETAGTNG 170
Db 118 -----SGKDFYSLKELDLTISVETEKLSFGANGKNVNTSDTKGINFAKETAGTNG 170
Qy 171 DPTVHLNGIGSTLDTLGGSSASHVDAGNOST--HYTRASIKDVLNAGWNKIKVKTGST 228
Db 171 DPTVHLNGIGSTLDTLGGSSASHVDAGNOST--HYTRASIKDVLNAGWNKIKVKTGST 228
Qy 229 TGQSENVDPVRTYDVEEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIEKEDKLVTKG 288
Db 229 TGQSENVDPVRTYDVEEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIEKEDKLVTKG 288
Qy 289 KKGKENGSSSTDEGEGLVTAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTFA 348
Db 289 KKGKENGSSSTDEGEGLVTAKEVIDAVNKAQWRMKTATTANGOTGQADKFEETVTSCTKVTFA 348
Qy 349 SGNGTATVSKDQGNITVYKDVAVNVDALNVLNOLNSGWNLDKAVAGSSGKVTSGVNSP 408
Db 349 SGNGTATVSKDQGNITVYKDVAVNVDALNVLNOLNSGWNLDKAVAGSSGKVTSGVNSP 408
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Db 359 SKGGTATVSKDDGQNIITVKYDVNVGDALNVQLONSGNNLDSKAVAGSSGKVISGNVSP 418
QY 409 SKGKDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLSDVDDGALNV 468
Db 419 SKGKDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLSDVDDGALNV 478
QY 469 GSKDANKPVRITNVAPGVEGSDVTNVAOLKGYAQNUNNRIDVNGNARAGIAQAIATAGL 528
Db 479 GSKDANKPVRITNVAPGVEGSDVTNVAOLKGYAQNUNNRIDVNGNARAGIAQAIATAGL 538
QY 539 AQAATPGKSMMAIGGGTYLGEAGYALGYSSISDGTGMWVTKGTASGNSRGHFGTSASVGYO 588
Db 539 VQAYLPGKSMMAIGGGTYLGEAGYALGYSSISDGTGMWVTKGTASGNSRGHFGTSASVGYO 598
QY 589 W 589
Db 599 W 599
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## RESULT 4

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US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15
```

```
Query Match 90.0%; Score 2694; DB 4; Length 599;
Best Local Similarity 89.7%; Pred. No. 3.4e-190;
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;
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QY 1 MNKIYRIINWSALNMAVWVSELTRNHTKRASATVATVATLTLISATVQANATDDEDEEL 60
Db 1 MNKIYRIINWSALNMAVWVSELTRNHTKRASATVATVATLTLISATVQANATDDEDEEL 60
QY 61 ESVARSALVLOFMIDKEGEGIESTGDIWSTIYYDDHNTLHGATVYLLKAGDNLKIKO--- 117
Db 61 ESVARSALVLOFMIDKEGEGIESTGDIWSTIYYDDHNTLHGATVYLLKAGDNLKIKO--- 120
QY 118 -----SGKDPYLSLKKELKDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 170
Db 121 KNTNENTNDSFTYSLKLDLTLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
QY 171 DPTVHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKTGST 228
Db 181 DPTVHLNGIGSTLTDLTLNLTGATTVNTNDVTDKKRAASVYKDVNLAGMNIKGVKPGTT 240
QY 229 TGQSENVDFVRYDYVEFLSADTKTTTVNVEKDNKRTVEIKGATSVYIKKDGKLVYTG 288
Db 241 A--SDWVDFVRYDYVEFLSADTKTTTVNVEKDNKRTVEIKGATSVYIKKDGKLVYTG 298
QY 289 KKGGENGSTDEGEGLVTAKEVIDAVNKGAWMRKTTTANGQTGOADKFEVTVSGTKVTPA 348
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Db 299 KKGGENGSTDEGEGLVTAKEVIDAVNKGAWMRKTTTANGQTGOADKFEVTVSGTKVTPA 358
QY 349 SKGGTATVSKDDGQNIITVKYDVNVGDALNVQLONSGNNLDSKAVAGSSGKVISGNVSP 408
Db 359 SKGKDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLSDVDDGALNV 418
QY 409 SKGKDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLSDVDDGALNV 468
Db 419 SKGKDEVTNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGADAPTLSDVDDGALNV 478
QY 469 GSKDANKPVRITNVAPGVEGSDVTNVAOLKGYAQNUNNRIDVNGNARAGIAQAIATAGL 528
Db 479 GSKDANKPVRITNVAPGVEGSDVTNVAOLKGYAQNUNNRIDVNGNARAGIAQAIATAGL 538
QY 529 AQAATPGKSMMAIGGGTYLGEAGYALGYSSISDGTGMWVTKGTASGNSRGHFGTSASVGYO 588
Db 539 VQAYLPGKSMMAIGGGTYLGEAGYALGYSSISDGTGMWVTKGTASGNSRGHFGTSASVGYO 598
QY 589 W 589
Db 599 W 599
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## RESULT 5

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US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5
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Query Match 87.4%; Score 2616.5; DB 4; Length 598;
Best Local Similarity 87.7%; Pred. No. 1.7e-184;
Matches 527; Conservative 18; Mismatches 41; Indels 15; Gaps 4;
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QY 1 MNKIYRIINWSALNMAVWVSELTRNHTKRASATVATVATLTLISATVQANATDDEDEEL 60
Db 1 MNKIYRIINWSALNMAVWVSELTRNHTKRASATVATVATLTLISATVQANATDDEDEEL 59
QY 61 ESVARSALVLOFMIDKEGEGIESTGDIWSTIYYDDHNTLHGATVYLLKAGDNLKIKO--- 120
Db 60 EPOARTAAVLSFRSDKEGEGIEGTEGDSMWAVYFDEKRVLLKAGATVLLKAGDNLKIKO--- 119
QY 121 D-----FTYSLKKELKDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 170
Db 120 ENTNENTNDSFTYSLKLDLTLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
QY 171 DPTVHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKTGST 228
Db 180 DPTVHLNGIGSTLTDLTLNLTGATTVNTNDVTDKKRAASVYKDVNLAGMNIKGVKPGTT 239
QY 229 TGQSENVDFVRYDYVEFLSADTKTTTVNVEKDNKRTVEIKGATSVYIKKDGKLVYTG 288
Db 240 A--SDWVDFVRYDYVEFLSADTKTTTVNVEKDNKRTVEIKGATSVYIKKDGKLVYTG 297
QY 289 KKGGENGSTDEGEGLVTAKEVIDAVNKGAWMRKTTTANGQTGOADKFEVTVSGTKVTPA 348
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Db 298 KKGKENGSSSTDEGEGLTAKAEVIDAVNKAQRMKTTTANGOTGADKEFTVTSCTKTFFA 357
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Db 358 SGNCTTATVSKDOGNITTVKYDVAVGDLNVNOLONGMNLDSKAVAGSSGKVTSGVWSP 417
QY 409 SKGKMDFTVINMAGNNIEITRNGKNIDIAISMPQFSSVSLGACADAPTLVSDEGALNV 468
Db 418 SKGKMDFTVINMAGNNIEITRNGKNIDIAISMPQFSSVSLGACADAPTLVSDEGALNV 477
QY 469 GSKDANKPVRITTNVAPGVKEDGDTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 528
Db 478 GSKDANKPVRITTNVAPGVKEDGDTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 537
QY 529 AQAALPKSKMMAIGGGTYLGBAGYAIGYSSISDTGNVYIKGTASGSRGHGTSASVGYQ 588
Db 538 AQAALPKSKMMAIGGGTYLGBAGYAIGYSSISDTGNVYIKGTASGSRGHGTSASVGYQ 597
QY 589 W 589
Db 598 W 598
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RESULT 6
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-669-974-5
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Query Match 87.4% Score 2616.5; DB 4; Length 598;
Best Local Similarity 87.7% Pred. No. 1.7e-184;
Matches 527; Conservative 18; Mismatches 41; Indels 15; Gaps 4;
QY 1 MNKIRITIMNSALNAAVVSSELTNRHTRKASATVATATLTLATLTSATVQANATDDEDEL 60
Db 1 MNKIRITIMNSALNAAVVSSELTNRHTRKASATVATATLTLATLTSATVQANATDDEDEL 59
QY 61 ESVARSAVLIOFMIDKEGNGEIESTGDIWSIYYDHNHTLHGATVTLKAGNLIKIKOSGK 120
Db 60 EPVORTAVLISFRSDKEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG 119
QY 121 D-----FTYSIKKELKDLTSVEFEKLSFGANGKVNITSDFGLNFAKETAGNG 170
Db 120 ENTNENTNDSSFTYSKLDLTLTSVEFEKLSFGANGKVNITSDFGLNFAKETAGNG 179
QY 171 DPTVHLNIGISTLIDTLTAGSSASHVDAGNOST--HYTPAASIKDVLNAGNMIKGVKTGST 228
Db 180 DPTVHLNIGISTLIDTLTAGSSASHVDAGNOST--HYTPAASIKDVLNAGNMIKGVKTGST 239
QY 229 TGQSENVDVFRYDTVEFLSADTKTTTVNVESKONGKRETEVIGAKTSVIEKDGKLVYG 288
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Db 240 A--SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKRETEVIGAKTSVIEKDGKLVYG 297
QY 289 KKGKENGSSSTDEGEGLTAKAEVIDAVNKAQRMKTTTANGOTGADKEFTVTSCTKTFFA 348
Db 298 KKGKENGSSSTDEGEGLTAKAEVIDAVNKAQRMKTTTANGOTGADKEFTVTSCTKTFFA 357
QY 349 SGNCTTATVSKDOGNITTVKYDVAVGDLNVNOLONGMNLDSKAVAGSSGKVTSGVWSP 408
Db 358 SGNCTTATVSKDOGNITTVKYDVAVGDLNVNOLONGMNLDSKAVAGSSGKVTSGVWSP 417
QY 409 SKGKMDFTVINMAGNNIEITRNGKNIDIAISMPQFSSVSLGACADAPTLVSDEGALNV 468
Db 418 SKGKMDFTVINMAGNNIEITRNGKNIDIAISMPQFSSVSLGACADAPTLVSDEGALNV 477
QY 469 GSKDANKPVRITTNVAPGVKEDGDTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 528
Db 478 GSKDANKPVRITTNVAPGVKEDGDTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 537
QY 529 AQAALPKSKMMAIGGGTYLGBAGYAIGYSSISDTGNVYIKGTASGSRGHGTSASVGYQ 588
Db 538 AQAALPKSKMMAIGGGTYLGBAGYAIGYSSISDTGNVYIKGTASGSRGHGTSASVGYQ 597
QY 589 W 589
Db 598 W 598
```

```
RESULT 7
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-377-155-13
```

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Query Match 87.2% Score 2610.5; DB 4; Length 598;
Best Local Similarity 87.4% Pred. No. 4.6e-184;
Matches 525; Conservative 19; Mismatches 42; Indels 15; Gaps 4;
QY 1 MNKIRITIMNSALNAAVVSSELTNRHTRKASATVATATLTLATLTSATVQANATDDEDEL 60
Db 1 MNKIRITIMNSALNAAVVSSELTNRHTRKASATVATATLTLATLTSATVQANATDDEDEL 59
QY 61 ESVARSAVLIOFMIDKEGNGEIESTGDIWSIYYDHNHTLHGATVTLKAGNLIKIKOSGK 120
Db 60 EPVORTAVLISFRSDKEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG 119
QY 121 D-----FTYSIKKELKDLTSVEFEKLSFGANGKVNITSDFGLNFAKETAGNG 170
Db 120 ENTNENTNDSSFTYSKLDLTLTSVEFEKLSFGANGKVNITSDFGLNFAKETAGNG 179
QY 171 DPTVHLNIGISTLIDTLTAGSSASHVDAGNOST--HYTPAASIKDVLNAGNMIKGVKTGST 228
Db 180 DPTVHLNIGISTLIDTLTAGSSASHVDAGNOST--HYTPAASIKDVLNAGNMIKGVKTGST 239
QY 229 TGQSENVDVFRYDTVEFLSADTKTTTVNVESKONGKRETEVIGAKTSVIEKDGKLVYG 288
```



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:|||||
Db 240 A--SDNVDEVRRTDYVEFLSADTKTTTVNVEESKDNCKRTEVKIGAKTSYIKEDGKLVYG 297
QY 289 KKGEGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTOAQKFEVYSGTVFTA 348
Db 298 KKGEGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTOAQKFEVYSGTVFTA 357
QY 349 SCNGTATVSKDDQGNITVYKVDVNGDALNVNOLNSGNMLDSKAVAGSSGKVISGNVSP 408
Db 358 SCNGTATVSKDDQGNITVYKVDVNGDALNVNOLNSGNMLDSKAVAGSSGKVISGNVSP 417
QY 409 SKGKMDETVYNAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNV 468
Db 418 SKGKMDETVYNAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNV 477
QY 469 GSKDANKPVRITNVAVGVEGEGVTNVAOLKGVANLNINRNDVNGNARAGIAQAIATAGL 528
Db 478 GSKDANKPVRITNVAVGVEGEGVTNVAOLKGVANLNINRNDVNGNARAGIAQAIATAGL 537
QY 529 AQAYLPGKSMMAIGGGTYLGEAGYATGYSISDPTGMWVJKGTASGNSRGHFGTSASVGYO 568
Db 538 AQAYLPGKSMMAIGGGTYLGEAGYATGYSISDPTGMWVJKGTASGNSRGHFGTSASVGYO 597
QY 589 W 589
Db 598 W 598

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RESULT 8
US-09-669-974-13
: Sequence 13, Application US/09669974
: Patent No. 6333173

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: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 13
: LENGTH: 598
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-13

```

```

Query Match 87.2%; Score 2610.5; DB 4; Length 598;
Best Local Similarity 87.4%; Pred. No. 4.6e-184;
Matches 525; Conservative 19; Mismatches 42; Indels 15; Gaps 4;

```

```

QY 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATVATLTLASATVQAATDDEDEL 60
Db 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAANATD-DDDLVL 59
QY 61 ESVAARSALVLOEMIDKEGNEIESTGDIWSIYDDHNTLHGATVTLKAGDNLKIKOSGK 120
Db 60 EYQVQRTAVVLSFRSDKEGEGEGEDSDSNMAYVFEDEKRVYLKAGAITLKAQDNLIKQNTN 119
QY 121 D-----FTYSLKKEKLDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 170
Db 120 ENTNEENTDSFYSLSKKDLTLDTLSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
QY 171 DPTVHLNGIGSTLDTLDTLAGSSASHVDAGNOST--HYTRAASIKOVNAGNINIGVATGTST 228

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Db 180 DPTVHLNGIGSTLDTLDTLAGSSASHVDAGNOST--HYTRAASIKOVNAGNINIGVATGTST 239
QY 229 TQOSENVNDEVRRTDYVEFLSADTKTTTVNVEESKDNCKRTEVKIGAKTSYIKEDGKLVYG 288
Db 240 A--SDNVDEVRRTDYVEFLSADTKTTTVNVEESKDNCKRTEVKIGAKTSYIKEDGKLVYG 297
QY 289 KKGEGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTOAQKFEVYSGTVFTA 348
Db 298 KKGEGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTOAQKFEVYSGTVFTA 357
QY 349 SCNGTATVSKDDQGNITVYKVDVNGDALNVNOLNSGNMLDSKAVAGSSGKVISGNVSP 408
Db 358 SCNGTATVSKDDQGNITVYKVDVNGDALNVNOLNSGNMLDSKAVAGSSGKVISGNVSP 417
QY 409 SKGKMDETVYNAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNV 468
Db 418 SKGKMDETVYNAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNV 477
QY 469 GSKDANKPVRITNVAVGVEGEGVTNVAOLKGVANLNINRNDVNGNARAGIAQAIATAGL 528
Db 478 GSKDANKPVRITNVAVGVEGEGVTNVAOLKGVANLNINRNDVNGNARAGIAQAIATAGL 537
QY 529 AQAYLPGKSMMAIGGGTYLGEAGYATGYSISDPTGMWVJKGTASGNSRGHFGTSASVGYO 568
Db 538 AQAYLPGKSMMAIGGGTYLGEAGYATGYSISDPTGMWVJKGTASGNSRGHFGTSASVGYO 597
QY 589 W 589
Db 598 W 598

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RESULT 9
US-09-377-155-7
: Sequence 7, Application US/09377155
: Patent No. 6197312

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: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-7

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Query Match 86.0%; Score 2573.5; DB 4; Length 594;
Best Local Similarity 86.6%; Pred. No. 2.4e-181;
Matches 517; Conservative 20; Mismatches 49; Indels 11; Gaps 4;

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QY 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATVATLTLASATVQAATDDEDEL 60
Db 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAANATD-DDDLVL 59
QY 61 ESVAARSALVLOEMIDKEGNEIESTGDIWSIYDDHNTLHGATVTLKAGDNLKIKOSGK 120
Db 60 EYQVQRTAVVLSFRSDKEGEGEGEDSDSNMAYVFEDEKRVYLKAGAITLKAQDNLIKQNTN 119
QY 121 D-----FTYSLKKEKLDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 174
Db 120 ENTNEENTDSFYSLSKKDLTLDTLSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
QY 175 HLNGIGSTLDTLDTLAGSSASHVDAGNOST--HYTRAASIKOVNAGNINIGVATGTST 232

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Db 180 HUNGISTLDTLLNTGATNTVNDVTDDEKKRAASVKVLNAGWNKGVKPGTTA--S 237
      |||:|||||:|:|:|||||:|||||:|:|:|
Oy 233 ENDFVFTYDVEFLSADTKTTTVNVESKDNKGRTEVKAITSVKEKGLVTKGKG 292
      :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 238 DNDVFRTYDVEFLSADTKTTTVNVESKDNKGRTEVKAITSVKEKGLVTKGKG 297
Oy 293 ENGSTDEGGLVYAKVDAVNAKGRMKTTPANGOTGADFEVYTSCTKTPASGNG 352
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 298 ENGSTDEGGLVYAKVDAVNAKGRMKTTPANGOTGADFEVYTSCTKTPASGNG 357
Oy 353 TTATVSKDDGNTTVKDVAVNGDALNVNOLNSGWNLSKAVAGSSGKVISGNVSPSKG 412
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 358 TTATVSKDDGNTTVKDVAVNGDALNVNOLNSGWNLSKAVAGSSGKVISGNVSPSKG 417
Oy 413 MDETVINAGNIEITRNKNIDIAISMTPQFSSVSLGAGADAPTLVSDEGALNVGSKD 472
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 418 MDETVINAGNIEITRNKNIDIAISMTPQFSSVSLGAGADAPTLVSDEGALNVGSKD 477
Oy 473 ANKPRITTNVAPGVKEDVTVNAOLKGVNAQNLNRRIDNVGNARAGIAQAIATAGLQAY 532
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 478 TNKPRITTNVAPGVKEDVTVNAOLKGVNAQNLNRRIDNVGNARAGIAQAIATAGLQAY 537
Oy 533 LPKSMAAIGGTYLGEAGYAIIGYSSISDTGNWYIKGTASGNSRGHGTSAVGYOW 589
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 538 LPKSMAAIGGTYLGEAGYAIIGYSSISDTGNWYIKGTASGNSRGHGTSAVGYOW 594

```

RESULT 10  
US-09-669-974-7  
Sequence 7, Application US/09669974  
Patent No. 633173

```

: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669, 974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-7

```

Query Match 86.0%; Score 2573.5; DB 4; Length 594;  
Best Local Similarity 86.6%; Pred. No. 2.4e-181;  
Matches 517; Conservative 20; Mismatches 49; Indels 11; Gaps 4;

```

Oy 1 MNKIYRIIWNALNAAWVVSSELTNRNHTKRASATATATATATLLSTVQANATDDEDEL 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MNKIYRIIWNALNAAWVVSSELTNRNHTKRASATATATATATLLSTVQANATDDEDEL 59
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 61 ESVARSALVLOFMIDKEGNEIESTGDIIGMSIYYDDHNTLGATVTLKAGDLKIKQSGK 120
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 60 EPVQRTAVVLSFRSDKESTGEKEGEDSNMAVPEDEKRVLAGATTLKAGDLKIKQNTN 119
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 121 D-----FTYSLKRELKDLTSVETEKLSFGANGKRVNTSDTKGINFAKETAGTNGDPTV 174
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 120 ENTNDSFTYSIKDLTDLTJVSVEEKLSTFGANGKRVNTSDTKGINFAKETAGTNGDPTV 179
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 175 HUNGISTLDTLLNTGATNTVNDVTDDEKKRAASVKVLNAGWNKGVKPGTTA--S 232
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

Db 180 HUNGISTLDTLLNTGATNTVNDVTDDEKKRAASVKVLNAGWNKGVKPGTTA--S 237
      |||:|||||:|:|:|||||:|||||:|:|:|
Oy 233 ENDFVFTYDVEFLSADTKTTTVNVESKDNKGRTEVKAITSVKEKGLVTKGKG 292
      :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 238 DNDVFRTYDVEFLSADTKTTTVNVESKDNKGRTEVKAITSVKEKGLVTKGKG 297
Oy 293 ENGSTDEGGLVYAKVDAVNAKGRMKTTPANGOTGADFEVYTSCTKTPASGNG 352
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 298 ENGSTDEGGLVYAKVDAVNAKGRMKTTPANGOTGADFEVYTSCTKTPASGNG 357
Oy 353 TTATVSKDDGNTTVKDVAVNGDALNVNOLNSGWNLSKAVAGSSGKVISGNVSPSKG 412
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 358 TTATVSKDDGNTTVKDVAVNGDALNVNOLNSGWNLSKAVAGSSGKVISGNVSPSKG 417
Oy 413 MDETVINAGNIEITRNKNIDIAISMTPQFSSVSLGAGADAPTLVSDEGALNVGSKD 472
      |||:|:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 418 MDETVINAGNIEITRNKNIDIAISMTPQFSSVSLGAGADAPTLVSDEGALNVGSKD 477
Oy 473 ANKPRITTNVAPGVKEDVTVNAOLKGVNAQNLNRRIDNVGNARAGIAQAIATAGLQAY 532
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 478 TNKPRITTNVAPGVKEDVTVNAOLKGVNAQNLNRRIDNVGNARAGIAQAIATAGLQAY 537
Oy 533 LPKSMAAIGGTYLGEAGYAIIGYSSISDTGNWYIKGTASGNSRGHGTSAVGYOW 589
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 538 LPKSMAAIGGTYLGEAGYAIIGYSSISDTGNWYIKGTASGNSRGHGTSAVGYOW 594

```

RESULT 11  
US-09-377-155-9  
Sequence 9, Application US/09377155  
Patent No. 6197312

```

: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 9
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-9

```

Query Match 84.1%; Score 2516.5; DB 4; Length 594;  
Best Local Similarity 85.3%; Pred. No. 3.7e-177;  
Matches 509; Conservative 19; Mismatches 58; Indels 11; Gaps 4;

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Oy 1 MNKIYRIIWNALNAAWVVSSELTNRNHTKRASATATATATATLLSTVQANATDDEDEL 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MNKIYRIIWNALNAAWVVSSELTNRNHTKRASATATATATATLLSTVQANATDDEDEL 59
      |||:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 61 ESVARSALVLOFMIDKEGNEIESTGDIIGMSIYYDDHNTLGATVTLKAGDLKIKQSGK 117
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 60 EPVQRTAVVLSFRSDKESTGEKEGEDSNMAVPEDEKRVLAGATTLKAGDLKIKQNTN 119
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 118 ---SGKDFYSLKRELKDLTSVETEKLSFGANGKRVNTSDTKGINFAKETAGTNGDPTV 174
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 120 ENTNDSFTYSIKDLTDLTJVSVEEKLSTFGANGKRVNTSDTKGINFAKETAGTNGDPTV 179
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 175 HUNGISTLDTLLNTGATNTVNDVTDDEKKRAASVKVLNAGWNKGVKPGTTA--S 232
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 180 HUNGISTLDTLLNTGATNTVNDVTDDEKKRAASVKVLNAGWNKGVKPGTTA--S 237
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 233 ENDFVFTYDVEFLSADTKTTTVNVESKDNKGRTEVKAITSVKEKGLVTKGKG 292
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

Db 238 DNWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 297
Qy 293 ENGSSSTDBEGGLVTAKEVIDAVNKAQMRKTTTANGQTOAQKFEVTVSGTVTFASGNG 352
Db 298 ENDSSSTDBEGGLVTAKEVIDAVNKAQMRKTTTANGQTOAQKFEVTVSGTVTFASGNG 357
Qy 353 TTAATSKDQGNITVYKDYDYNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 412
Db 358 TTAATSKDQGNITVYKDYDYNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 417
Qy 413 MDETVINAGNNIEITRNCKNIDIAISMTPOFSSVSLGAGADAPTLSDVEGALNVGSKD 472
Db 418 MDETVINAGNNIEITRNCKNIDIAISMTPOFSSVSLGAGADAPTLSDVEGALNVGSKD 477
Qy 473 ANKPRVITVAVGKVEGDTVNAOLKGVAQNLNRRIDVNGNARACIAAIAATAGLAQAY 532
Db 478 ANKPRVITVAVGKVEGDTVNAOLKGVAQNLNRRIDVNGNARACIAAIAATAGLAQAY 537
Qy 533 LPEKSMMAIGGGTYLGEAGYTAIGYSSISPTGMNVIKGTASGNSRGHFGTSASVGYOM 589
Db 538 LPEKSMMAIGGGTYLGEAGYTAIGYSSISPTGMNVIKGTASGNSRGHFGTSASVGYOM 594
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RESULT 12
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9
```

```

Query Match 84.1%; Score 2516.5; DB 4; Length 594;
Best Local Similarity 85.3%; Pred. No. 3.7e-177;
Matches 509; Conservative 19; Mismatches 58; Indels 11; Gaps 4;

Qy 1 MKKIRIINNSALNMAVVSSELTRNHTKRASATVATVATLTLASATVQANATDDEDEL 60
Db 1 MKKIRIINNSALNMAVVSSELTRNHTKRASATVATVATLTLFAVQASTTD-DDDLVL 59
Qy 61 ESVAASALVQFMIDKEGGEIESTGDIQMSIYDDHNTLHG-ATYTLKAGDNLKIKO-- 117
Db 60 EYVQATVAVLSFRSDEKEGEKEVEDSMWGYFEDKKGVLTACTITLTKAGDNLKIKONN 119
Qy 118 ---SGKDFYSLKKELKDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNDPTV 174
Db 120 ENTNASSFTYSLKKDLTDLTSVETEKLSFANSKNVNTSDTKGLNFAKETAGTNDPTV 179
Qy 175 HNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIGVTKGSTTGS 232
Db 180 HNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIGVTKGSTTGS 237
Qy 233 ENWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 292
Db 238 DNWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 297
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Db 238 DNWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 297
Qy 293 ENGSSSTDBEGGLVTAKEVIDAVNKAQMRKTTTANGQTOAQKFEVTVSGTVTFASGNG 352
Db 298 ENDSSSTDBEGGLVTAKEVIDAVNKAQMRKTTTANGQTOAQKFEVTVSGTVTFASGNG 357
Qy 353 TTAATSKDQGNITVYKDYDYNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 412
Db 358 TTAATSKDQGNITVYKDYDYNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 417
Qy 413 MDETVINAGNNIEITRNCKNIDIAISMTPOFSSVSLGAGADAPTLSDVEGALNVGSKD 472
Db 418 MDETVINAGNNIEITRNCKNIDIAISMTPOFSSVSLGAGADAPTLSDVEGALNVGSKD 477
Qy 473 ANKPRVITVAVGKVEGDTVNAOLKGVAQNLNRRIDVNGNARACIAAIAATAGLAQAY 532
Db 478 ANKPRVITVAVGKVEGDTVNAOLKGVAQNLNRRIDVNGNARACIAAIAATAGLAQAY 537
Qy 533 LPEKSMMAIGGGTYLGEAGYTAIGYSSISPTGMNVIKGTASGNSRGHFGTSASVGYOM 589
Db 538 LPEKSMMAIGGGTYLGEAGYTAIGYSSISPTGMNVIKGTASGNSRGHFGTSASVGYOM 594
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```

RESULT 13
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17
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```

Query Match 83.2%; Score 2490.5; DB 4; Length 592;
Best Local Similarity 85.5%; Pred. No. 3e-175;
Matches 511; Conservative 18; Mismatches 54; Indels 15; Gaps 6;

Qy 1 MKKIRIINNSALNMAVVSSELTRNHTKRASATVATVATLTLASATVQANATDDEDEL 60
Db 1 MKKIRIINNSALNMAVVSSELTRNHTKRASATVATVATLTLFAVQANATDDEDEDEL 60
Qy 61 ESVAASALVQFMIDKEGGEIESTGDIQMSIYDDHNTLHG-ATYTLKAGDNLKIKO-- 117
Db 61 ESVOAS-VVGSIQASMEGSEVLET---ISLMTNDSKEVEDPYTVTLKAGDNLKIKONT 116
Qy 118 ---SGKDFYSLKKELKDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNDPTV 173
Db 117 NENTNASSFTYSLKKDLTGLINVEETKLSFGANGKNVNTSDTKGLNFAKETAGTNDPTV 176
Qy 174 VHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIGVTKGSTTGS 231
Db 177 VHLNGIGSTLTDLTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIGVTKGSTTGS 234
Qy 232 ENWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 291
Db 233 SDWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 294
Qy 292 GENGSSSTDBEGGLVTAKEVIDAVNKAQMRKTTTANGQTOAQKFEVTVSGTVTFASGNG 351
Db 238 DNWDFRVTDFVEFLSADTKTTTAVNESKDNCKRTEVKIGAKTSVIKEDGKLVYTGKDG 297
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Db 295 GENSSSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSCTKYTFASGN 354  
Qy 352 GTTATVSKDDGNTTVKDYVAVNGDALNVNQLONGMNLDSKAVAGSSGKTVISGNVSPSKG 411  
Db 355 GTTATVSKDDGNTTVKDYVAVNGDALNVNQLONGMNLDSKAVAGSSGKTVISGNVSPSKG 414  
Qy 412 KMDETVINAGNNIEITFRNGKNIDIAISMTPOFSSVSLGACADAPTLVSDDEGALNVGSK 471  
Db 415 KMDETVINAGNNIEITFRNGKNIDIAISMTPOFSSVSLGACADAPTLVSDDEGALNVGSK 474  
Qy 472 DANKPVRTNVAPEGVKBEDVTNVAQLKGVAONLNRRIDNVGNARAGIAOLAATAAGLVOA 531  
Db 475 DANKPVRTNVAPEGVKBEDVTNVAQLKGVAONLNRRIDNVGNARAGIAOLAATAAGLVOA 534  
Qy 532 YLPKSMMAIGGTYLGEAGYAIGYSSISDPTGNVYIKGTASGNSRGHGTASVGYOM 589  
Db 535 YLPKSMMAIGGTYLGEAGYAIGYSSISDPTGNVYIKGTASGNSRGHGTASVGYOM 592

## RESULT 14

US-09-669-974-17  
: Sequence 17, Application US/09669974  
: Patent No. 6333173  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/669, 974  
: PRIOR FILING DATE: 2000-09-26  
: PRIOR APPLICATION NUMBER: US 09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 17  
: LENGTH: 592  
: TYPE: PR  
: ORGANISM: Neisseria meningitidis  
US-09-669-974-17

Query Match 83.2%; Score 2490.5; DB 4; Length 592;  
Best Local Similarity 85.3%; Pred. No. 3e-175;  
Matches 511; Conservative 18; Mismatches 54; Indels 15; Gaps 6;

Qy 1 MNKIYRIIWNLSALNANWVYSELTRNHTKRASATYATATVATLTLSTATVOANATDDEDEEL 60  
Db 1 MNKIYRIIWNLSALNANWVYSELTRNHTKRASATYATATVATLTLSTATVOANATDDEDEEL 60  
Qy 61 ESVARSAVLQFMIDKEGNGEIESTGDIGMSIYYDDHNTLHG-ATVTLKAGDNLIKIKO-- 117  
Db 61 ESVARSAVLQFMIDKEGNGEIESTGDIGMSIYYDDHNTLHG-ATVTLKAGDNLIKIKO-- 117  
Qy 118 -----SGADFTYSLKELKDLTSETEKLSFGANGKNVITSDTKGLNPAKETAAGTNGDPT 173  
Db 117 NENTNASSFTYSLKELKDLTSETEKLSFGANGKNVITSDTKGLNPAKETAAGTNGDPT 176  
Qy 174 VHLNGIGSTLDTLTLGSSASHVDAGNOST--HYTRAASIKQVLNAGMNIKGVKGTSTGO 231  
Db 177 VHLNGIGSTLDTLTLGSSASHVDAGNOST--HYTRAASIKQVLNAGMNIKGVKGTSTGO 234  
Qy 232 SENVDVRYDYVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVIEKXGKLVTKGKG 291  
Db 235 SDNDVRYDYVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVIEKXGKLVTKGKG 294  
Qy 292 GENSSSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSCTKYTFASGN 351

Db 295 GENSSSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSCTKYTFASGN 354  
Qy 352 GTTATVSKDDGNTTVKDYVAVNGDALNVNQLONGMNLDSKAVAGSSGKTVISGNVSPSKG 411  
Db 355 GTTATVSKDDGNTTVKDYVAVNGDALNVNQLONGMNLDSKAVAGSSGKTVISGNVSPSKG 414  
Qy 412 KMDETVINAGNNIEITFRNGKNIDIAISMTPOFSSVSLGACADAPTLVSDDEGALNVGSK 471  
Db 415 KMDETVINAGNNIEITFRNGKNIDIAISMTPOFSSVSLGACADAPTLVSDDEGALNVGSK 474  
Qy 472 DANKPVRTNVAPEGVKBEDVTNVAQLKGVAONLNRRIDNVGNARAGIAOLAATAAGLVOA 531  
Db 475 DANKPVRTNVAPEGVKBEDVTNVAQLKGVAONLNRRIDNVGNARAGIAOLAATAAGLVOA 534  
Qy 532 YLPKSMMAIGGTYLGEAGYAIGYSSISDPTGNVYIKGTASGNSRGHGTASVGYOM 589  
Db 535 YLPKSMMAIGGTYLGEAGYAIGYSSISDPTGNVYIKGTASGNSRGHGTASVGYOM 592

## RESULT 15

US-09-377-155-21  
: Sequence 21, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 21  
: LENGTH: 591  
: TYPE: PR  
: ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 82.8%; Score 2479; DB 4; Length 591;  
Best Local Similarity 84.2%; Pred. No. 2.1e-174;  
Matches 502; Conservative 28; Mismatches 54; Indels 12; Gaps 6;

Qy 1 MNKIYRIIWNLSALNANWVYSELTRNHTKRASATYATATVATLTLSTATVOANATDDEDEE- 59  
Db 1 MNKIYRIIWNLSALNANWVYSELTRNHTKRASATYATATVATLTLSTATVOANATDDEDEE- 60  
Qy 60 -LESVARSAVLQFMIDKEGNGE---IESTGDIGMSIYYDDHNTLHGATVTLKAGDNLIK 115  
Db 61 YLDPQRTVAALVINSDEGEGEKEEENSND--WAYFENEKGYLTAREILTKAGDNLIK 118  
Qy 116 KOSGKDDFTYSLKELKDLTSETEKLSFGANGKNVITSDTKGLNPAKETAAGTNGDPTVH 175  
Db 119 KONGNFTYSLKELKDLTSETEKLSFGANGKNVITSDTKGLNPAKETAAGTNGDPTVH 178  
Qy 176 LNGIGSTLDTLTLGSSASHVDAGNOST--HYTRAASIKQVLNAGMNIKGVKGTSTGOSE 233  
Db 179 LNGIGSTLDTLTLGSSASHVDAGNOST--HYTRAASIKQVLNAGMNIKGVKGTSTGOSE 236  
Qy 234 NVDFVRYDYVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVIEKXGKLVTKGKG 293  
Db 237 NVDFVRYDYVEFLSADTKTTTVNVEESKDNKRTEVKIGAKTSVIEKXGKLVTKGKG 296  
Qy 294 NGSSSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSCTKYTFASGN 353  
Db 297 NGSSSTDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEYVTSCTKYTFASGN 356  
Qy 354 TATVSKDDGNTTVKDYVAVNGDALNVNQLONGMNLDSKAVAGSSGKTVISGNVSPSKG 413

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Db 357 TATVSKDDGNTVTMYDVNVGDALNVNLQNSGMNLDKAVAGSSGKVTSGNVSPSKGM 416
QY 414 DETVNINAGNNIEITRNGKNIDIAITSMTPQESSVSLGAGADAPTLSVDEGALNVGSKDA 473
Db 417 DETVNINAGNNIEITRNGKNIDIAITSMTPQESSVSLGAGADAPTLSVDGD-ALNVGSKRD 475
QY 474 NKPVRTTNVAPGVKEDDYTNVAQLKGVAQNLRNIDNVNGNARAGTAQAATAAGLAQAYL 533
Db 476 NKPVRTTNVAPGVKEDDYTNVAQLKGVAQNLRNIDNVNGNARAGTAQAATAAGLAQAYL 535
QY 534 PKSMMAIGGTYLGEAGYAIGYSSISDTPGNVYIKGTASGNSRGRHGTASVGYOW 589
Db 536 PKSMMAIGGTYRGEAGYAIGYSSISDGNWLIKGTASGNSRGRHGTASVGYOW 591

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Search completed: July 3, 2002, 08:10:15  
 Job time: 527 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:05 ; Search time 95.27 Seconds  
(without alignments)  
594.065 Million cell updates/sec

Title: US-09-771-382-3

Perfect score: 2994

Sequence: 1 MNKIYRIINMSALNMAWVVS.....TASGNSRGHFGTSASVGYQW 589

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 2626.5 | 87.7        | 592    | 2     | A81888      |
| 2          | 2479   | 82.8        | 591    | 2     | G81133      |
| 3          | 600.5  | 20.1        | 298    | 2     | I64138      |
| 4          | 423    | 14.1        | 2059   | 2     | D82671      |
| 5          | 399    | 13.3        | 1190   | 2     | A82615      |
| 6          | 358    | 12.0        | 1588   | 2     | A86036      |
| 7          | 358    | 12.0        | 1588   | 2     | H91188      |
| 8          | 352    | 11.8        | 1107   | 2     | AC0976      |
| 9          | 332.5  | 11.1        | 658    | 2     | AH0110      |
| 10         | 257.5  | 8.6         | 1004   | 2     | C82672      |
| 11         | 245    | 8.2         | 1325   | 2     | A64905      |
| 12         | 235    | 7.8         | 1417   | 2     | A83080      |
| 13         | 232.5  | 7.8         | 1018   | 2     | H81335      |
| 14         | 228    | 7.6         | 1343   | 2     | E90893      |
| 15         | 225.5  | 7.5         | 5188   | 2     | B85547      |
| 16         | 225.5  | 7.5         | 5291   | 2     | F90696      |
| 17         | 225    | 7.5         | 1343   | 2     | D85724      |
| 18         | 223    | 7.4         | 1910   | 2     | AF0394      |
| 19         | 219.5  | 7.3         | 949    | 2     | D90803      |
| 20         | 219.5  | 7.3         | 1005   | 2     | H85611      |
| 21         | 218    | 7.3         | 4919   | 2     | G49664      |
| 22         | 216.5  | 7.2         | 1091   | 2     | T31105      |
| 23         | 216.5  | 7.2         | 1361   | 2     | T03415      |
| 24         | 216.5  | 7.2         | 1608   | 2     | A28182      |
| 25         | 210    | 7.0         | 1536   | 2     | A43855      |
| 26         | 209.5  | 7.0         | 1286   | 2     | S28634      |
| 27         | 209    | 7.0         | 918    | 2     | AB2445      |
| 28         | 207.5  | 6.9         | 3705   | 2     | AD0123      |
| 29         | 205.5  | 6.9         | 1651   | 2     | JC1340      |

|    |       |     |      |   |        |                     |
|----|-------|-----|------|---|--------|---------------------|
| 30 | 203.5 | 6.8 | 1275 | 2 | T33369 | hypothetical prote  |
| 31 | 203.5 | 6.8 | 2249 | 2 | A41477 | 190k surface anti   |
| 32 | 203   | 6.8 | 1327 | 2 | B90674 | Aida-I adhesin-lik  |
| 33 | 203   | 6.8 | 1349 | 2 | E85524 | probable beta-bar   |
| 34 | 202   | 6.7 | 936  | 2 | I40711 | sapB protein - Cam  |
| 35 | 202   | 6.7 | 1366 | 2 | S57664 | IGA-specific meta   |
| 36 | 201.5 | 6.7 | 1109 | 2 | A56143 | surface-array prot  |
| 37 | 201   | 6.7 | 1238 | 2 | AH0038 | probable exported   |
| 38 | 200   | 6.7 | 1430 | 2 | AF0351 | probable autotrans  |
| 39 | 197   | 6.6 | 2703 | 2 | H81193 | hemagglutinin/hemo  |
| 40 | 196   | 6.5 | 1477 | 2 | B43855 | high-molecular-wel  |
| 41 | 196   | 6.5 | 1567 | 2 | S11672 | ice nucleation pro  |
| 42 | 195   | 6.5 | 3013 | 2 | AB0480 | probable invasion y |
| 43 | 194   | 6.5 | 2020 | 2 | C48399 | ABC-type transpor   |
| 44 | 192.5 | 6.4 | 4936 | 2 | AH2515 | hypothetical prote  |
| 45 | 191.5 | 6.4 | 980  | 2 | H90681 | probable flagellin  |

## ALIGNMENTS

RESULT 1  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence-revision 05-May-2000 #text-change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491  
A:Reference number: A81775; M01D:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84461.1; PID:9737  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

| Query Match | Best Local Similarity | 87.7%               | Score 2626.5         | DB 2               | Length 592 |
|-------------|-----------------------|---------------------|----------------------|--------------------|------------|
| Matches 531 | Conservative 13       | Mismatches 41       | Indels 11            | Gaps 4             |            |
| QY 1        | MNKYRIINMSALNMAWVVS   | ELTRNHTKRASATVATLTL | LSATVQANATPDEDEEL    | 60                 |            |
| DB 1        | MNKYRIINMSALNMAWVVS   | ELTRNHTKRASATVATLTL | LSATVQANATPDEDEEL    | 60                 |            |
| QY 61       | ESVARSALVQEMIDKEGNGE  | IESTGDIQMSIYYDHN    | TLHG-ATYTLKAGDNLKIKO | 117                |            |
| DB 61       | ESVARSALVQEMIDKEGNGE  | IESTGDIQMSIYYDHN    | TLHG-ATYTLKAGDNLKIKO | 117                |            |
| QY 118      | -----SKDKFTYSLKKE     | LKDLTSTYETELKLSFG   | ANGKVNITSDPKGLNFAK   | ETAGTNDPT 173      |            |
| DB 117      | NENTNASSFTYSLKDKD     | LTGLINETERKLSFG     | ANGKVNITSDPKGLNFAK   | ETAGTNDPT 176      |            |
| QY 174      | VHLNGIGSTLTDRLAG      | SSASHVDAGNOSTHYT    | PAASIKDVLNAGWNIKG    | VTGOSTGOST 233     |            |
| DB 177      | VHLNGIGSTLTDRLAG      | SSASHVDAGNOSTHYT    | PAASIKDVLNAGWNIKG    | VTGOSTGOST 236     |            |
| QY 234      | NDVFVTTYDTEFLSAD      | TKTTTVNVEKDKNGK     | TEVAKIGAKTSVIEKDG    | KLVYTGKGKE 293     |            |
| DB 237      | NDVFVTTYDTEFLSAD      | TKTTTVNVEKDKNGK     | TEVAKIGAKTSVIEKDG    | KLVYTGKGKE 296     |            |
| QY 294      | NGSSTDEGEGIVTAKE      | VIDAVNKAQRMTTNT     | ANGOTGODKRETYSGT     | KVFPASGNGT 353     |            |
| DB 297      | NGSSTDEGEGIVTAKE      | VIDAVNKAQRMTTNT     | ANGOTGODKRETYSGT     | KVFPASGNGT 356     |            |
| QY 354      | TATVSKDDOGNITVKY      | DVNVGALNVNOLONG     | SGMNLDSKAVAGSSG      | KVVISGNTSPSKGM 413 |            |
| DB 357      | TATVSKDDOGNITVKY      | DVNVGALNVNOLONG     | SGMNLDSKAVAGSSG      | KVVISGNTSPSKGM 416 |            |

|    |     |                                                            |     |
|----|-----|------------------------------------------------------------|-----|
| Oy | 414 | DETVMNNGNNIETTRNCKNIDITSMTPQSSSVSLAGADAPLTVDDDEALNVGSKDA   | 473 |
| Db | 417 | DETVMNNGNNIETSRNCKNIDITSMAPQSSSVSLAGADAPLTVDDDEALNVGSKDA   | 476 |
| Oy | 474 | NKPVKITVNAVGVEGDVTVNAOLKQVAAQNNNRINDVNGNARIGIQAOTATAGLAAYL | 533 |
| Db | 477 | NKPVKITVNAVGVEGDVTVNAOLKQVAAQNNNRINDVNGNARIGIQAOTATAGLAAYL | 536 |
| Oy | 534 | PKKSMMAIGGGTYLGEAGYAIGYSSISDPTGMMWVTKGTASNGSRGHPGTSASVGTQW | 589 |
| Db | 537 | PKKSMMAIGGGTYLGEAGYAIGYSSISDGTGMMWVTKGTASNGSRGHPGTSASVGTQW | 592 |

## RESULT 2

adhesin NMB0992[imported] - *Neisseria meningitidis* (strain MC58 serogroup B)  
C.Species: *Neisseria meningitidis*  
C.Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C.Accession: G81133  
R.Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qin, H.; Vamthyan, J.; Gill, J.; Scarlatti, V.; Masiugnani, V.; Pizze, M. Science 287, 1809-1815, 2000  
A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Ver  
A.Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A.Reference number: A61000; MUID:2017575  
A.Accession: G81133  
A.Status: Preliminary  
A.Molecule type: DNA  
A.Residues: 1-591 <TE>  
A.Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AA41395.1; PID:g722622  
A.Experimental source: serogroup B, strain MC58  
C.Gene: NMB0992

|                           |       |                    |            |            |
|---------------------------|-------|--------------------|------------|------------|
| Query Match               | 82.8% | Score 2479         | DB 2       | Length 591 |
| Best Local Similarity     | 84.2% | Pred. No. 6.4e-121 |            |            |
| Matches 502; Conservative | 28;   | Mismatches 54;     | Indels 12; | Gaps 6;    |

|    |     |                                                                 |     |
|----|-----|-----------------------------------------------------------------|-----|
| OY | 1   | MNKYRIITNSALNAMYVSVSELTENHNRKRASATYATVILATLLSATVOANLTDJDEEE-    | 59  |
| Dd | 1   | MNKYRIITNSALNAMYVSELTRNHKRASATYATVILATLLSATVOASNNNEQDEDL        | 60  |
| OY | 60  | -LESVARSALYLOFMIDKEGNGE--IESTGDIGMSIYDDHNLHGATVYLTKAGMDLKI      | 115 |
| Dd | 61  | YLDPOQTFAVILIYNSDEKGEKEKEVENSND--MAVYFEGGYLTAREITLTKAGMDLKI     | 118 |
| OY | 116 | KOSGDEFTYSLKKELEKDLTSLVEYKELSPGANGKVNITSDPKGLNPAKERTAGNGDPTVH   | 175 |
| Dd | 119 | KONGNFYSLKDKDLTDLTSLVGEKLSFSAANGKNVNTSDPKGLNPAKERTAGNGDPTVH     | 178 |
| OY | 176 | LNGLIGSTLTDLTLAGSSAHVDAGNQST--HYTRASAIKIDVYLNAGMNLKGYVTSQTQOSE  | 233 |
| Dd | 179 | LNGLIGSTLTDLTLNLTGATNTVNTNNTDDEKKRAASVAKDYLNAGMNLKGYVPGTTLA--SD | 236 |
| OY | 234 | NVDYPRYTDYVEFLSADPKTTTVANVESKDNCKRPEVKIIGAKTSYIKERDGLVYTGKKE    | 293 |
| Dd | 237 | NVDYPRYTDYVEFLSADPKTTTVANVESKDNCKRPEVKIIGAKTSYIKERDGLVYTGKKE    | 296 |
| OY | 294 | NGSSTDEGEGLVTAKEVYDAVNKAGMRKTTTANGQFQGAOKPEFYVSGTVYFPAASNGT     | 353 |
| Dd | 297 | NGSSTDEBEGLVTAKEVIDAVNKGWRKTKTTANGQFQGAOKPEFYVSGTVYFPAASRGT     | 356 |
| OY | 354 | TATVSKDDQGNITVYKYDVNVGDALNVLNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKGM   | 413 |
| Dd | 357 | TATVSKDDQGNITVYKYDVNVGDALNVLNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKGM   | 416 |
| OY | 414 | DETVMNNGNNIEITRNCKNIDITASMPPOSSVSLAGADAPLTVSDDEBALNVGSKDA       | 473 |
| Dd | 417 | DETVMNNGNNIEITRNCKNIDITASMPPOSSVSLAGADAPLTVSDG--ALNVGSKKD       | 475 |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| OY | 474 | NKPVRITVAVAGVEGDVTNYAOLCKGYAQNINNTIDVNWGNARAGIAQOALATATGLQAYL | 533 |
| Db | 476 | NKPVRITVAVAGVEGDVTNYAOLCKGYAQNINNTIDVNWGNARAGIAQOALATATGLQAYL | 535 |
| OY | 534 | PKSMAALGGGTYYLGEAGYALCYGISIDTGYMMVTKGTAAGSRNRHPTSAVGYOM       | 589 |
| Db | 536 | PKSMAALGGGTYYLGEAGYALCYGISIDTGYMMVTKGTAAGSRNRHPTSAVGYOM       | 591 |

### RESULT 3

adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: 164138  
R:Flatschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: 164138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:U42023; NID:g1574588; PID:g1574589; TIGR:HI1732

|                       |                 |                   |           |            |
|-----------------------|-----------------|-------------------|-----------|------------|
| Query Match           | 20.1%           | Score 600.5       | DB 2      | Length 298 |
| Best Local Similarity | 46.0%           | Pred. No. 3.2e+24 |           |            |
| Matches 150           | Conservative 32 | Mismatches 87     | Indels 57 | Gaps 11    |

```

OY      1 MNRIRITMNSALNAAVVVSELTENHRRKRSATVAATVTLTLLSATVOA-----NAT 52
Db      1 MNRIFKVIMNVVQTVWVVSELTEHRHKRISATVATAVLAVLTSATVQAOLINDAGTFVKYG 60
OY      53 DTDEBEELSESARSAKLVLQFMIDKEGNGEISTEDIGMSIYYDDHNLTGHATYTLKRGDN 112
Db      61 STEDIE--DSATRK-----DNNKQAKLA-----GDTLTLIAAGKN 94

```

```

QY 113 LKIK--GSGKDPYLSIKKELKDLDSVEHEKLSFAN-----GNKNYISDPKGINFAK 163
Db 95 LKAKIDOGGKSVTLALADLDVYKAKVSDTLTIGGNTPAAGATPKVSTLSTADGLKLA 154
QY 164 ETAGNGDPYTHLNGISGTLTDLTLAGSSAS--HYDAGNOSTHYTPAASIKDVLNAGNWK 222
Db 155 ---GNNGDTAHLNGLASTLTPDYVTNNGASISVTFPSRDIETKPAATIKDVLNAGNWK 211
QY 223 VKTSGTSGSENVDFVRTYDVTVEFLSADTKTTTVNVEBKONGKRTVEYICAKTSVYKEK 282
Db 212 AKVAG--GNTENVDLVAGYDVAVEFTGDKNTLDVLTAKENGKTTVEYFKPKTSVIGDN 269
QY 283 GKLYTK-----GKGNGS--STDE 300
Db 270 GKLLTGKQLKANTGTATNATEDDE 295

```

## RESULT 4

surface protein Xp1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:Anonymous: The Xylella fastidiosa Consortium of the Organisation for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: D82671  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2059 <STM>



A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H.  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,  
A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1529

Query Match 14.1%; Score 423; DB 2; Length 2059;

Best Local Similarity 24.9%; Pred. No. 5.9e-14;  
Matches 173; Conservative 97; Mismatches 225; Indels 200; Gaps 32;

```
OY 58 EELESVARSALVLOFMIDKEGNGEISTGDIQMSIYYDDHN---TLHGATVTLKAGD-NL 113
DB 1402 EETDAVNRSOL-----KSISTAVDQCVITLITASANGSKVAAGCTVILKNTDNL 1450
OY 114 KIKOSG--KDFYSLKKEIKDL-----TSVTEKLSFGAN---GNKVNITSDT----- 156
DB 1451 TISKSGDNDVYFNLESDLEKSIYVNTQDLKDGKVVSNVLLSNELVITSHSSTSSV 1510
OY 157 ---KGLNFAKETA-----GTNCDPVLHNGIGSTLTD---TLASSA-----SHVDAGN 199
DB 1511 KTLANGESVNVNFTVNGDGVNIDVYVNDGLSTVGASLTLISIMAGSHKRTVNTAGT 1570
OY 200 QST---HYTRASIKDVLNAGNIGV--KTGSGTQSENVDFVRT-----YDT 243
DB 1571 EETDAVNRSOLKSVSEAVDKMTLITASANGSKVAAGCTVILKNTDNLITKSGSDNDV 1630
OY 244 VEELISADTK-----TTTVNESKDNKGRTEVKIGAKTSVIREKDGKLVTKKGEN-- 294
DB 1631 VFNLSKDFEVDVTAAGNIVYNTDGVKVG--SDVSLGAMGLFANGPSVYASGFNAGDKVI 1688
OY 295 ---GSSTDEEGGLVTAKEVDVANKAGWRMKTTTANGCQ-----QADKEFYTS 341
DB 1689 SHVAVGMADTDAVNVSOLKQAVQSVYKATRYSTNDGCTGGNVDGCGATSKAIAAGV 1748
OY 342 GTKVT-----FASNGT-----ATVSKD-----DOG-----NITVKKYD- 370
DB 1749 GTQASGEGAAVAGSAAASGKSTAIGRNALIASADGVALGCGANDGCGAESYTGKYSG 1808
OY 371 ---VNVG-----DALNVNQL-----QNSGMNLDL----- 391
DB 1809 VQNTVGVTVSGVDAKGETRISINVAADAKAMDADVNLRLQDLDAVQKSNLQTDMDMHEINN 1868
OY 392 ---KAVAGSGKVIISGVNSPSKGMDETIVINA---GNNIETRN-----GKNIDIAT 438
DB 1869 IEDVEKIKTKGSASSVKG-----MGVNAIAIGTNAVSGTESVALGKNTNVA 1916
OY 439 SMTPOFSSVSLGAGADPTLSVDDEGALNVGSKDANKPVRITNVAPGVREGVTVNAOLK 498
DB 1917 D-----NAVAINGSYA-----DRANSYVSGGSSER--QVTNVAAGTADTDAVNVSQNL 1964
OY 499 GVAQNLNRRIDNVNGNAR---AGIAQIATAGLAQVLPKSSMAIGGGTILGEGYAI 554
DB 1965 OGLITAKQYTDGVMGNLNRRTSGVAAAIATATNLPAQVYQGGKMTSVGVSSVQGGSAIATV 2024
OY 555 GYSSISIDPQNMVYIKGTASGNSRGHGTASVGYOW 589
DB 2025 GYSAVSESHVWFKEFGSANTRSHVGVAGVGYOW 2059
```

RESULT 5

AB2615  
Surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: AB2615

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: AB2615  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-1190 <STM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN

A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,  
A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1981

Query Match 13.3%; Score 399; DB 2; Length 1190;

Best Local Similarity 26.3%; Pred. No. 5e-13;  
Matches 162; Conservative 92; Mismatches 219; Indels 144; Gaps 29;

```
OY 25 NHTKRASATVAT---AVLATLISA-----TVOANATDMD--EDELLESVARSALVLOFM 73
DB 666 NTLTGSTGLVITDGPSTVSSGINSAGNOKITVNAAGTADDAVNFSQLQVS----- 716
OY 74 IDKEGNGEISTGDIQMSIY---YDDHNTLHGATVTLKAGD-NLKT-KOSG-KDFYSLK 127
DB 717 ---STASKGMNLLASGANSNVAPEESVDLTKFTDGIYISKESGSDVLENTLS 766
OY 128 KELKDLTSVETEKLSPGANGKVNITSDFKLNFAGETAGTNDPVLHNGIGSTLTDPL 187
DB 767 SSLK-----LDKLVG-----DIYMTNGV-----TYGSG-----VTLSGKGLVTD-- 803
OY 188 AGSS--ASHVADAGNOS--THYTRASIKDVLNAGNIGVKTGSGTQSENVDFVRTDVT 244
DB 804 -GSPVTSIGINAGSKITVNAAGTADTDAV---NLSQNTAMAGSGASVHYSTYD-- 856
OY 245 EFLSADTKTTTVNESKDNKGRTEVKIGAKTSVIREKDGKLVTKKGENG--SSTDEGG 303
DB 857 ---GCTGGNNGCDATGTRSIANGVGLASA---EGATAVGSAAASGKSTAIGRN 908
OY 304 LVTAKEVIDAVNKKAGWRMKTTTANGCTGOADKFEFVTSCTKYTFASGNGTATATSKDDG 363
DB 909 AVASADGVALD--GAKDARGAESTYTKYSGLQNTTIVTIVSGADSKETRTVS----- 962
OY 364 NITVRYDVNVGALNVNQL---QNSGMNLDKAVAGSGSKVYISGVNSPSKGMDETIVNI 419
DB 963 NVAADAKAAT--DAVNLRLQDLDAVQKSNLQTDMDMHEINN-----VAV 1006
OY 420 NAGNNIETRNKGNKIDIASMTPOFSSVSLGAGADA-----PLTVDDDEGAL-- 466
DB 1007 NSLNN-----SAPPIAGVADATAIAGVATASGADSIAMGNKASASADNAVALGN 1055
OY 467 -----NVGSKDANKPVRITNVAPGVKEGDTVNVQNLGVQVQNLNRRIDNVNGNAR 516
```



```
QY 314 VN-----KAGRMKTTTANGOTGOADKFFETVTSQTK----- 344
DB 1179 IGAVALTPPKYFPHANSTEDSLAVGTDSLAMGAKTIVNDKRGITGIGYAVDANALNGIA 1238
QY 345 -----VTFASNGTTFAT-----VSKDDGQNTTVKYD 370
DB 1239 IGSNAQVIHVNIAIGNGSTTRGCAQNTYATYNDAPQNSVEGSEFVSADGQROLT--- 1295
QY 371 VNVG-----DALNVNLOL-----NSGMJLDSK----- 392
DB 1236 VAAGADPTDAVNVGQLKTYTDAQVSONTOSITNLDNRVTNLDLRVTNIENGIDIVTTGST 1355
QY 393 -----AVAGSGKVISGNVSPSKG-----KMDETVINAGNNIEIR 429
DB 1356 KYFKNTDGVNDSAGQKDSVALGSSIAADNSVALGTGSVATEENTIVSGSTNORRT 1415
QY 430 N---GKNIDIATSMTPQPSFVSVLGAGADAPTLVDEGALNVGSKDANKPVRITNAPCV 486
DB 1416 NVAAGKNAITDAVNAVQLKSESEAGVRYDTPKADGSIDYSNITLGCGNGG--TTRISNVAGV 1474
QY 487 KEGDVTNVAQLKGVAQ-----NLNNRIDNVNGNARGICIAQALITAGLAQAYLPF 535
DB 1475 NNNDVNVNAQOLKQSVQETKQYTDQRMVEMDNKLSKTESKLSGGLASAMAMTGLPQAYTPG 1534
QY 536 KSMMAIGGTYLGEAGYALGYSSISDTGCMVTKGTASGNSRGHFGTSASVGYOW 589
DB 1535 ASMASTGGTNGESAVALGSMVANSANGRVYKLOGSTNSQGEFYSALGAGIOW 1588
```

```
RESULT 8
AC0976
probable autotransporter sapsb [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
  th., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
  S.; Moule, S.; O'Gaora, P.
  Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
  A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CA00303.1; PID:q16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapsb
```

```
Query Match 11.8%; Score 352; DB 2; Length 1107;
Best Local Similarity 20.3%; Pred. No. 1.2e-10;
Matches 174; Conservative 111; Mismatches 256; Indels 316; Gaps 29;

QY 27 TKRASATVATAVLATLLSATVQANATDDEDELSVARSALVLOFMIDKEGNGELE--- 83
DB 273 TFSASRNGSASKITMLAAGTTLAADSDAVNGSQLYETNOK-----VDQNTSAIDIMT 325
QY 84 -----STGIGMSIYYDDHNTLHGATVTLK-----AGD-----NLKIK 116
DB 326 SITNLSDDLNSNNETNNSFSASHGSTTKKTINNAAGELSESTDAVNGSQLFETNEKVD 385
QY 117 QSGKDFVYSLKELDLTVSETEKLS-----FGAN--GNKV 150
DB 386 QUTTILAAATNTITQNSAIEMLNITSVDINTSITGLTDNALMDEDTGAFSANHGGS 445
QY 151 NITSOTKGINFKKETAAGTNGDPTVHLN-----GIGSTLT-----DTLAG 189
DB 446 KITNVAAGALSDESDTDAVNGSQLYETNOKVDONTSAIADINTSITMLGTDALSWDEDEGA 505
QY 190 SSASHVDAG--NOSTHYTRAASIKDVLNAGWNIKGVKTSSTGQSENVDPVRYDYEFIS 248
```

```
DB 506 FSASHGTSCTNKTITNVAAGEIASDSTDA---INGSQLYET-----NMLISQYNEISQOLA 557
QY 249 ADTKTTTVN-----VSKDNGKRTVEYKIGAKTSVIEKDGKLVYTG--KENGSS 297
DB 558 GDTSEFYITENGTVKYIIRTNDNGLEGODAYATGNCATVAGDAVAGACIALGONSSS 617
QY 298 TDEG-----EGLY-----TAKEVIDAVNKA-----GWRMKT 323
DB 618 STEGSIALGSGTSNRAITTTGIRETSATSDGVYIGINTTDRELGLALSLCTDGESTRQIT 677
QY 324 TTANGGQ-----ADKFETVTSQTFVTFASNGTTFATVSKDDQGN 365
DB 678 NVADGSEADATVAYROLQNAIGAVTTTPKRYHANSTEDSLAVGTDSLAMGAK----- 732
QY 366 TVKYDVNVGDALNVNOLN--SGWNIDSKAVAGSSGKVISGNVP----- 408
DB 733 IYNADAGIGIGINTLVMAINGIAIGSNARANHANSIMAGNSQTTTGAQOTDYATVNMND 792
QY 409 -----SKGMD-----ETVINMAGN-----NEIIRNGKNI----- 434
DB 793 TPQNSYGEFVSSEDEQROITNVAAGSADPTDAVNVGQLKYTDQVSRNTQSTINLNTQVS 852
QY 435 -----DIATSMTPQF-----SSVSLGAGADAP-----T 457
DB 853 NIDFRTYNTIENGIDLVYTTGSKTYFKTNTDADANAGADSVAILGSSIAAENSVALGT 912
QY 458 LSVDE--GALNVGSKDANKPVRITNAPCVKEGDVTNVAQLK----- 498
DB 913 NSVADENAVTVSVGSSFTQQR--RITNVAAGVNNMTDAVNAVQLKASEAGSVRYETNADGSVN 970
QY 499 -----GVNQ-----NLNNRIDNVN 512
DB 971 YSVNLGDSGGTTRIGNVSAAVNDTDAVNAVQLKRSVEBANTYTDQKMGEMSKIKGLE 1030
QY 513 GNARAGIAOAITAGLAQAYLPKSKMAIGGTYLGEAGYALGYSSISDPTGNNVITGTAS 572
DB 1031 NKMSGIASAMAMAGLPQAYARPAANTSTIAGTFNESAVALGVSNSGCGVYTYLQGT 1090
QY 573 GNSRGHFGTSASVGYOW 589
DB 1091 SNSQGDYSAATGAGFCOW 1107
```

```
RESULT 9
AH0110
probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M
  deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
  11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
  Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:q15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YP00902
```

```
Query Match 11.1%; Score 332.5; DB 2; Length 658;
Best Local Similarity 23.9%; Pred. No. 6.3e-10;
Matches 154; Conservative 80; Mismatches 239; Indels 171; Gaps 26;

QY 27 TKRASATVAT---AVLATLLSATVQ-----ANATDDED--EELSVARSALVLOFM 73
DB 105 TNLAPATISSTPTDAVVGSQLVNLVQDGRYFPHANSVNPFTDSLASGLERIA----- 155
```

A:Gene: XF1516

```
Query Match      8.68; Score 257.5; DB 2; Length 1004;
Best Local Similarity 21.38; Pred. No. 8.2e-06;
Matches 158; Conservative 105; Mismatches 264; Indels 207; Gaps 33;

OY 2 NKIIRIINSALNMMVWVSELTNR-----HTKRASATVATVATLATLATVQANAT 52
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 NOITRKFENSLSGSVASVASHMTNDGCGSDVYLRRISGVRNRLVLALIGALTSTV 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 53 DTDEDELESVARSL-----VLQFMIDKEGNGEIE-STGD-----IGMSIYYDD 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 -----HQSVKSPAMVYASKVVAHVDSQVNPFRADRIPTGDSSELTMTMALDMKFFPF 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 97 -HNTL-----HGATVTLKADNLIKIKOSGDFPFLSLKELKDLTSVETE 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 112 NNSIIGFESKAFAPNALALGYNSSVTQSANNGVAL--GSNSTVS-----GVNSV 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 140 KLSFPAANKNNIYS-----DTKGLNFAKETAGTGGDPVTHLNGIG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 ALGASMSASLELVISVGGGCVTGPVARIYVNGDIGNNDVAVKSQLDQ-VTASVNDVA 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 181 ST-----LTDTLAGSSASHVDAGNOSTHY---TRAASIKDYLNAGWNLIKGVKTSGTSGS 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 ASVKIATLNTQVYTGSSVASA-SGKESTALIGSAQAVADNTVAFGRAITANVGSALGFD 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 223 ENVDVFRTYDVEFLADTKTYYNVEESK-----NKRTEYKIGAKTSV 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 SHAKGI-----NSTVTGTQSVSLGOGGVSLGYNSEFVGESEFNLALGSNSLV 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 278 IKERKGLVTKGK--KGENSSSTDEGGL--VTAKEYI-----DAVNKAGMRKPT 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 ILQGVDSVALGSGMSASEPNVYVSGSGDLKGPVARIYVNGDIGNNDVAVKSQLDQVT 384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 324 TTANGOTGQADKFETV--TSGTKYTFASGNGTTAT-VSKDDGNITVYKYDVVNGDALNVN 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 ASVNDVVASVKKIACAIQITGSGVASVSGDSPTAGASQAQAGDSISA---LGRSPAN 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 381 OLONGSGWLD-----SKAVAGSSGKVIYSGNVSPSKGMDETVMINAGNNIEITRNCKN 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ALGSSALGVDGHALGANSTALGOSTAISSEGTSTIG--YNSFVQASATNGIALGSN--- 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 434 IDIATSMTPQFSSVSLGAGADAPTLSDVEDEALANGSKD-ANKPY--RTIYVAPGKEGD 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 -----AIVSGVNSVALGAGSVASELNV-----ISVGGDCGYTGPVARIYVNGDIGNND 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 491 VTNVAOLKVAQNLNN--RIDNVNGNAR--AGIAQAI--ATAGLAQAYLPGKSMMAI 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 AVNKSOLDGVTAIVNDVYASVKKIYGTIQTIGSGVASAIGKRSFTGASQAQVGDSSVAL 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 542 G-----GCTYLGECAGYAIGYSISDPTGMWYK-----GTASAGN 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 605 GTRATVANAIGSSVILGVDNRARGINSTALGRQSNALIGDGSVSLGFNSFVROSGEGHVALGT 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 575 SRGHFG-TSASVGY 587
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 DAGVSGKDSIALGY 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
A64905
ydek protein - Escherichia coli
N:Alternate names: protein T
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 02-Feb-2001
C:Accession: A64905; 152440; S34315
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perina, N.T.; Butland, V.; Riley, M.;
A:; Rose, D.J.; Mau, B.; Shao, Y.
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: A64905
```





RESULT 15  
B85547  
Probable Rfx family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: B85547  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallantha, E.; Potamoukis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B85547  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-5188 <STO>  
A:Cross-references: GB:AF005174; NID:q12513368; PIDN:ANG54838.1; GSPDB:GN00145; UWGP:206  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: 20615

Query Match 7.5%; Score 225.5; DB 2; Length 5188;  
Best Local Similarity 21.2%; Pred. No. 0.0031;  
Matches 157; Conservative 94; Mismatches 250; Indels 241; Gaps 33;

OY 10 NSALNAMYVSELTFRNHRKASATATATVLAFLSATVQANATDDEDELESVARSLV 69  
DB 1409 DGAANVOASVSNVAGNSTO--ATHAYSVDATAPSVTINTIATD----- 1449  
OY 70 LQFMIDKEGNGEISTGDIQMSIYDDHNTLHGATVTLKAGDNLIKQSGKDFYSLKE 129  
DB 1450 -----DILNAEAGSAL-----TISG-TSTAAGOTVYTLNGVYSGNVQAD 1491  
OY 130 LKDLTSVETEKL-SFGANGKNVNTSDTKGLNFAKETAGTNGD---PTVHLNGISTLTLD 185  
DB 1492 GSWSVSPTGLDASLTASSYTNASVSDKARNSASATHNLVLDLAAPVYIN----- 1543  
OY 186 TLAGSSASHVDAGNSTHYTRAISKDVLNAGWN-----IKVKTGSTTGQSENVDF-VR 239  
DB 1544 TVAGD-----DIIMTEHGOAOIISGATGATTGNTVSITGTT 1582  
OY 240 TYDVEFLSAD-----TKTTVNESKDKNGKRTK---VKIGAKTS 276  
DB 1583 TYTTY--LDANGNMSIGVPASVIALAGDVTITATVTDASGNSGTASHITVVALGAPVL 1640  
OY 277 VIK-----EKDKL-VTKG-----KENGSSPTDEGE--LVTAKE 309  
DB 1641 AINTIAYDDIINAIEKAGADLAITGTSNOPAGTOITVTLNGQNYTTTADASGMSVTPAS 1700  
OY 310 VIDANKAGWM--KTTTANQGTQAD--KEEYTSGTKYTFASG---NGTITATVSKD 360  
DB 1701 RVSAIGEATVYTAATADAGSGSASHNVQNTALPGVTINNVATDDIINAIEAGVEQT 1760  
OY 361 DQGNIT-----VKYDVNVDALNVQLO-NSGMNLSKAVA-----GSSGKVISGNVSPSK 410  
DB 1761 ISGQVTGAAGGTAVTTLGATYTTAQNLSMSYDVPAASLOELNGELTISASVTSNV 1820  
OY 411 GKM-----DETUNI-----NAGNNIEITRNG 431  
DB 1821 GNTGNGTRETITDANLPGLRVDTVAGDDVNIIEHQALVITGSSSSGLAAGSVTLTING 1880  
OY 432 KNIDIAITSMTPOFSSVSLGAGADAPTLVSVDDEGALNV---GSKDANKPYRITNVAP---- 484  
DB 1881 Q-----TYVAALADGTWSVGPVAVDSAMPASVYTIASGSTSAGNPVSVTHPYTVDL 1935  
OY 485 -----GVKEGDVYNNVQLKGVAQNLLNNRIDNVNGNARAGI-----AGAIATAGLAQ 530  
DB 1936 AAVASINMITADVDYINAAE-KGAALLTSGSTSGVAGOTVYTFEGKITYSATVAANGSWS 1994  
OY 531 AYLPGKSMIAIGGTYLGEA-----GYAIGYSSISDPTGMNVYIK----- 569  
DB 1995 TSVPAADMAALRDBDASAOASVSNVNGNSATTTTHAYSVDASAPVYIN-TIAGDDILNAA 2053

OY 570 -----TASGNSRGHFGTSASV 585  
DB 2054 EAGALITIGSSSTAAGOTVTV 2075

Search completed: July 3, 2002, 08:12:12  
Job time: 434 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:29:46 ; Search time 48.34 Seconds

(without alignments)  
471.779 Million cell updates/sec

Title: US-09-771-382-3

Perfect score: 2994

Sequence: 1 MNKIVRIINMSALNAMYVS.....TASGNSRGHFGTSASVGYQW 589

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description          |
|------------|-------|-------------|--------|--------------|----------------------|
| 1          | 245   | 8.2         | 1325   | 1 YDEK_ECOLI | P32051 escherichia   |
| 2          | 216.5 | 7.2         | 1039   | 1 AG43_ECOLI | P39180 escherichia   |
| 3          | 216.5 | 7.2         | 1608   | 1 HUYA_SERMA | P15320 serratia ma   |
| 4          | 209.5 | 7.0         | 1286   | 1 AIDA_ECOLI | O03155 escherichia   |
| 5          | 203.5 | 6.8         | 2249   | 1 OMPA_RICRI | P15921 rickettsia    |
| 6          | 196   | 6.5         | 1567   | 1 ICEN_XANCT | P18127 xanthomonas   |
| 7          | 196   | 6.5         | 1656   | 1 OMPB_RICJA | O06653 r outer mem   |
| 8          | 195.5 | 6.5         | 1953   | 1 BIGA_SALTY | P25927 salmonella    |
| 9          | 194   | 6.5         | 2003   | 1 YDBA_ECOLI | P33666 escherichia   |
| 10         | 188.5 | 6.3         | 1577   | 1 HUYA_PROMI | P16466 proteus mir   |
| 11         | 187.5 | 6.3         | 1569   | 1 YPOA_ECOLI | P52143 escherichia   |
| 12         | 186.5 | 6.2         | 1300   | 1 120K_RICRI | P14914 rickettsia    |
| 13         | 186.5 | 6.2         | 1654   | 1 OMPA_RICRI | O53047 r outer mem   |
| 14         | 186.5 | 6.2         | 2021   | 1 OMPA_RICRI | O52657 rickettsia    |
| 15         | 186   | 6.2         | 1655   | 1 OMPB_RICCN | O9Kk33 r outer mem   |
| 16         | 184.5 | 6.2         | 1025   | 1 SIAP_CAUCR | P35828 callobacter   |
| 17         | 180   | 6.0         | 933    | 1 SIAP_CAMEE | P35827 campylobact   |
| 18         | 179.5 | 6.0         | 1645   | 1 OMPB_RICRY | P96989 r outer mem   |
| 19         | 176   | 5.9         | 1210   | 1 ICEN_PSEFL | P25915 pseudomonas   |
| 20         | 175.5 | 5.9         | 1694   | 1 IGA2_HAEIN | P44969 haemophilus   |
| 21         | 175.5 | 5.9         | 1702   | 1 IGA2_HAEIN | P44969 haemophilus   |
| 22         | 174.5 | 5.8         | 1148   | 1 ICEN_PSEFL | O30611 pseudomonas   |
| 23         | 174.5 | 5.8         | 1200   | 1 ICEN_PSEFL | P06620 pseudomonas   |
| 24         | 174   | 5.8         | 550    | 1 FLIC_SHEFL | Q08860 shigella fl   |
| 25         | 172.5 | 5.8         | 1643   | 1 OMPB_RICPR | O53020 r outer mem   |
| 26         | 172   | 5.7         | 439    | 1 ACWA_LACLA | O9c1a lactococcus    |
| 27         | 170.5 | 5.7         | 1848   | 1 CBPA_CLOCL | P38058 clostridium   |
| 28         | 170.5 | 5.7         | 2329   | 1 YS89_CAEEL | O09624 caenothabdi   |
| 29         | 169   | 5.6         | 1150   | 1 APMU_PIG   | P12021 sus scrofa    |
| 30         | 168.5 | 5.6         | 918    | 1 YKWB_CAEEL | P34487 caenothabdi   |
| 31         | 168   | 5.6         | 1861   | 1 APV_THETU  | P38536 t amylolpulli |
| 32         | 167   | 5.6         | 1228   | 1 SIAP_BACST | P35825 bacillus st   |
| 33         | 166.5 | 5.6         | 1770   | 1 PMPC_CHLTR | O84419 chlamydia t   |

|    |       |     |      |              |                     |
|----|-------|-----|------|--------------|---------------------|
| 34 | 165   | 5.5 | 1258 | 1 ICEN_ERWHE | P16239 erwinia her  |
| 35 | 165   | 5.5 | 1322 | 1 ICEA_PANAN | P20469 pantoea ana  |
| 36 | 165   | 5.5 | 2334 | 1 WAPA_BACSU | O07833 bacillus su  |
| 37 | 164.5 | 5.5 | 948  | 1 HP11_DEIRA | P56867 delinococcus |
| 38 | 164   | 5.5 | 1005 | 1 Y456_CHLTR | O84462 chlamydia t  |
| 39 | 164   | 5.5 | 1007 | 1 Y741_CHLMU | O9p1t6 chlamydia m  |
| 40 | 164   | 5.5 | 1034 | 1 ICEN_PANAN | O47879 pantoea ana  |
| 41 | 163.5 | 5.5 | 814  | 1 SLAI_BACAN | P49051 bacillus an  |
| 42 | 163.5 | 5.5 | 1196 | 1 ICEN_PSEFL | O33479 pseudomonas  |
| 43 | 160.5 | 5.4 | 1250 | 1 YPAL_ECOLI | P45508 escherichia  |
| 44 | 159   | 5.3 | 1153 | 1 PVDB_PLAKN | P50493 plasmodium   |
| 45 | 158.5 | 5.3 | 504  | 1 FLIC_SALMO | P06177 salmonella   |

## ALIGNMENTS

```

RESULT 1
YDEK_ECOLI STANDARD: PRT: 1325 AA.
AC P32051: P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-9742617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97251357; PubMed-9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Ohnita T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horinouchi T.;
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE-94100243; PubMed-8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochem. Biophys. Acta 1153:345-347(1993).
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (potential).
CC -I- SIMILARITY: TO E-COLI YFAL.
CC -I- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -I- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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 CC -----  
 DR EMBL: A5000248; AAC74583.1; -  
 DR EMBL: D90793; BAA15190.1; ALT\_INIT.  
 DR EMBL: D90794; BAA15197.1; ALT\_INIT.  
 DR EMBL: X73295; CAA51730.1; ALT\_FRAME.  
 DR PIR: S34315; S34315.  
 DR EcoGene: EG11780; Ydek.  
 DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
 DR Hypothetical protein; Membrane; Lipoprotein; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
 FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT CONFLICT 884 884 N->K (IN REF. 3).  
 FT CONFLICT 1317 1317 M->S (IN REF. 3).  
 FT SEQUENCE 1325 AA; 136514 MW; 26A3A06FA19AD7D CRC64;

Query Match 8.2%; Score 245; DB 1; Length 1325;  
 Best Local Similarity 24.8%; Pred. No 4,4e-05;

Matches 164; Conservative 67; Mismatches 253; Indels 176; Gaps 35;

QY 1 MNKIRIIMNSALNAVWVSELTRNHR-----RASATVAT---AVLATLSATVQAN 50  
 DB 1 MNRIRYIMNCTQVQACSELRFRAGKTSVNLKSSGLTKFSRLTGLVALLSGSAS 60  
 QY 51 ATPDDEBELESVARSAVLQFMIDKEGNGESTGD---IGNSIYYDDHTLTGATY-T 106  
 DB 61 GASLEVN-----DOITNIDTDAVAYLVGW-----YGTGLN 94  
 QY 107 LKAGDNLIKQSGKDFYSLKELDLTSVETKLSFGANGK---VNITSDTKGLNPAK 163  
 DB 95 ILAGN-----ASLTITTSYI---GANDSGTYAVLGTRML----- 130  
 QY 164 ETAGTNGDPYVHLNGISLTLDLAGSSASHADAGNOSTHYTRAASIKDVLAQMNIKGV 223  
 DB 131 YDSGNMNR--LN-VGSGTGTINIKQKHVDCG-----YLRGSSGTGV 172  
 QY 224 KTGSTGSENVDFRYDYEFISADTKITTVAVESKDNKRE-----VAIGAKTS 276  
 DB 173 GTVNEGE---DSVLTTELEFISYSGSLNIT---DKGYVTSSIVAILGYAGSNGQ 224  
 QY 277 VIREKDK-LVYTGK-----GKGNGSSSTDEGEGLTAAKEVDVAVKAGMRKKTTPAN 327  
 DB 225 VVERKGEMLIKNDSSIEFOIGNOGTGEATIREGLVTAENTIIIGNATG-----IGTLN 280  
 QY 328 GGTGADKFEFTVSGTKVTFASGNGTATVSKDOGNITV-YD-VNVDALN--VNQLQ 383  
 DB 281 VQ-----DQDSVITVRLYNGVFGNG--TVNISNNGLINNKEYSLVGVDQDSHGIVANTD 333  
 QY 384 NSGNL-----DSKAVAGSGKYISGVNSVSKGMDTVINAGN----- 423  
 DB 334 KGHNFLOTGEAFRYIYIGDAGDELNVSEKVDSGITAG---MKET---GTGNITVK 387  
 QY 424 --NIEIRPNKGNIDIANSMTPQFSSVSLGAGADAPTLISVDEDEGALN-----GSKDANKP 476  
 DB 388 DKSNTITNLGTYDGHGEMNISNOGLVNSGSSSLGTYGTGNVSTITTGMEVKN 447  
 QY 477 VRITNAPVEGDVTNVAQLKGAVALNLRIDVNGNARAGIAQALA---TAGIAQAYL 533  
 DB 448 VYTTIGVAGVGNLNIISDGC--KPVSONITFLGDKASGIGTILINDATSSPFTVGINVNF 505  
 QY 534 PGKSMALIGGTLYGEAGYAI-----GYSSISDTGNWYIKTAGSANSR---GHGCT 581  
 DB 506 -GSGIVVNSGATINSTGYFIGNASCKGIIVNISTDLNMLK-TSTNAQLQGVGLGT 563

RESULT 2  
 AG43\_ECOLI STANDARD; PRT; 1039 AA.

AC P39180; P76360; P75614; P97241; Q46771;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Antigen 43 precursor (AG43) (Flufluffing protein).  
 GN Ftu OR B2000.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OC NCBI\_Taxid=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=9742617; PubMed=9278503;  
 RA Blatter F.R., Plunkett G., Ili, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97251358; PubMed=9097040;  
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
 RA Kasai H., Kimura S., Kitakawa M., Kitakawa M., Makino K., Miki T.,  
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
 RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
 RA Yamamoto Y., Horiochi T.;  
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 40.1-50.0 min region on the linkage map.";  
 RL DNA Res. 3:379-392(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ML 308-225;  
 RA Henderson I.R., Owen P.;  
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP PRELIMINARY SEQUENCE OF 53-78.  
 RX MEDLINE=89291704; PubMed=2661530;  
 RC STRAIN=ML 308-225;  
 RA Caffrey P., Owen P.;  
 RT "Purification and N-terminal sequence of the alpha subunit of antigen  
 RT 43, a unique protein complex associated with the outer membrane of  
 RT Escherichia coli.";  
 RL J. Bacteriol. 171:3634-3640(1989).  
 RN [5]  
 RP SEQUENCE OF 53-63.  
 RC STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [6]  
 RP GENE NAME.  
 RX MEDLINE=97257509; PubMed=9103983;  
 RA Henderson I.R., Meehan M., Owen P.;  
 RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
 RT determines colony morphology and autoaggregation in Escherichia coli  
 RT K-12.";  
 RL FEMS Microbiol. Lett. 149:115-120(1997).  
 CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY  
 CC FUNCTION AS AN ADHESIN.  
 CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
 CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
 CC CHAIN).  
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.  
 CC -1- SIMILARITY: TO ADHESIN AIDI-1 AND TO BORDETTELLA PERTACTIN.  
 CC -----  
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      396 REQLQAGSTVAASGSAKLLSTQEDVVKILGANVASRADRALSVKAAARDVHLAAGLVKDKSSE 455
      82 -----IESTGDIGMSIYYDDHNTLHGA-----TYTLKAGDNLIKIK-----QSGKDPTY 124
      456 RGYORNTHTSLRTGRWS-NSDESESLKASELRSECELTIKGRVNTVGAAVHQRDLTI 514
      125 SLKRELK-----DLTSVETEKLSFGANG--NKVNTSDTKGINFAKETAGTNGDPTV 174
      515 DADQIOGVQVKTANAKAVRDKTSMGIGGGDKNN--SNRREISHASEL--TSGG-TL 569
      175 HLNG-IGSTLTDTLA-GSSASHVDAGNOSTYTRAAATK-DVLAAGNMIKVKGTST--- 228
      570 RLNQOQVLTITGSKARQKGEVATPAGLRIDNALSTTVYKIDA-----RTGTAPNI 622
      229 TGOSENVDFVATYDVEFLASDTKTTTVNVESKD-NGKRT-----EVKIGAKTSVYKEKG 283
      623 TSSHKADNVSQSTASLKDSDTNLTLSHKDADVIGQVASGGELESSTGNTGNV-- 680
      284 KLVYTGKKGNGSSTDEGEGLVT---AKEVIDAVNKAQWRM-----KTT----- 324
      681 -----AERQONIDEQKTLTVNGYAKEAGDKQYRAGLRIEHTRDEKKTRTENSASS 733
      325 -----TANGOTGOADKFEVYTGCTVTFASGNGTAA----- 355
      734 LSGGSVKIKAEKDYTFSGSKLVADKDAVSNGNVSFLAADKTAASNTQRTKIGGFEYTT 793
      356 -----TSKPDQGNITVYKDYVNVGDALVANYNOLNSGMN 388
      794 GGDIKLGSVAGYENNKTKQAOSSKAITSGSDVAGNLT-----INARDKLTQOQAGHSHVG 849
      389 LDSRAVAGSSGKVIYSGNVSFKGMDFTVNIAGNIEITRNKNIDIAITMTPOFSSVS 448
      850 AYOENAGVDHLAADFTSTTTTKTDVGNV-----GANVDYSAVTRPERAVG 898
      449 LGAQADAPTLISVDEG-----ALNVSCKANKPVRTN---VAPGVKEDV----- 491
      899 KAAKIDA-TGVINIDIGIGAPNVGLDIGAGGSSSEKSSSQAVVSSVQASIDINAKGE 957
      492 -----TNYAQLKGYAQNIN-----NRIDVNGNARAGIAQAIATAGLAQAYLPKG 536
      958 VRDQGTQVQAKG-AVNLTLASHSHSEAAANRODQDSRTRBSAGRYVTITGSDLTIVAK 1016
      537 SMAAGGTYLGEAGYALGYSISDFTGNW-----VIKGTASGNSRGHGTSA 583
      1017 G-----EGGTORSNSSASQAVTGSIDAANGINVMYKKAIDAYGTALNGRGKTAANA 1068

RESULT 4
AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC 003155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aida-I precursor.
OS AIDA-I.
OS Escherichia coli.
OC Plasmid PIB6.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (0126:H27);
RX MEDLINE=9232638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is
RT synthesised via a precursor molecule."
RL Mol. Microbiol. 6:1539-1546(1992).
CC -I- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI

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      CC TO EPITHELIAL CELLS.
      CC -I- SUBCELLULAR LOCATION: Outer membrane.
      CC -----
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      CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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      CC modified and this statement is not removed. Usage by and for commercial
      CC entities requires a license agreement (See http://www.isb.ch/announce/
      CC or send an email to license@isb-sib.ch).
      CC -----
      DR EMBL: X65022; CA46156.1; -.
      DR PIR: S28634; S28634.
      KW Cell adhesion; Signal; Outer membrane; Plasmid.
      FT SIGNAL 1 49
      FT CHAIN 50 7 ADHESIN AIDA-I.
      FT PROPEP ? 1286
      SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 7.0%; Score 209.5; DB 1; Length 1286;
Best Local Similarity 19.4%; Pred. No. 0.0024;
Matches 136; Conservative 122; Mismatches 257; Indels 185; Gaps 32;

      QY 1 MNKRIITMNSALAAVYVSELTNRH-----IKRASATYATA--VLATLISATVQANA 51
      DB 1 MNKAYSIITMNSHROAVIASELARGHGFVLAKNTLLVLAAYSTIGMAFAYNISGTVSSGG 60
      QY 52 TDTDEDELESVAR---SALVQFMIDKEGNG-----EIESTG-DIGMSIYYDDHNTL 100
      DB 61 TVSSGEFQIVYSGRNSATYVNSGTOIVNNGKTTATTVVSSSQNVGTS----- 111
      QY 101 HGATVT--LKAGDNLIKQSGKDEFTYSLK---KELKDLTSVETEKLSFGAN-----GNKV 150
      DB 112 -GATISTIVNSGGIORVSSGVAATNLGGAQNTVNLGHASNTVIFRSGNOITFSGIFT 170
      QY 151 NITSDTKLANFAKETAGTNGDPTVHLNGIGSTLDTLADSSASHVDAGNOSTHTTRASTI 210
      DB 171 DSTNISGGQGVSSGGVASTMTTINSSGAQNLISE--EGALSTHISGGNOYISAGANAT 228
      QY 211 KDVNLNAGW---NIKGYKTGST-TGOSENVND-----FVRTYD---VEFLADPTKTTTV 256
      DB 229 ETIVNSGGFORVNSGAVATGTVLSGCTONVSSGSAISTSVYNSGVQTVFAGATVTTTV 288
      QY 257 NVESKDN-----GKRTVEKIGARTSVIKE-----KDKELVYTGKKGNGSSTDEG- 301
      DB 289 NSGNQNTISSGIVSEFTVNVSGTQNIYVSGSALSANIKGSOIYNSGTAINTLVSDGY 348
      QY 302 -----EGLVTAKEVIDAVNKAQWRMKTITTANGOTGOADKFEVYTGCTVTFASGNGTATV 357
      DB 349 QHIRNGGIASGTI---VNQSGY---VNISG--GYAESTIINSGLTLRLVSDGARCTIL 400
      QY 358 SKDOGNITVYKDYVNVGDALVNOLONSGMNL-----DSKAAVAGSSG-KVIYSGNVS 408
      DB 401 NSGRENVS-----NGVSYNMAINTNGNOYIYSDGEAFAALVNTSPGRINSQIAP 453
      QY 409 SKGMDFTVNIAGN---NIEITRNKNI-----DIATSMTPQFSSVSLGAGADA 455
      DB 454 VQNSVAVTRVTSAAKPEDAEVYSGKQTVYLMRGIMYSNFLTAWSMFPTASGA----- 509
      QY 456 PTLVYDDEGALN-----VGSKDANKPVATITVAAPVK 487
      DB 510 ---NVNLSGRINAFAGNVGTITLNOGQROYVYSGATATSTGNGREGYV---LSGKIT 562
      QY 488 EGDVTNVAQLKGVQNLNRRIDVNVGNARAGIAQAIATAGLAQAYLPKSMMAIGGTYL 547
      DB 563 DGTVLN-----SGDLAVSSGGKASA-----TVINBGAGQFV 594
      QY 548 GEAGYALGYSSISDPTGMNVIKGTASG-----NSRGHFTS 582
      DB 595 YDGGQVYTG-TNKKNGTITRVDSGASALNIALSSGNGLTFS 633

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RESULT 5
OMPA_RICRI STANDARD: PRT: 2249 AA.
ID OMPA_RICRI
AC P15921:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
  antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
  Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R:
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
  repeated, near-identical sequences."
RL Infect. Immun. 58:2760-2769(1990).
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
  S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTH: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC -----
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CC -----
DR EMBL: M31227; AAA26380.1;
DR PIR: A41477; A41477.
DR InterPro: IPR003858; rompa_rOmpB; 1.
DR Pfam: PF02708; rompa_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 2249
FT DOMAIN 212 1180
FT REPEAT 212 286
FT REPEAT 287 358
FT REPEAT 359 430
FT REPEAT 431 505
FT REPEAT 506 577
FT REPEAT 578 652
FT REPEAT 653 724
FT REPEAT 725 799
FT REPEAT 800 874
FT REPEAT 875 949
FT REPEAT 950 1021
FT REPEAT 1022 1093
FT REPEAT 1094 1165
FT REPEAT 1166 1180
FT REPEAT 1181 1249
FT SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.8%; Score 203.5; DB 1; Length 2249;
Best Local Similarity 22.4%; Pred. No. 0.0093;
Matches 153; Conservative 72; Mismatches 257; Indels 201; Gaps 32;

OY 30 ASATV-ATAVATLTATLFAVVOANATDDEDELESVARSAVLVQFMIDKENGCE----- 81
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 730 ALATVNVAGAGRTLGAVIKATTTKLTNAASVLTITNANAVLTGADITDGTGDNVGLNL 789
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 82 ----TESTGIDGWSITYDDHNTLGCATVTLKAGDNLIKQSGKDPYSLKELKDLTGYE 137
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 790 NGALSGVTVGIDG-----NTNSLATISVAGGTATLGAVIKATTTKLTNAASVLTITLN 841
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
```

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OY 138 TEKLSFGANGKNVNTSDPKGLNFAKETAGTNGDPTVHLNIGSLTLDPLAGSSA---SH 194
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 842 ANAVLTGAVDN-----TTGGDNVGLNLNGLALSOVDTGDTNLSLATIS 885
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 195 VDAGN-----OSTHYTPRAASIKDVLNAGWNKIKGKYG---STTGQSENVDFVPTY 241
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 886 VAGATATLGAGAVIKATTTKLTNAASVLTITNANAVLTGADITDGTGDNVGLNL 940
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 242 DTVEFLSADFTKT---TVNVEKSD---NG---KRTYKIGAKTVYIKEDGKLVYTG--- 288
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 941 GALSOVTCIDIGNTNLSLATISVAGGTATLGAVIKATTTKLTNAASVLTITNANAV 1000
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 289 -KRGKENGSSPDEGEGVLTAKE---EVIDAVKKA---GWRKKTITAN----- 327
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1001 NTGNANNGIYVFTGNSVTYGVNGVNTNATVNVAGAGLLOVGGVVKANTINTDNASAVT 1060
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 328 -----GOTGOADKFEVTVSGTKVTFASGNGTATVASKDOGNITVYKVDNVGDAL----- 377
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1061 FTNPVYVGTGALDNTGNANNGI-VTTGNSVTYGVN-----GNTNATVNVAGAGLLOV 1114
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 378 -----NVN-----OLONGMNLDSKAAVAGSSGKYISGVNPSKGM 413
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1115 GVVKANTINTDNASAVTFTNPVYVGTGALDNTG-NANNGIYVFTGNSVTYGVN-----GNT 1169
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 414 DETVIMAGNNIETIRNG---KNIDIASMTPOSSSVSLGAGAP-----TLSVDEG 464
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1170 NALATVNVAGAGITLQAGSLAANNIDFGARSTLEFNGPLDGGKAIPLYFKGALINGNA 1229
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 465 ALNVGSKDANK-----PVRTNVAPG-----VREGDVTNAQLKAVQNLNLR----- 507
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1230 ILNVMTFKLTASHLTIGVYAEINIGAGNLTITDASVGDVITLN-----AQNTNPARDSV 1284
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 508 --IDNVNGNARAGIAQAATATAGLAQVLPKSKMAIGGTYLGEAGVYAGYSSISDPTGM 565
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1285 IVLNMLTG--VGVNIIILADLV--APG-----ADEGTV 1314
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 566 VIKGTASGNSRCH--FGTSASVG 586
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1315 VENGGVNGLNVGNAVGTARNIG 1337
  1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 6
ICEN_XANCT STANDARD: PRT: 1567 AA.
ID ICEN_XANCT
AC P16127:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
  Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inx from
  Xanthomonas campestris pv. translucens."
RL Mol. Gen. Genet. 223:163-166(1990).
CC -1- FUNCTION: ICE NUCLEATION PROTEIN ENABLE BACTERIA TO NUCLEATE
  CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS (BY SIMILARITY).
CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS (BY SIMILARITY).
CC -1- REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
  NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
  FAMILY.
CC -----
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OY 419 I-----NAGNNIEIT-----RNGKNIDIATSMF 441
DB 867 FENSSGLAVLPSGIPENDAGNTPLTKSTVGNETAEGESVPSVIVSGDVSTADQOV 926
OY 442 --POFSSVSLGAGAD-----APTLSV-----DDEGALNVGSKDANKPVRTTNPAPGVK 487
DB 927 IGDNNIYGLIGSDNGIIVNATITLYAGGITINNNGVTITLSGVNPNPGIYGLGTGIG 986
OY 488 EG-----DVTNVAOLKGVANLNN-----RIDNVNGNA 515
DB 987 ASKFQVTFETDYNNLGNITATNTTINDGVVYTGIAAGIAGIDFQKITLSGVNGNA 1046
OY 516 RAGIQAATATAGLAQAVLPKSKMAI-----GGTYLGEAGATATGSSISDPTGNVVIKGT 570
DB 1047 NVREFADGI-----FNSNSTSMIVTTRANNGTVTYLGNA--FVGNIGSDPTPVASVRET 1096
OY 571 ASGNSRG-----HFEGT 581
DB 1097 GSNNGAGLKGNITYSQVIDEPT 1117

RESULT 8
BIGA_SALTY STANDARD: PRT: 1953 AA.
AC P25927: P25928: Q9XCQ3:
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein biga precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rbs homolog.";
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [13]
RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=91100301; PubMed=1987123;
RA Wu J.Y., Siegel L.M., Kredich L.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysg plasmid to overcome limiting sholeme
RT cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -I- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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DR EMBL: AF133696; AAD39458.1; -
DR EMBL: AE008859; AAL22340.1; -
DR EMBL: M64606; AAA27042.1; ALT_FRAME.
DR EMBL: M64606; AAA27043.1; ALT_FRAME.
DR PIR: C39200; C39200.
DR PIR: D39200; D39200.
DR StyGene: SG10437; biga.
KW Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 1953
FT DOMAIN 101 252
FT REPEAT 101 103
FT REPEAT 104 113
FT REPEAT 114 122
FT REPEAT 123 133
FT REPEAT 134 144
FT REPEAT 145 155
FT REPEAT 156 166
FT REPEAT 167 177
FT REPEAT 178 188
FT REPEAT 189 199
FT REPEAT 200 210
FT REPEAT 211 221
FT REPEAT 222 232
FT REPEAT 233 243
FT REPEAT 244 252
FT CONFLICT 207 207
FT CONFLICT 514 514
FT CONFLICT 1698 1698
FT CONFLICT 1795 1798
FT CONFLICT 1836 1837
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C934D91AE CRC64;

Query Match 6.5%; Score 195.5; DB 1; Length 1953;
Best Local Similarity 22.0%; Pred. No. 0.02;
Matches 136; Conservative 96; Mismatches 249; Indels 137; Gaps 29;
```

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OY 41 TLLSATVQANATDTDEDELESVARSAVLQPMIDKEGNGEISGTGIGMSIYDDHNTL 100
DB 347 TVISGDDQAH--NSDRGMDISGDRGTVII-----SDDRVTNLTGSSVT 390
OY 101 HCATVTLKAGDNLKITKOSKDTTYSIKELKDLTVEYEKLSFGANGKVNITSDTKLN 160
DB 391 DEATGMVTSIGDDETTNTISGH-----STVD-----NATGALISGNGTTN 429
OY 161 FAKETAGTNGDPTVHLNGLSTLTDT-----LAGSSASHVDAGNOSTHYTRAASIKDV 214
DB 430 FAGDIAVSGGTAIIIIIDGNATIKNTGTSIDSGASTGTIVGNNARVNNDGDMITTDGG 489
OY 215 NAGW-----NIKGVKTSGTSGSENVDFRTYDVEFLADPTTYYVNESKDNKRTVEK 270
DB 490 TCGHITGDVNVIDNAGSTVSGADA-----TALYIEGDNLVINEGQITSGAVGTR 542
OY 271 ICAKTSVIREKKGKLVYTGK-----KGENGSTDEGEIYV--AKEVI--DAVNKAGNR 320
DB 543 IGDGAHTTNTGDIVVDGASAAVIINGDNGSLTGAADLVLDGAMGIIYGTGMEA-- 599
OY 321 KMTTANGTGQADKFEYVTSKRVTF-----ASGNTTGVTSKDDGNTVTKYDVNV 373
DB 600 --KNTGNATVRADSVGVFVYVAGEKNTFKKKGIDIVSLNCTGALVS--GDMSQVTLGDDIV 656
OY 374 GDALVNVQLONSGWNLDKRAVAGSSGV--ISGNVSPS-----KGMDETVINAGN 423
DB 657 --VSQVSEGVFFSATGTGVSAGDSNAVDITGNVNISADYVGGDDLAAGAPPLTGVVYVN 713
OY 424 NIETIRNCK-NI---DIATSMTPQFSSVSLGAGADAPILSYDDEGALNVGSKDANKPVKI 479
DB 714 GNTVTLNGALNIDDDLSATGCGYLDVYGLSVTGDNDVEID--GGINI--THSEDPILGG 769
OY 480 TNVAGVKKGDVTNVAOLKGV-----VAQNLNRRIDN--VNGN--RAGTAQAI-----AT 525
```







OX NCBI\_TaxID=584;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.  
 RC STRAIN-ISOLATE 477-12;  
 RA MEDLINE-90170827; PubMed-2407716;  
 RX Upjohn T.S., Welch R.A.;  
 RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent  
 hemolysin genes (hpmA and hpmB) reveals sequence similarity with the  
 Serratia marcescens hemolysin genes (shlA and shlB).";  
 RL J. Bacteriol. 172:1206-1216(1990).  
 CC - FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
 CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
 DEFINED.  
 CC - FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
 ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPM  
 REQUIRES HPMB FUNCTION.  
 CC - SUBCELLULAR LOCATION: Outer membrane.  
 CC - MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPM  
 MAY BE RESPONSIBLE FOR PORE FORMATION.  
 CC - SIMILARITY: TO S. MARCESCENS HEMOLYSIN (SHLA).  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, M30186; AAA25657.1; -  
 DR PIR, A35140; A35140.  
 RM Hemolysin; Toxin; Outer membrane; Signal.  
 FT SIGNAL  
 FT CHAIN 30 1577 HEMOLYSIN.  
 SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;  
 Query Match 6.3%; Score 188.5; DB 1; Length 1577;  
 Best Local Similarity 22.3%; Pred. No. 0.034;  
 Matches 160; Conservative 99; Mismatches 244; Indels 215; Gaps 40;  
 OY 15 AWWVSELTRNHTKRASATVATAVLATLTSATVQANATDDEDELESVARSALVQPMI 74  
 DB 607 AENIRKSHKNEKNOTST-----GSELISDAQLTVVSGNDVNVIGSLIKSA----- 653  
 OY 75 DEKGKEISTDDIGMS-----IYDDHNTLHGATVTLKAGDNLTKQSGKDEFTSLKKE 129  
 DB 654 DLIG---IHSLGDINVKSAQOVTAKIDDEKTSLATIGHAKEVED-KOYSAGFHTHTNNKN 709  
 OY 130 LKDLTSVEREKLSPFGANGKKNVITSPTKGLNFA---KETAGT---NGDPYHLNIGIST 182  
 DB 710 ---TSTETQANSTISGANVVDLQAN-KQVTRAGSGLKTTAGASITGDNVAFVSENKK 764  
 OY 183 LNDTL-----AGSSAS-HVDAGNOSTHTTR-----AASIKD 212  
 DB 765 GTDNDTDTISGSESVYTGVDKXSKADPQYDKOHTQTEVTKKRGSTEVAGDLITIANKD 824  
 OY 213 VLNAG--WIKGVKGTGSGTGOSENDVFTYPTVEFLSADTKTTVNV----- 258  
 DB 825 LHEGASHHEVEROYES---GENIOHLAVND---SETSKTDLNGLVDGVNLDYSG 875  
 OY 259 -----ESKDNKRREVKIGAKTSVKE---KD-----GKLVGKGKE 293  
 DB 876 YRKPKAKALEDVNT--TKGNNTDILTKVTARDALANLANLNLETNPVNGVEGKIGGS 934  
 OY 294 NCSSTDE---GGLVYAKEVIDAVNK---AGWRMKT-----TANGOTGOA--DKFEV 339  
 DB 935 QOSQOTDSQAVSTISNAGKIDIDSNNKLHDOGHYSTOGISLTANTHTSEATIDKHQTT 994  
 OY 340 TSGTK---VTRASGNGTATVYKSKDQGNITVYKVDVNGDALNVNOLNSGW--NIDSKA 393  
 DB 995 FHETKGGQIGVSTGTGSDITVAIKGEGOTT-----DNALMETKAKSGQFTSNDISI 1047

OY 394 VAGSSGKVISGNVPSKGMDETVINAGNIEFTR-----NGK-NIDIATSM 440  
 DB 1048 NGENAHYEGAOEDQAKGR---TV-INAGDGLTAAQTHTSHRSOSNGSANKLAKGT--- 1101  
 OY 441 TPQSSSVSLAGADAPTL-SVDEGALNVGSKDANKPVRITVAPGVKGDVTNVAQLKG 499  
 DB 1102 TPE--SKDYGCGFNACTHTHSKQRTAKVGTITGSGIELNGHNLTGG--THLSQED 1157  
 OY 500 VAOANLNRIID-----NVGNARAGIAQAIATAGLAQVALPKSM---MAIG 542  
 DB 1158 IALMATNKVDLOSASSEHTEKGNLSGVQAGF-----GKKMTDASSVN 1202  
 OY 543 GGYLGEAGVAYGY-----SSIDPTGMVVIKGT-----AGNSRGHGTSAS 584  
 DB 1203 G---LGSQAFALGKDEKSVREGCTINNNGLTINGSVHLQAGVNSKDTQLTSQS 1257  
 RESULT 11  
 ID YPJA\_ECOLI STANDARD: PRT; 1569 AA.  
 AC P52143; P76610; P77017; P77019;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical outer membrane protein ypja.  
 GN YPJA OR B2647.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE-97426617; PubMed-9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE-97349980; PubMed-9205837;  
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yamagata S., Horiuchi T.;  
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
 K-12 genome corresponding to 50.0-68.8 min on the linkage map and  
 analysis of its sequence features";  
 RL DNA Res. 4:91-113(1997).  
 CC - SUBCELLULAR LOCATION: Outer membrane (Potential).  
 CC - SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, U36840; AAA79815.1; ALT\_SEQ.  
 DR EMBL, AE000350; AAC75695.1; -  
 DR EMBL, D90889; BAA16514.1; ALT\_INIT.  
 DR EMBL, D90890; BAA16518.1; ALT\_INIT.  
 DR EcoGene; EGI3213; ypja.  
 KW Hypothetical protein; Outer membrane; Complete proteome.  
 SQ SEQUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;

Query Match 6.3%; Score 187.5; DB 1; Length 1569;  
 Best Local Similarity 21.4%; Pred. No. 0.038;  
 Matches 149; Conservative 94; Mismatches 249; Indels 203; Gaps 37;

26 HTKRAS--ATVATAVATLTLATVQANATDTDEDELESV---ARSALYV--QFMIDK- 76  
 581 HVEOSGSGALIASTSTGLTIEGINSYGDAFYIRNSEAKNVLENAGSLTYTGRADVTI 640  
 77 -EGGEIESG-DIGMSIYDDHNTLHGATVTLKAGDNLIKSGKQFETSLKELDLT 134  
 641 INANGKMDYGVKDYGLVNSAGTOTTASATSDKA--NIK---GCKOTVGLANE----A 691  
 135 SVEN-EKLSFGANGKNVNTSDTKGL-NFAKETAINGDPTVHLNGIGSTLTDTLAGSSA 192  
 692 NIEGSEIDVGGSTFKHNGIGTQVONYGK---AINTD-----IVSGLOQIMANGTA 741  
 193 -SHVDAGNOSTHYTRAASKVDVLAAGMNTKGVKGTSTG--QSENVDPVPT----- 240  
 742 EGSIIINGSGQVNVNEGGLAE--NSVINDGCTLDVREKGSATGQOOSGALVATPRATVGT 800  
 241 --YDTVEFLSADTKTTV-----NVESKDNKGRTEVKIGATSVYKEK----- 281  
 801 TRADVAFSTIEGGAANNILLANGVLTVESDPTSDKTQVANGGR-ETVKTATATGTTLT 859  
 282 -----DGKLVTKGKG-----ENGSTDEGEGLVTAKEVIDAVANKA 317  
 860 GGEIVGAVANETTINDGQIOTVSANGELIKTKINEGTLTVNDNGKAT-----DIVONS 914  
 318 GWRKKTITANGQOAGDKFEVTSCTKV--TFASGNGTATVSDDOGNT-----TYKYD 370  
 915 GAALOTSTANG-----TEISGTHOYGFSTISGLATMLNGLNLLVAGTEARD 965  
 371 VNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKMDETVINANGNIETIRN 430  
 966 STVKG---GAMQNLG--QDSATRVNSGGQYTLGRSKDEPALARAEDLOVAGGTAIYYA 1020  
 431 GKNIDIAIS-----WTPQ-----FSSVSLGAGADA--PTLSVDEG 464  
 1021 GTLDASVSGATGSLSLMTPRDNTPVKLEGAVRTDSATLTLLNGVDTTLADLTAAISRG 1080  
 465 ALANGSKD-----ANKPRITINAVAPVKEGDY----- 491  
 1081 SVMLSNNSCAGTSCNCEYRVSLL--LNDGCVLYLSAQTAADATNGIYNTLTNELSSG 1138  
 492 -----TNYAOLKGYAQNINRINDVNGNARAGIAOAITAGLAQAYLPKSMMAIGGTY 546  
 1139 NFYLTINAVASRGDQLYVNN---NATGNFKI-----FYODTGVSPQSDAMTLVITGG--- 1188  
 547 LGEAGYAGVSSISDTGMVITKGT-----ASGNS 575  
 1189 -GDASFILG-----NTGCFVLDLGYEYVLKSDGNS 1217

RESULT 12  
 ID 120K\_RICRI STANDARD; PRT: 1300 AA.  
 AC P14914;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE 120 kDa surface-exposed protein.  
 GN P120.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=90136087; PubMed=2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the

RT 120 kDa surface-exposed protein of Rickettsia rickettsii.  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
 CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPTTOES  
 CC CONFERRING ANTIGENICITY TO THE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPA FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: X16353; CA34402.1; --  
 DR PIR: S07575; S07575.  
 DR InterPro: IPR003858; ROMP\_A; ROMP.  
 DR Pfam: PF02708; ROMP\_A; ROMP; 1.  
 KW Antigen; Glycoprotein; Cell wall; S-layer.  
 FT CARBOHYD 7  
 FT CARBOHYD 66  
 FT CARBOHYD 86  
 FT CARBOHYD 103  
 FT CARBOHYD 147  
 FT CARBOHYD 268  
 FT CARBOHYD 330  
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 FT CARBOHYD 424  
 FT CARBOHYD 430  
 FT CARBOHYD 436  
 FT CARBOHYD 444  
 FT CARBOHYD 515  
 FT CARBOHYD 547  
 FT CARBOHYD 593  
 FT CARBOHYD 655  
 FT CARBOHYD 698  
 FT CARBOHYD 710  
 FT CARBOHYD 799  
 FT CARBOHYD 800  
 FT CARBOHYD 826  
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 FT CARBOHYD 1140  
 FT CARBOHYD 1146  
 FT CARBOHYD 1211  
 FT CARBOHYD 1211  
 SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

Query Match 6.2%; Score 186.5; DB 1; Length 1300;  
 Best Local Similarity 21.4%; Pred. No. 0.044;  
 Matches 166; Conservative 88; Mismatches 260; Indels 261; Gaps 38;

30 ASATVATVATLTLATVQANATDTDEDELESV-ARSALYVQFMIDKGN--GEIESTG 86  
 22 ADGTYAFAFTASKVITQDSNFGNTDFGNLAQIKVPAITLV-----TGNETDASMPG 75  
 87 DIGMSIYDDHNTLHGATVTLKAGDNLIKSGKQFETSLKELDLTSVETKLSFGAN 146  
 76 NTAGVITFDANGTLESAS---ADANVAV-----TWNNTAIE-----AS 110  
 147 GKNVNTSDTKGLNFAKETAAGT-----NGDPTVHLNG-----IGSTL---TDTLAGSSAS 193  
 111 GAGVQLSGTHAELRLGNAGSIFKLADGTV-INKNVQOTVYALGALAGATTITDGSAITI 169

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OY 194 HDVAGNOS-----THYTRASIKDVLN-AGWNKIKVGTGTTGQSEN----- 234
DB 170 TSDIGNAGGAALQRTITLANDAKKTLTLGGANITIGAGGIDIDQANGTITKLTSTONNIV 229
OY 235 VDF---VRYDT-----VEFLSADRT-----TTVNESKDNCK 265
DB 230 VDFDLAIDQDTGVNDASSLTNAQTLTLTKIGTIGANNKTLTGQFNIGSSKTVLSNGNVA 289
OY 266 RTEVKIGATSVIKEDKGLVT-----GKG-----GEN-GSSTD----- 299
DB 290 INELVINGDCAVOGFADHYTLITRTNAAGQKILFNPVNNGTTLAAGTILGATNPLAE 349
OY 300 -----EGEGLVTAKEVIDANVAKGMRKTTTAN-----GQTG---QADKFE 337
DB 350 INFGSGVAVNDVLANVEGNVLYATNTITTDANVGSFVNAGSTNIVSGTVGGQDGKFN 409
OY 338 TVT--SGTKVTF--ASGNGTTATVSKD---OGNTTVKIDVNVGDALVNOQNSG--- 386
DB 410 TVALENGTIVKFLGNATFNGNTTIANSTLQIGNTYTAOC-VASADGTGIVEVNTGPIT 468
OY 387 WNLDSKA-----VAGSSGKVLS--GNVSPSKGKDETVNI----- 419
DB 469 VTLNKAAPVNALKQITVSGPNVNVINEIGNAGNHGAVTDITAFENSSLGAVVFLPRGI 528
OY 420 ---MAGNNEIT-----RNGKNIDIATSMT-----POSSVSLGAGAD- 454
DB 529 PFNDAGNTMPLTITKSTVGNKTAAGFDPVPSVYVLGVDSVADGVIDDQNNITVGLGSDN 588
OY 455 -----APTLSV-----DDEGALNVGSKDANKFVRITNVAPG----- 485
DB 589 GILVNTTLYAGISTLNNNGVTYTLGSGVNPMPGTGYGLGTIGAGSKFQVTTTIDYNNL 648
OY 486 -----VKEGDVTNVAOLKGVACONLNRRIDNVGNAPAGIAQAIATAGLAQAVLPCK 536
DB 649 GNIATNATINDCVTTTGTGIGAGIGDGIKTLTGSVNGNGVRFADILSNSTG---MIGT 705
OY 537 SMMALIGGTVLGEAGVAGVSSISDQGNVYIKRTAGSNGSNG-----HNGT 581
DB 706 TKANNGTVYTLGNA--FVGNIGDSDTPVASVRFPSGSDSAGLOGNITYSOVIDRGT 758

RESULT 13
OMPB.RICRI STANDARD; PRT: 1654 AA.
ID OMPB.RICRI 053047;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rompB)
DE (romp B) [contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales;
OC Rickettsiaceae: Rickettsiinae: Rickettsia.
OX NCBI_TaxID=783;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=R:
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.B. Jr., Cieplik W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (romp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN (12)
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R:
RX MEDLINE=90336087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the

```

```

RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC
DR EMBL: X16353; CAA34403.1; -
DR InterPro: IPR003858; rompa, rompb.
DR Pfam: PF02708; rompa, rompb; 1.
KW Antigen, S-layer, Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087FE618 CRC64;

Query Match 6.2%; Score 186.5; DB 1; Length 1654;
Best local similarity 21.4%; Pred. No. 0.045;
Matches 166; Conservative 88; Mismatches 260; Indels 261; Gaps 38;

OY 30 ASATVATVAVLATILSTNVQANATDDEDELESEV-ARSALVDFMIDKEEN-GEIESTG 86
DB 376 ADGTTAFKTAASKAVVTTQDSNFGNTDFGNLAQIKVPNATTL-----TGNFTGDSNPG 429
OY 87 DIMSIIYDDNHTLHGATVTLKAGDNLIKIKSGKDFYLSKELKDLTVSETEKLSGAN 146
DB 430 NTAGVITTFDANGTLESAS-----ADANVAV-----TNNTTALB-----AS 464
OY 147 GNRVNITSDTKGLNFAKTAGT---NGDPTVHLNG-----IGSTL---TDPLAGSSAS 193
DB 465 GAGVYOLSGTHAELRLGNAGSIFKLADGTIV-INGKVNQTAGALAACTITLDSAT 523
OY 194 HDVAGNOS-----THYTRASIKDVLN-AGWNKIKVGTGTTGQSEN----- 234
DB 524 TGDIGNAGGAALQRTITLANDAKKTLTLGGANITIGAGGIDIDQANGTITKLTSTONNIV 583
OY 235 VDF---VRYDT-----VEFLSADRT-----TTVNESKDNCK 265
DB 584 VDFDLAIDQDTGVNDASSLTNAQTLTLTKIGTIGANNKTLTGQFNIGSSKTVLSNGNVA 643
OY 266 RTEVKIGATSVIKEDKGLVT-----GKG-----GEN-GSSTD----- 299
DB 644 INELVINGDCAVOGFADHYTLITRTNAAGQKILFNPVNNGTTLAAGTILGATNPLAE 703
OY 300 -----EGEGLVTAKEVIDANVAKGMRKTTTAN-----GQTG---QADKFE 337
DB 704 INFGSGVAVNDVLANVEGNVLYATNTITTDANVGSFVNAGSTNIVSGTVGGQDGKFN 763
OY 338 TVT--SGTKVTF--ASGNGTTATVSKD---OGNTTVKIDVNVGDALVNOQNSG--- 386
DB 764 TVALENGTIVKFLGNATFNGNTTIANSTLQIGNTYTAOC-VASADGTGIVEVNTGPIT 822
OY 387 WNLDSKA-----VAGSSGKVLS--GNVSPSKGKDETVNI----- 419
DB 823 VTLNKAAPVNALKQITVSGPNVNVINEIGNAGNHGAVTDITAFENSSLGAVVFLPRGI 882
OY 420 ---MAGNNEIT-----RNGKNIDIATSMT-----POSSVSLGAGAD- 454
DB 883 PFNDAGNTMPLTITKSTVGNKTAAGFDPVPSVYVLGVDSVADGVIDDQNNITVGLGSDN 942
OY 455 -----APTLSV-----DDEGALNVGSKDANKFVRITNVAPG----- 485

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Db 943 GIIVATTLVAGISITLNNNGVTLGGVPMPTGVYIGTGIGASKRFQVTTDYNNL 1002  
OY 486 -----VKEGDVNTVAOLKGVANLNNDVNGNARAGIAAIAATAGIAQAYLCK 536  
Db 1003 GNITATNFATINDGVTVTTGGTIGTGFDDKITIGSVNGNNTVFAAGIILSNST---MGT 1059  
OY 537 SMAAGGTGTYGAGYAIGYSSISDPTGMVTKGTASGNSRG-----HFGT 581  
Db 1060 TRANGTGTVYLGNA--FVGNIGSDPTPAVASVFTGSDSGAGIAGNITGVSDVDFGT 1112  
RESULT 14  
OMPA\_RICCN STANDARD: PRT: 2021 AA.  
ID OMPA\_RICCN P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
AC Q52670; Q52674;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rompa) (romp A).  
GN OMPA OR RC1273.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=94171067; PubMed=8125327;  
RA Croquet-Valdes P.A., Weiss K., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";  
RL Gene 140:115-119(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).  
RL [3]  
RN SEQUENCE OF 8-204 FROM N.A.  
RC STRAIN=Indian tick typhus, MI, Malish 7, and Moroccan;  
RX MEDLINE=97015921; PubMed=8662558;  
RA Roux V., Fournier P.E., Raoult D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rompa."; J. Clin. Microbiol. 34:2058-2065(1996).  
RN [4]  
RP SEQUENCE OF 953-2012 FROM N.A.  
RC STRAIN=Indian tick typhus, MI, Malish 7, and Moroccan;  
RA Raoult D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompa."; Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PMW: GLYCOSYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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DR EMBL: U01028; AAA17405.1; -  
DR EMBL: AE008674; AAL03811.1; -  
DR EMBL: U43794; AAB49549.1; -  
DR EMBL: U43798; AAB49550.1; -  
DR EMBL: U43806; AAB49551.1; -  
DR EMBL: U45244; AAB49556.1; -  
DR EMBL: U46918; AAB49563.1; -  
DR EMBL: U83440; AAC35176.1; -  
DR EMBL: U83443; AAC35179.1; -  
DR EMBL: U83448; AAC35184.1; -  
DR EMBL: U83453; AAC35189.1; -  
DR InterPro: IPR003858; rompa\_rompB.  
DR Pfam: PF02708; rompa\_rompB; 1.  
DR Antigen: Repeat; signal; Cell wall; s-layer; Glycoprotein;  
KW Complete proteome.  
FT SIGNAL 1 38  
FT CHAIN 39 2021  
FT DOMAIN 238 946  
FT DOMAIN 1424 1528  
FT VARIANT 60 60  
FT VARIANT 76 76  
FT VARIANT 86 137  
FT VARIANT 126 133  
FT VARIANT 953 954  
FT VARIANT 1245 1245  
FT VARIANT 1308 1308  
FT VARIANT 1877 1877  
FT CONFLICT 10 10  
FT CONFLICT 92 92  
FT CONFLICT 126 126  
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FT CONFLICT 1872 1872  
FT CONFLICT 1875 1875  
FT CONFLICT 1878 1879  
FT CONFLICT 1936 1936  
FT CONFLICT 1965 1970  
FT CONFLICT 1997 1997  
SQ SEQUENCE 2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;  
Query Match 6.2%; Score 186.5; DB 1; Length 2021;  
Best Local Similarity 21.3%; Pred. No. 0.057;  
Matches 163; Conservative 84; Mismatches 245; Indels 273; Gaps 37;  
OY 10 NSALNAMYVSELFTRN-HTKRASATVAT-AVLATLLSATVQANATDTDEDELESVARSA 67  
DB 850 NNGIVTFGTGSDVNTGNITNALTATISVAGAKATLGAIKATTKTKLDNMSAVFT- NP 908  
OY 68 LVLOQMIIDKEGN-----GEISTGDIGMSITYDDHNTLH-----GATVTLKAGDNL- 113  
DB 909 VVVTGAIIDNTGNANNGIVTFGTGSDVNTGNIG-----NTNALATVNVGAVTLQAGGSLD 962

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OY 114 -----KIKOSGKDFYSLKKEKLDTSVETKLSFGANGKNVITSDTK 157
DB 963 ANNIDEGARSTLEFNGPLDGGGNAIPYFKGAL-----ANNNNAILNVNKT 1008
OY 158 GLMFAKETAGT-----NDDPTV-----HLNGISGT 182
DB 1009 LLTAHYHLTGTVAEINIGAGNLFPAIDASAGDVTLLNAODIHFRAIDSLVSLMTGCVGN 1068
OY 183 LDTTLAGSSSHVDAGNOSHHTYRAASIKDYVLNAGNNIKGVKGS--TTGSEVNDVY--R 239
DB 1069 NILAADLVAAPVDEGTV-----VFDGG--VNLGINSVNAAGAAINIGDVGNN 1114
OY 240 TYDVEELASDRTKTYTVNVS-----KDKGRTE-----VKIGAKTSVKERDGL 285
DB 1115 KFTTLLIYNAVTITDDVNEGLIONVLINNADTSTAFAAGTIQIDATYTTIDANNGL 1174
OY 286 VTGGR-----GENGSSTDEGEGLVTAKEVIDAVNKGAWRM 321
DB 1175 NIPAGNIKFAHADAOILNNGSSGNDRTITLGNMIDPDNDDEGIIVINSV-----TAG--K 1227
OY 322 KITTAGNQT--GQADKEFTV-----TSGTVTFASGN-----GTATV-- 357
DB 1228 KLTIAGKGTFFGAHKLQDIFKEGEGFTAGT--TFNTTNIVIDITGQLELGAATTANVVL 1285
OY 358 SKD-----DGNITVVKYDVNVDALNVNOLNSGNNLDSKAIVAGSSG 399
DB 1286 EKDAVOLITGNGIGFLDFPAKNGTYTLNNNVNAGTVK-----NTGCTNNGTILVIGASN 1341
OY 400 -----KVISGNVSPSG-----KMDETVINAGNNIET 427
DB 1342 LNRVNGIAMLKVGAGNVTKAGNVKIGETGTNTLTLPAHFKLIGSINTKGQALKL 1401
OY 428 T-RNGKNID--IATSMTPQSSVSLG--AGADAPILSYDDGALNVGSKDANKPRIT 480
DB 1402 NPNNGSVSVSGVGTAAAN-----SVDDITTAGATSFASVNAAGTATLGGTTFEHAFTTN 1455
OY 481 NVAPGVKEGDTV-----NVAOLKGVQAO--NLNNRI--DNVGNNAAGIAQAIAATAGLA 529
DB 1456 TGAVTTLAKGSTITFAKNVATFSAVNSATINFGNSLAFNSNITGSG-----TTLILGAN 1509
OY 530 QAVLPKSKMW-----AIGGGTYLGEAGYAIGYSSISD 561
DB 1510 QVMTYTGSPFTDTLITLPTFPDGAAGKSGNLIKSGTILDSGVSN 1554

RESULT 15
OMPB_RICCN STANDARD: PRT; 1655 AA.
ID OMPB_RICCN O9KRA3; O9KRA3; O9XC45;
AC O9KRA3; O9KRA3; O9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (OMPb)
DE (Omp B) [contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptidol.
OMPb OR RC1085.
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Reout D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;

```

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RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raout D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein ompb (ompb).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AEO08659; AAL03623.1; -
DR EMBL: AF123721; AAF34124.1; -
DR EMBL: AF123726; AAF34129.1; -
DR EMBL: AF149110; AAD39533.1; -
DR InterPro: IPR003858; OMPA_OmpB.
DR Pfam: PF02708; OmpA_OmpB; 1.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334
FT 1335 1655
FT VARIANT 61 61
FT VARIANT 75 75
FT VARIANT 78 78
FT VARIANT 251 251
FT VARIANT 413 413
FT VARIANT 959 959
FT VARIANT 988 988
FT VARIANT 1139 1139
FT CONFLICT 353 354
FT CONFLICT 776 776
FT CONFLICT 1159 1159
FT CONFLICT 1177 1177
FT CONFLICT 1492 1492
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5CE37 CRC64;

Query Match 6.2%; Score 186; DB 1; Length 1655;
Best Local Similarity 22.6%; Pred. No. 0.048; Indels 208; Gaps 39;
Matches 169; Conservative 77; Mismatches 293;

OY 10 NSALNMAVVVSELT-----RNH-----TRASATVTAVALATLLSA 45
DB 95 NTANNLDVYREDTTLGFTITNVNNAHFMMLNACKTLLITTOGCTINVOAAATKNNNV 154
OY 46 TVOANATDDEDELESVAR-----SALVLOF-----MIDKEGNET 82
DB 155 VAOVNMGAAIDNNDLOGVGRIDCGAAASTVLFVNLANPTQKADLLIDGNVIVNGANGTL 214
OY 83 EST-----GDIGMSIY-----DGHNTL-----HGATVTLAAGN--- 112
DB 215 NVATNGFIKVSSEPAIVYINIGD--GGGIMFNPDADVNTLNLQANCAATTFNGTSDTGR 273
OY 113 ---LKIKSGKDF--TYSLKKEKLDTSVETE-----KLSFGANGKNVITSDTKGLNF 161

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:39 ; Search time 168.02 Seconds  
(without alignments)  
606.440 Million cell updates/sec

Title: US-09-771-382-3  
Perfect score: 2994  
Sequence: 1 MNKIVRIIWNLSALNMMVVS.....TASGNSRGHFGTSASVGYOW 589

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2994   | 100.0       | 589    | 2  | Q93QY1 neisseria m |
| 2          | 2979   | 99.5        | 589    | 2  | Q93PI0 neisseria m |
| 3          | 2862   | 95.6        | 595    | 2  | Q93PH0 neisseria m |
| 4          | 2738   | 91.4        | 599    | 2  | Q93PS8 neisseria m |
| 5          | 2713.5 | 90.6        | 600    | 2  | Q93PS5 neisseria m |
| 6          | 2694   | 90.0        | 599    | 2  | Q93PS8 neisseria m |
| 7          | 2684   | 89.7        | 592    | 16 | Q93PR7 neisseria m |
| 8          | 2625.5 | 87.7        | 592    | 16 | Q93QW4 neisseria m |
| 9          | 2625.5 | 87.7        | 598    | 2  | Q93PT0 neisseria m |
| 10         | 2616.5 | 87.4        | 598    | 2  | Q93QY5 neisseria m |
| 11         | 2610.5 | 87.2        | 598    | 2  | Q93PS0 neisseria m |
| 12         | 2573.5 | 86.0        | 594    | 2  | Q93PH7 neisseria m |
| 13         | 2571.5 | 85.9        | 598    | 2  | Q93PR9 neisseria m |
| 14         | 2569.5 | 85.8        | 590    | 2  | Q93PS3 neisseria m |
| 15         | 2561.5 | 85.6        | 594    | 2  | Q93PS2 neisseria m |
| 16         | 2557.5 | 85.4        | 594    | 2  | Q93PI3 neisseria m |

|    |        |      |      |    |                    |
|----|--------|------|------|----|--------------------|
| 17 | 2516.5 | 84.1 | 594  | 2  | Q93QY4 neisseria m |
| 18 | 2512.5 | 83.9 | 600  | 2  | Q93PS6 neisseria m |
| 19 | 2490.5 | 83.2 | 592  | 2  | Q93QY2 neisseria m |
| 20 | 2479   | 82.8 | 591  | 2  | Q93PS7 neisseria m |
| 21 | 2479   | 82.8 | 591  | 16 | Q93RI8 neisseria m |
| 22 | 2475.5 | 82.7 | 592  | 2  | Q93PS9 neisseria m |
| 23 | 2467   | 82.4 | 591  | 2  | Q93QY3 neisseria m |
| 24 | 2462.5 | 82.2 | 592  | 2  | Q9AOF0 neisseria m |
| 25 | 2343.5 | 78.3 | 526  | 2  | Q93PS4 neisseria m |
| 26 | 2341.5 | 78.2 | 530  | 2  | Q93PS1 neisseria m |
| 27 | 1179.5 | 39.4 | 2353 | 2  | P71401 haemophilus |
| 28 | 1169.5 | 39.1 | 1098 | 2  | Q48152 haemophilus |
| 29 | 444.5  | 14.8 | 1299 | 16 | Q9F3X6 pasteurilla |
| 30 | 423    | 14.1 | 2059 | 16 | Q9PD50 xylella fas |
| 31 | 399    | 13.3 | 1190 | 16 | Q9PC04 xylella fas |
| 32 | 352    | 11.8 | 1107 | 2  | Q9F2D8 salmonella  |
| 33 | 330.5  | 11.0 | 2712 | 16 | Q9F3X5 rhizobium l |
| 34 | 262    | 8.8  | 1291 | 16 | Q92KQ7 rhizobium m |
| 35 | 257.5  | 8.6  | 1004 | 16 | Q9PD63 xylella fas |
| 36 | 246    | 8.2  | 1953 | 16 | Q9BHJ2 rhizobium l |
| 37 | 239.5  | 8.0  | 1265 | 2  | Q9FDA0 xanthomonas |
| 38 | 235.5  | 7.9  | 989  | 2  | Q9XD84 escherichia |
| 39 | 235    | 7.8  | 1417 | 16 | Q9HVN6 pseudomonas |
| 40 | 232.5  | 7.8  | 1018 | 16 | Q9HWU6 pseudomonas |
| 41 | 225.5  | 7.5  | 873  | 2  | Q9L960 moraxella c |
| 42 | 221    | 7.4  | 945  | 2  | Q93F03 shigella fl |
| 43 | 220.5  | 7.4  | 3930 | 16 | Q98E20 rhizobium l |
| 44 | 218.5  | 7.3  | 2747 | 2  | Q9L800 aeromonas s |
| 45 | 218    | 7.3  | 4919 | 2  | Q9ZH10 haemophilus |

#### ALIGNMENTS

| RESULT | ID                                                                    | PRELIMINARY:                         | PRT: | 589 AA. |
|--------|-----------------------------------------------------------------------|--------------------------------------|------|---------|
| Q93QY1 | Q93QY1                                                                | Q93QY1                               |      |         |
| AC     | Q93QY1                                                                | 01-DEC-2001 (TREMBLrel. 19, Created) |      |         |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                     |                                      |      |         |
| DR     | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                   |                                      |      |         |
| DE     | NHHA OUTER MEMBRANE PROTEIN.                                          |                                      |      |         |
| GN     | NHHA.                                                                 |                                      |      |         |
| OS     | Neisseria meningitidis.                                               |                                      |      |         |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |                                      |      |         |
| OX     | NCBI_TaxID=487;                                                       |                                      |      |         |
| RM     | [1]                                                                   |                                      |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |                                      |      |         |
| RC     | STRAIN=P20.                                                           |                                      |      |         |
| RA     | Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.:      |                                      |      |         |
| RT     | "Identification and characterization of a gene encoding a novel outer |                                      |      |         |
| RL     | membrane protein of Neisseria meningitidis."                          |                                      |      |         |
| DR     | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.               |                                      |      |         |
| EMBL:  | AF157610; AAK68871.1; -                                               |                                      |      |         |
| DR     | SEQUENCE 589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;                    |                                      |      |         |

| Query Match | Best Local Similarity | Score                                                         | 2994;                              | DB 2; | Length     | 589; |
|-------------|-----------------------|---------------------------------------------------------------|------------------------------------|-------|------------|------|
| Matches     | 589;                  | Conservative                                                  | 100.0%;                            | 0;    | Mismatches | 0;   |
|             |                       |                                                               |                                    |       | Indels     | 0;   |
|             |                       |                                                               |                                    |       | Gaps       | 0;   |
| QY          | 1                     | MNKIVRIIWNLSALNMMVVS                                          | ELTRNHTKASATVATATLISATVQANATDDEDEL | 60    |            |      |
| DB          | 1                     | MNKIVRIIWNLSALNMMVVS                                          | ELTRNHTKASATVATATLISATVQANATDDEDEL | 60    |            |      |
| QY          | 61                    | ESVARSALVLOPMIDKEGGEIESTGDISIYYDDHNTLHGAATYTLKAGDMLIKIOSK     | 120                                |       |            |      |
| DB          | 61                    | ESVARSALVLOPMIDKEGGEIESTGDISIYYDDHNTLHGAATYTLKAGDMLIKIOSK     | 120                                |       |            |      |
| QY          | 121                   | DEFTYSLKKELKDLTSVETEKLSFGANGKRVNITSDTKGINFAKETAGTNGDPTVHLNGIG | 180                                |       |            |      |
| DB          | 121                   | DEFTYSLKKELKDLTSVETEKLSFGANGKRVNITSDTKGINFAKETAGTNGDPTVHLNGIG | 180                                |       |            |      |

QY 181 STLDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNKIKVGTGSGTGOSENVDEVRT 240  
| | | | |  
DB 181 STLDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNKIKVGTGSGTGOSENVDEVRT 240  
QY 241 YDVEFLSADPKTTTAVVESKDNKRTEVRKIGAKTSYIKKEDGLVYKKGKGENGSSTDE 300  
| | | | |  
DB 241 YDVEFLSADPKTTTAVVESKDNKRTEVRKIGAKTSYIKKEDGLVYKKGKGENGSSTDE 300  
QY 301 GEGLVTAKEVIDAVNKAQWKRKTTTANGQTGOADKFEFTVSGKVTYPAASNGTATVSKD 360  
| | | | |  
DB 301 GEGLVTAKEVIDAVNKAQWKRKTTTANGQTGOADKFEFTVSGKVTYPAASNGTATVSKD 360  
QY 361 DQGNITVYKVDVNGDALNVNOLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETYNIN 420  
| | | | |  
DB 361 DQGNITVYKVDVNGDALNVNOLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETYNIN 420  
QY 421 AGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPLTVSDEGALNVGSKDANKPVIRIT 480  
| | | | |  
DB 421 AGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPLTVSDEGALNVGSKDANKPVIRIT 480  
QY 481 NVAPGVEGDTVNTVAQLKGAQNLNNRIDVNGNARAGIAQAIATAGLAQAYLPKGSMA 540  
| | | | |  
DB 481 NVAPGVEGDTVNTVAQLKGAQNLNNRIDVNGNARAGIAQAIATAGLAQAYLPKGSMA 540  
QY 541 IGGGTVYGEAGYATGYSISDGTGMWIKGTASGNSRGHFTGSASVGYQW 589  
| | | | |  
DB 541 IGGGTVYGEAGYATGYSISDGTGMWIKGTASGNSRGHFTGSASVGYQW 589

RESULT 2  
Q9JPH0 PRELIMINARY; PRT; 589 AA.  
ID Q9JPH0  
AC Q9JPH0;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGP165, 90/18311, AND 93/4286;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226384; AAF42533.1; -;  
DR EMBL: AF226362; AAF42511.1; -;  
DR EMBL: AF226363; AAF42512.1; -;  
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95DA868566A6 CRC64;

Query Match 99.5%; Score 2979; DB 2; Length 589;  
Best Local Similarity 99.5%; Pred. No. 1.5e-117;  
Matches 586; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATVATVATLTLASATVQANATDDEDEL 60  
| | | | |  
DB 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATVATVATLTLASATVQANATDDEDEL 60  
QY 61 ESVARSALVLOFMIDKEGNGEISTGDIQMSIYYDDHNTLHGATVTLKAGDNLIKOSGK 120  
| | | | |  
DB 61 ESVARSALVLOFMIDKEGNGEISTGDIQMSIYYDDHNTLHGATVTLKAGDNLIKOSGK 120

QY 121 DFTYSLKELKDLTSTVTEKLSFGANGKNYNTSDTKGLNFAKTAETAGNDPPYHLNGIG 180  
| | | | |  
DB 121 DFTYSLKELKDLTSTVTEKLSFGANGKNYNTSDTKGLNFAKTAETAGNDPPYHLNGIG 180  
QY 181 STLDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNKIKVGTGSGTGOSENVDEVRT 240  
| | | | |  
DB 181 STLDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNKIKVGTGSGTGOSENVDEVRT 240  
QY 241 YDVEFLSADPKTTTAVVESKDNKRTEVRKIGAKTSYIKKEDGLVYKKGKGENGSSTDE 300  
| | | | |  
DB 241 YDVEFLSADPKTTTAVVESKDNKRTEVRKIGAKTSYIKKEDGLVYKKGKGENGSSTDE 300  
QY 301 GEGLVTAKEVIDAVNKAQWKRKTTTANGQTGOADKFEFTVSGKVTYPAASNGTATVSKD 360  
| | | | |  
DB 301 GEGLVTAKEVIDAVNKAQWKRKTTTANGQTGOADKFEFTVSGKVTYPAASNGTATVSKD 360  
QY 361 DQGNITVYKVDVNGDALNVNOLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETYNIN 420  
| | | | |  
DB 361 DQGNITVYKVDVNGDALNVNOLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETYNIN 420  
QY 421 AGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPLTVSDEGALNVGSKDANKPVIRIT 480  
| | | | |  
DB 421 AGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPLTVSDEGALNVGSKDANKPVIRIT 480  
QY 481 NVAPGVEGDTVNTVAQLKGAQNLNNRIDVNGNARAGIAQAIATAGLAQAYLPKGSMA 540  
| | | | |  
DB 481 NVAPGVEGDTVNTVAQLKGAQNLNNRIDVNGNARAGIAQAIATAGLAQAYLPKGSMA 540  
QY 541 IGGGTVYGEAGYATGYSISDGTGMWIKGTASGNSRGHFTGSASVGYQW 589  
| | | | |  
DB 541 IGGGTVYGEAGYATGYSISDGTGMWIKGTASGNSRGHFTGSASVGYQW 589

RESULT 3  
Q9JPH0 PRELIMINARY; PRT; 595 AA.  
ID Q9JPH0  
AC Q9JPH0;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=528, AND 1000;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226360; AAF42509.1; -;  
DR EMBL: AF226356; AAF42505.1; -;  
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;

Query Match 95.6%; Score 2862; DB 2; Length 595;  
Best Local Similarity 95.0%; Pred. No. 1.2e-112;  
Matches 565; Conservative 7; Mismatches 17; Indels 6; Gaps 1;

QY 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATVATVATLTLASATVQANATDDEDEL 60  
| | | | |  
DB 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATVATVATLTLASATVQANATDDEDEL 60  
QY 61 ESVARSALVLOFMIDKEGNGEISTGDIQMSIYYDDHNTLHGATVTLKAGDNLIKIKO--- 117



[illegible]

|            | Query Match | Similarity                                                | Score | DB 2       | Length |
|------------|-------------|-----------------------------------------------------------|-------|------------|--------|
| Best Local | 91.48%      | 90.58%                                                    | 2738  | 599        |        |
| Matches    | 542         | Conservative                                              | 14    | Mismatches | 33     |
|            |             |                                                           |       | Indels     | 10     |
|            |             |                                                           |       | Gaps       | 1      |
| QY         | 1           | MNKIRIITNSALNMAVVVSELTNRHTRKASTVATATATLLSATVCANATDDEDEEL  | 60    |            |        |
| Db         | 1           | MNKIRIITNSALNMAVVVSELTNRHTRKASTVATATATLLSATVCANATDDEDEEVL | 60    |            |        |

|    |     |                                                                 |     |
|----|-----|-----------------------------------------------------------------|-----|
| QY | 61  | ESVANSALVLOFMJDICEENGELIESTGOLGSIYXDHNHLLHGAUVTLTKADGNLKINO---  | 117 |
| Db | 61  | BPVKRTAVVLRSRSGESTGKEVETEDSHMVKVDFEDEVGLAKAGITITLTKAGDNLTIKONTD | 120 |
| QY | 118 | -----SGKDFPTYSLKKRELKDLTVSEFEKLSFPGANGKNVITSDTGLGFPACKETACTNG   | 170 |
| Db | 121 | ENTDEBNTWASSPSTYSLKKDLFDLTSVETEKLSFGANGKNVITSDTGLGMPACKETACTNG  | 180 |
| QY | 171 | DPTVHLNIGSTLUDPTLGLGSSASHVDAGNOSTHTTPRAASIKDVLNACMNLIKVYTGSTTG  | 230 |
| Db | 181 | DTTVHLNIGSTLUDPTLGLGSSASHVDAGNOSTHTTPRAASIKDVLNACMNLIKVYTGSTTG  | 240 |
| QY | 231 | QSENDPFRPTDYEFEFSADPKRTTTVNANESKDNKRTPEVKIGARTSVIKEKDGKLVYKGK   | 290 |
| Db | 241 | QSENDPFRPTDYEFEFSADPKRTTTVNANESKDNKRTPEVKIGARTSVIKEKDGKLVYKGK   | 300 |
| QY | 291 | KGENSSSTDEBEGVLAYAKEVIDAANKKGRMKTTPANGOTGQADKFEYVNSGTRYVPFASG   | 350 |
| Db | 301 | KGENSSSTDEBEGVLAYAKEVIDAANKKGRMKTTPANGOTGQADKFEYVNSGTRYVPFASG   | 360 |
| QY | 351 | NGTTATVSKDQGNITTVKYDVNVGDALVNOLDJONGSNGNLDSKAAVAGSSGKVISGNTVPSK | 410 |
| Db | 361 | KGTATVSKDQGNITTVKYDVNVGDALVNOLDJONGSNGNLDSKAAVAGSSGKVISGNTVPSK  | 420 |
| QY | 411 | GKMDETVINAGNNIETIRNCKNIDDIATSMTPQSSSVSLGAGADAPLTVSDDBEGALNVGS   | 470 |
| Db | 421 | GKMDETVINAGNNIETIRNCKNIDDIATSMTPQSSSVSLGAGADAPLTVSDDBEGALNVGS   | 480 |
| QY | 471 | KDANKPVRITVNAVAPVEKGDVTYNAOLKGVAKQNLNNRINDYNGNARAGIAQALITATAGLQ | 530 |
| Db | 481 | KDANKPVRITVNAVAPVEKGDVTYNAOLKGVAKQNLNNRINDYNGNARAGIAQALITATAGLQ | 540 |
| QY | 531 | AYLPKSSMAALGGGTGYLDEAGYALGYSSIDTGMWVTKGTASGNSRCHFTSASVGTQM      | 589 |
| Db | 541 | AYLPKSSMAALGGGTGYLDEAGYALGYSSIDTGMWVTKGTASGNSRCHFTSASVGTQM      | 599 |

| RESULT | 5                                                                     |                           |
|--------|-----------------------------------------------------------------------|---------------------------|
| Q9JPSS | Q9JPSS                                                                | PRELIMINARY; PRT; 600 AA. |
| AC     | Q9JPSS5;                                                              |                           |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Created)                                  |                           |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                     |                           |
| DT     | 01-MAR-2001 (TREMBLrel. 16, Last annotation update)                   |                           |
| DE     | OUTER MEMBRANE PROTEIN GNA992.                                        |                           |
| GN     | GNA992.                                                               |                           |
| OS     | Neisseria meningitidis                                                |                           |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |                           |
| OX     | NCBI_TaxID=487;                                                       |                           |
| RN     | [1]                                                                   |                           |
| RP     | SEQUENCE FROM N.A.                                                    |                           |
| RC     | STRAIN=E32;                                                           |                           |
| RX     | MEDLINE=20175756; PubMed=10710308;                                    |                           |
| RA     | Pizza M., Scarlato V., Masiugnani V., Giuliani M.M., Arico' B.,       |                           |
| RA     | Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,   |                           |
| RA     | Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  |                           |
| RA     | Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,     |                           |
| RA     | Brooker M., Hunt E., Knapp B., Blair E., Mason T., Tettelein H.,      |                           |
| RA     | Mood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,     |                           |
| RA     | Hoxon E.R., Grandi G., Rappunoli R.;                                  |                           |
| RT     | "Identification of Vaccine Candidates Against Serogroup B             |                           |
| RL     | Meningococcus by Whole-Genome Sequencing.";                           |                           |
| SC     | Science 287:1816-1820(2000).                                          |                           |
| SR     | EMBL; AF226372; AAF42521.1;                                           |                           |
| DQ     | SEQUENCE 600 AA; 62606 MW; 13C35F1C46392524 CRC64;                    |                           |

|                       |                  |                   |            |             |
|-----------------------|------------------|-------------------|------------|-------------|
| Query Match           | 90.6%            | Score 2713.5;     | DB 2;      | Length 600; |
| Best Local Similarity | 90.0%            | Pred. No. 2e-106; |            |             |
| Matches 540;          | Conservative 15; | Mismatches 34;    | Indels 11; | Gaps 2;     |

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||||| 1 MNKTYRIIMNSALNAAWVVSSELTNRNHRKRASATVATVLAATLATSATVQOANATDEEDNDL 60
61 ESVARSLVLOFMIDKNGENGEIESTG--DIGMSIYDDHNTLHGATVTLKAGDNLIKIKO-- 117
62 EPVVRATPVLVSFHDKDEGTGKEVEGASSNLTYTFDKNRVLKAGTTTLKAGDNLIKIKONT 120
118 -----SGKDFYSLKELKDLTSVETEKLSFGANGKNVITSPTKGLNFAKETAGTN 169
121 NENTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKNVITSPTKGLNFAKETAGTN 180
170 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 229
181 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 240
230 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 289
241 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 300
290 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 349
301 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 360
350 GNGTTATVSKDDGNTYKYDVNNGDALNVQLONSGWNLDKSAVAGSSGKVIISGNVSPS 409
361 GNGTTATVSKDDGNTYKYDVNNGDALNVQLONSGWNLDKSAVAGSSGKVIISGNVSPS 420
410 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 469
421 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 480
470 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 529
481 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 540
530 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 589
541 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 600

RESULT 6
O9JPR8 PRELIMINARY: PRT: 599 AA.
AC Q9JPR8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=2015756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).

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DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
SQ SEQUENCE 599 AA; 62844 MW; BBA16B5F3C1970C CRC64;

Query Match          90.0%; Score 2694; DB 2: Length 599;
Best Local Similarity 89.7%; Pred. No. 1,3e-105;
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;

OY 1 MNKTYRIIMNSALNAAWVVSSELTNRNHRKRASATVATVLAATLATSATVQOANATDEEDNDL 60
DB 1 MNKTYRIIMNSALNAAWVVSSELTNRNHRKRASATVATVLAATLATSATVQOANATDEEDNDL 60
OY 61 ESVARSLVLOFMIDKNGENGEIESTG--DIGMSIYDDHNTLHGATVTLKAGDNLIKIKO-- 117
DB 61 ESVARSLVLOFMIDKNGENGEIESTG--DIGMSIYDDHNTLHGATVTLKAGDNLIKIKONT 120
OY 118 -----SGKDFYSLKELKDLTSVETEKLSFGANGKNVITSPTKGLNFAKETAGTN 170
DB 118 -----SGKDFYSLKELKDLTSVETEKLSFGANGKNVITSPTKGLNFAKETAGTN 180
OY 121 NENTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKNVITSPTKGLNFAKETAGTN 228
DB 121 NENTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKNVITSPTKGLNFAKETAGTN 240
OY 170 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 288
DB 170 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 298
OY 181 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 348
DB 181 GDFPVHLNGISSTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNIKGYKTGSTT 358
OY 230 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 408
DB 230 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 418
OY 241 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 468
DB 241 GOSENVDFVRYDYVEFLSADTKTTTNNVESKDNKRTVEYIGAKTSYIKEDKGLVTGK 478
OY 290 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 528
DB 290 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 538
OY 301 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 588
DB 301 GKGNGSSDDEGLVYTAKEVIDAVNKAQMKRTTTANGOTGADKEFTVSGTKVTPAS 598
OY 350 GNGTTATVSKDDGNTYKYDVNNGDALNVQLONSGWNLDKSAVAGSSGKVIISGNVSPS 600
DB 350 GNGTTATVSKDDGNTYKYDVNNGDALNVQLONSGWNLDKSAVAGSSGKVIISGNVSPS 610
OY 410 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 658
DB 410 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 668
OY 421 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 708
DB 421 KKKMDEFVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGADAPLTVSDDEGALNVG 718
OY 470 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 758
DB 470 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 768
OY 481 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 808
DB 481 SKDANKPVRITTNVAPGVKESDVTNVAQLKGYAQNLNRRIDNVNGNARAGIAQAIATAGLA 818
OY 530 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 858
DB 530 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 868
OY 541 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 900
DB 541 QATLPKSMMAIGGTYLGEAGYAGTSSISDTGNNVYIKGTASGNSRGHFTSASVGYQ 910

RESULT 7
O9JPR7 PRELIMINARY: PRT: 598 AA.
AC Q9JPR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SW2107;
RX MEDLINE=2015756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

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RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.,  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.",  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226385; AAF42534.1;  
 SO SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 89.7%; Score 2686.5; DB 2; Length 598;  
 Best Local Similarity 89.6%; Pred. No. 2,7e-105;  
 Matches 537; Conservative 12; Mismatches 39; Indels 11; Gaps 2;

OY 1 MKKIRITNSALNMAVYVSELTRNHTKRASATVATVATLTLATVQAATDDEEL 60  
 DB 1 MKKIRITNSALNMAVYVSELTRNHTKRASATVATVATLTLATVQAATDDEEL 59  
 OY 61 ESVARSALVLOFMIDKEGNEIESTGDIQMSIYDDHNTLHGATVTLKAGDNKIKO--- 117  
 DB 60 EYVQRTAPLPSHASEGEGEKEVIGNTNLGIYFDEKRVLAKGTTLKLKAGDNKIKONTND 119  
 OY 118 -----SGKDEFTYSLKELKDLTSYETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 170  
 DB 120 EMTDETNASSFTYSLKDLTLDTLSTETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179  
 OY 171 DPTVHLNGISLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNMIKGYKTSSTG 230  
 DB 180 DPTVHLNGISLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNMIKGYKTSSTG 239  
 OY 231 OSENDVFTYDVEFLSADTKTTTVNVESSKONGKTEVKIGAKTSVIEKDKLVTGAG 290  
 DB 240 OSENDVFTYDVEFLSADTKTTTVNVESSKONGKTEVKIGAKTSVIEKDKLVTGAG 299  
 OY 291 KEENGSTDEGEGLYAKEVDAVNAKAGRMKTTTANGOTGADKFEYTSKTKVTFASG 350  
 DB 300 KEENGSTDEGEGLYAKEVDAVNAKAGRMKTTTANGOTGADKFEYTSKTKVTFASG 359  
 OY 351 NGTTATVSKDDOGNITVYKDVNVGDLNANOLONSGMNLSKRAVASSGKVISGNVSPSK 410  
 DB 360 KCTTATVSKDDOGNITVYKDVNVGDLNANOLONSGMNLSKRAVASSGKVISGNVSPSK 419  
 OY 411 GMDVETVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGS 470  
 DB 420 GMDVETVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGS 479  
 OY 471 KDAKPVRTTNVAPGVKEGDVTVNAOLKGVAAQLNNRINDVNGNARAGIAQATATAGLAA 530  
 DB 480 KDAKPVRTTNVAPGVKEGDVTVNAOLKGVAAQLNNRINDVNGNARAGIAQATATAGLAA 539  
 OY 531 AYLPGKSMAAIGGTYLGAGYAIGYSSISDTGNVWIKGTASGNSRGHFTSASVGYOW 589  
 DB 540 AYLPGKSMAAIGGTYLGAGYAIGYSSISDTGNVWIKGTASGNSRGHFTSASVGYOW 598

RESULT 8

O9JQW4 PRELIMINARY; PRT: 592 AA.

AC O9JQW4;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE PUTATIVE SURFACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).  
 GN NMA1200 OR GNA992.  
 OS Neisseria meningitidis (serogroup A), and  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699, 487;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;  
 RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,  
 RA Jagers K., Leather S., Moul S., Mungall K., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.,  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 RT meningitidis 22491".  
 RL Nature 404:502-506(2000).

RP SEQUENCE FROM N.A.  
 RC STRAIN=205900, B2133, F6124, AND 22491;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capocchi B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.,  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.",  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AL162755; CAB84461.1; -  
 DR EMBL: AF226357; AAF42506.1; -  
 DR EMBL: AF226365; AAF42514.1; -  
 DR EMBL: AF226373; AAF42522.1; -  
 DR EMBL: AF226386; AAF42535.1; -  
 DR EMBL: AF226386; AAF42535.1; -  
 KW Complete proteome.  
 SO SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 87.7%; Score 2626.5; DB 16; Length 592;  
 Best Local Similarity 89.1%; Pred. No. 8,7e-103;  
 Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

OY 1 MKKIRITNSALNMAVYVSELTRNHTKRASATVATVATLTLATVQAATDDEEL 60  
 DB 1 MKKIRITNSALNMAVYVSELTRNHTKRASATVATVATLTLATVQAATDDEEL 60  
 OY 61 ESVARSALVLOFMIDKEGNEIESTGDIQMSIYDDHNTLHG-ATVTLKAGDNKIKO-- 117  
 DB 61 ESVARS- VVGSIQASMEGSELET---ISLMTNDSKEFPDIYVTLKAGDNKIKONT 116  
 OY 118 -----SGKDEFTYSLKELKDLTSYETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 173  
 DB 117 NENTNASSFTYSLKDLTLDTLSTETKLSFGANGKNVNTSDTKGLNFAKETAGTNGDTT 176  
 OY 174 VHLNGISLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNMIKGYKTSSTG 233  
 DB 177 VHLNGISLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNMIKGYKTSSTG 236  
 OY 234 NVDVFTYDVEFLSADTKTTTVNVESSKONGKTEVKIGAKTSVIEKDKLVTGKGE 293  
 DB 237 NVDVFTYDVEFLSADTKTTTVNVESSKONGKTEVKIGAKTSVIEKDKLVTGKGE 296  
 OY 294 NGSTDEGEGLYAKEVDAVNAKAGRMKTTTANGOTGADKFEYTSKTKVTFASNGT 353  
 DB 297 NGSTDEGEGLYAKEVDAVNAKAGRMKTTTANGOTGADKFEYTSKTKVTFASNGT 356  
 OY 354 TATVSKDDOGNITVYKDVNVGDLNANOLONSGMNLSKRAVASSGKVISGNVSPSKGM 413  
 DB 357 TATVSKDDOGNITVYKDVNVGDLNANOLONSGMNLSKRAVASSGKVISGNVSPSKGM 416  
 OY 414 DETVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDA 473  
 DB 417 DETVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDA 476  
 OY 474 NKPVRTTNVAPGVKEGDVTVNAOLKGVAAQLNNRINDVNGNARAGIAQATATAGLAA 533  
 DB 477 NKPVRTTNVAPGVKEGDVTVNAOLKGVAAQLNNRINDVNGNARAGIAQATATAGLAA 536  
 OY 534 PGKSMAAIGGTYLGAGYAIGYSSISDTGNVWIKGTASGNSRGHFTSASVGYOW 589

Db 537 P6KSMMAIGGGTGYREAGATGYSISIDSGNMWIIIKGTASGNRHFQFASVASVGIOW 592

RESULT 9  
ID Q9JPT0 PRELIMINARY; PRT; 598 AA.  
AC Q9JPT0;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DI 01-MAR-2001 (TREMBLrel. 15, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria  
OX NCBI\_taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=20175756; PubMed=10710308;  
RX STRAIN=2996;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santoli L., Savino S., Scariselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetzelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moon E.R., Grandi G., Rappunoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.",  
RL Science 287:1816-1820(2000).  
DR ENBL; AF226359; AAF42308.1;-  
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0DF2EE3 CRC64;

|                           |       |                    |            |            |
|---------------------------|-------|--------------------|------------|------------|
| Query Match               | 87.7% | Score 2625.5       | DB 2       | Length 598 |
| Best Local Similarity     | 87.9% | Pred. No. 9.6e-103 |            |            |
| Matches 528; Conservative | 18;   | Mismatches 40;     | Indels 15; | Gaps 4;    |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| 0y | 1   | MNYIRIIMNSALNANWVYSELTRHNRKRAATATVNLATLISATVOANNTDDEBEL       | 60  |
| 0y | 1   | MNYIRIIMNSALNANWVYSELTRHNRKRAATATVNLATLISATVOANNTDDEBEL       | 60  |
| Db | 1   | MNKYIRIIMNSALNANWVYSELTRHNRKRAATATVNLATLISATVOANNTDDEBEL      | 59  |
| 0y | 61  | ESVARSLVLIQFMDICEKNGEJESTGDIQGSFYDDHHTLIGAVITLAKAGNEIKIKOSK   | 120 |
| Db | 60  | EPVQCTAVYLSFRSDKESTGEKEGETEDBSNNAVYDEKRVYLKAGAITLAKAGNLIKQNTN | 119 |
| 0y | 121 | D-----FTYSLKKEIKDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAAGNG        | 170 |
| Db | 120 | EWTNENTNDSFPTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAAGNG    | 170 |
| 0y | 171 | DPTVHLNIGSTLTDPLTAGSSASHVDAGNOST--HYTPAASIKOVNLNAGNIKCVKTGST  | 222 |
| Db | 180 | DPTVHLNIGSTLTDPLTNATATNTAVTNDNTDDEKRAASVKKVULNAGNIMKVCKPGTT   | 239 |
| 0y | 229 | TGQSENQVFETPTDVEFLSADTKTTTNNVNSKNGKRETKIDAKTSVYKEXGKXLTVG     | 288 |
| Db | 240 | A--SNDVFEVPTDVEFLSADTKTTTNNVNSKNGKRETKIDAKTSVYKEXGKXLTVG      | 297 |
| 0y | 289 | KKGGENSSTEDEGELVYAKVEIVAIYVNAKAGRMKTTTANCGTQGAQDFEYVTSCTKTPTA | 348 |
| Db | 298 | KKGGENSSTEDEGELVYAKVEIVAIYVNAKAGRMKTTTANCGTQGAQDFEYVTSCTKTPTA | 357 |
| 0y | 349 | SGNGTTFATVSKDDQGNITVKYDVNVNGDALNVNOLNSGWNLDKRAVAGSSGKVISGNVSP | 408 |
| Db | 358 | SGNGTTFATVSKDDQGNITVKYDVNVNGDALNVNOLNSGWNLDKRAVAGSSGKVISGNVSP | 417 |
| 0y | 409 | SKGKADDEVNINAGNIEITRNGKNIDATISMTQFSSVLSGACADAPTLISVDEGALNV    | 466 |
| Db | 418 | SKGKADDEVNINAGNIEITRNGKNIDATISMTQFSSVLSGACADAPTLISVDEGALNV    | 477 |
| 0y | 469 | GSKDANKVYRITNVAAPGVEGDDVTNVAGLKVCAONLNNRIDNVNGNARAGIAONIAFAGL | 528 |
| Db | 478 | GSKDANKVYRITNVAAPGVEGDDVTNVAGLKVCAONLNNRIDNVNGNARAGIAONIAFAGL | 537 |

|           |                                                                       |                                                             |              |
|-----------|-----------------------------------------------------------------------|-------------------------------------------------------------|--------------|
| QY        | 529                                                                   | AAATYLPKGSMAIGGCTGTGAGATGCAICGSSISDPGNVYICATGSGNRGHTGSASVGO | 568          |
|           |                                                                       |                                                             |              |
| Db        | 538                                                                   | AAATYLPKGSMAIGGCTGTGAGATGCAICGSSISDPGNVYICATGSGNRGHTGSASVGO | 597          |
| QY        | 589                                                                   | W 589                                                       |              |
|           |                                                                       |                                                             |              |
| Db        | 598                                                                   | W 598                                                       |              |
| RESULT 10 |                                                                       |                                                             |              |
| ID        | 0930Y5                                                                |                                                             | 0930Y5       |
| AC        | 0930Y5                                                                | PRELIMINARY;                                                | PRT; 598 AA. |
| DT        | 01-DEC-2001                                                           | (TREMBLrel, 19, Created)                                    |              |
| DT        | 01-DEC-2001                                                           | (TREMBLrel, 19, Last sequence update)                       |              |
| DT        | 01-DEC-2001                                                           | (TREMBLrel, 19, Last annotation update)                     |              |
| DE        | NHHA OUTER MEMBRANE PROTEIN.                                          |                                                             |              |
| GN        | NHHA.                                                                 |                                                             |              |
| OS        | Neisseria meningitidis.                                               |                                                             |              |
| OC        | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |                                                             |              |
| OX        | NCBI_Taxid=487;                                                       |                                                             |              |
| RN        | [1]                                                                   |                                                             |              |
| RC        | SEQUENCE FROM N.A.                                                    |                                                             |              |
| RP        | STRAIN=BZ10;                                                          |                                                             |              |
| RA        | Peak 1.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;      |                                                             |              |
| RT        | Identification and characterization of a gene encoding a novel outer  |                                                             |              |
| RT        | membrane protein of Neisseria meningitidis.";                         |                                                             |              |
| RL        | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.               |                                                             |              |
| DR        | EMBL; AF157603; AAK68864.1; -                                         |                                                             |              |
| SO        | SEQUENCE                                                              | 598 AA; 62687 MW; 18CEFFBE6410A150F CRC64;                  |              |

|                       |                 |                    |           |            |
|-----------------------|-----------------|--------------------|-----------|------------|
| Query Match           | 87.4%           | Score 2616.5       | DB 2      | Length 598 |
| Best Local Similarity | 87.7%           | Pred. No. 2.3e-102 |           |            |
| Matches 527           | Conservative 18 | Mismatches 41      | Indels 15 | Gaps 4     |

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0Y 1 MKKIIRIIMNSLNAWVYSELTRNHRKRAATVAATVILTLASATVQAAOTPDDEBEL 60
Db 1 MKKISRIIMNSLNAWVYSELTRNHRKRAATVAATVILTLAFATVQAAOTPD--DDLYL 59
0Y 61 ESVARSAVLQPMIDKEGENCELESTGDIQWGIYVDHNHTLGAFTVTLKADNLKIKOSG 120
Db 60 EYVQRTAVVYLSRSDKEGTEGKEGETEDSNAAVYDEKRYLKAGITLAKADNLKIKONTN 119
0Y 121 D-----FTYSLKELKDLTSVETELKLSFGANGKNVITSDTKGLNFAETAAG 170
Db 120 ENTMENTNDSSPTYSLKDLTLDSVETELKLSFGANGKNVITSDTKGLNFAETAAG 179
0Y 171 DPTVHLNGISLTLDTLGSSASHVDAGNST--HYRAASIKRYVLAAGNIKGVKTGST 228
Db 180 DPTVHLNGISLTLDTLNLGATNTVTDNDTDEKRAASVYKRYVLAAGNIKGVKPGT 239
0Y 229 TGQSENVDQFVRHYDVEFLSADTFTTNYNVSCKNGKRTKIGAKTSVLEKDGKLYTG 288
Db 240 A--SUNVDQFVRHYDVEFLSADTFTTNYNVSCKNGKRTKIGAKTSVLEKDGKLYTG 297
0Y 289 KKGKGENSSSTDEGEELVYAKFEVIAVNVKAGRMKTTTANGOTGADKFEFTVSGTKTFA 348
Db 298 KKGKGENSSSTDEGEELVYAKFEVIAVNVKAGRMKTTTANGOTGADKFEFTVSGTKTFA 357
0Y 349 SGNGTATVSKDDQGNITVYKYDVNVGDLANVQJONGSMNLDSKAVAGSSGKYISGNVSP 408
Db 358 SGNGTATVSKDDQGNITVYKYDVNVGDLANVQJONGSMNLDSKAVAGSSGKYISGNVSP 417
0Y 409 SKGKDEFTVNLNAGNNIEITFNKGNIDIATISMPQESSVSLGAGADAPTLSDVDEGALNV 468
Db 418 SKGKDEFTVNLNAGNNIEITFNKGNIDIATISMPQESSVSLGAGADAPTLSDVDEGALNV 477
0Y 469 GSKDANKVRVITTNAPGKYBEDDYTNVQJLKVQAONLNRRIDNVNGNARACIQAIAINAGL 528
Db 478 GSKDANKVRVITTNAPGKYBEDDYTNVQJLKVQAONLNRRIDNVNGNARACIQAIAINAGL 537

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|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                 |                    |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|--------------------|
| OY                    | 529                                                                                                                                                                                                                                                                                                                                                                                                                                             | AQALYPGKSMMAIGCGTTLVGEAGYVIAIGVSSISDGTGMWYIKGAASGRSHCFPTSAVSQVQ | 568                |
| Dd                    | 538                                                                                                                                                                                                                                                                                                                                                                                                                                             | AQAFLPGKSMMAIGCGTTRGEGAGYIATGISISDTGNWYIKGTAAGNSRSHFETISAVSQVQ  | 597                |
| OY                    | 589                                                                                                                                                                                                                                                                                                                                                                                                                                             | W 589                                                           |                    |
| Dd                    | 598                                                                                                                                                                                                                                                                                                                                                                                                                                             | W 598                                                           |                    |
| <hr/>                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                 |                    |
| RESULT                | 11                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                    |
| O9JPSO                | ID                                                                                                                                                                                                                                                                                                                                                                                                                                              | PRELIMINARY:                                                    | PRT: 598 AA.       |
| AC                    | O9JPSO                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                    |
| DT                    | 01-OCT-2000                                                                                                                                                                                                                                                                                                                                                                                                                                     | (TREMBLrel. 15. Created)                                        |                    |
| DT                    | 01-OCT-2000                                                                                                                                                                                                                                                                                                                                                                                                                                     | (TREMBLrel. 15, last sequence update)                           |                    |
| DT                    | 01-DEC-2001                                                                                                                                                                                                                                                                                                                                                                                                                                     | (TREMBLrel. 19, last annotation update)                         |                    |
| DE                    | OUTER MEMBRANE PROTEIN GNA992 (NHLA OUTER MEMBRANE PROTEIN).                                                                                                                                                                                                                                                                                                                                                                                    |                                                                 |                    |
| GNA992                | OR NHLA.                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                 |                    |
| OS                    | Neisseria meningitidis.                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                 |                    |
| OC                    | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.                                                                                                                                                                                                                                                                                                                                                                           |                                                                 |                    |
| OX                    | NCBL TaxID=487;                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                 |                    |
| RN                    | [1]                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                 |                    |
| RP                    | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                    |
| RC                    | STRAIN=NGH15;                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                 |                    |
| RX                    | MEDLINE=2017556; PubMed=10710308;                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                 |                    |
| RA                    | Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santoli L., Savino S., Scarcelli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; |                                                                 |                    |
| RA                    | "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."                                                                                                                                                                                                                                                                                                                                            |                                                                 |                    |
| RT                    | Science 287:1816-1820(2000).                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                 |                    |
| RL                    | [2]                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                 |                    |
| RN                    | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                    |
| RP                    | STRAIN=HI5;                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                 |                    |
| RC                    | Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                    |
| RT                    | "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis."                                                                                                                                                                                                                                                                                                                              |                                                                 |                    |
| RL                    | Submitted (JUN-1999) to the EMBL/Genbank/DBDJ databases.                                                                                                                                                                                                                                                                                                                                                                                        |                                                                 |                    |
| DR                    | EMBL: AF226381; AAAF2530.1; -                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                 |                    |
| DR                    | EMBL: AF157607; AAK6868.1; -                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                 |                    |
| SQ                    | SEQUENCE 598 AA; 62763 MW; EC67AEFB8BA63CB CRC64;                                                                                                                                                                                                                                                                                                                                                                                               |                                                                 |                    |
| <hr/>                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                 |                    |
| Query Match           | 87.2%;                                                                                                                                                                                                                                                                                                                                                                                                                                          | Score 2610.5;                                                   | DB: 2; Length 598; |
| Best Local Similarity | 87.4%;                                                                                                                                                                                                                                                                                                                                                                                                                                          | Pred. No. 4.1e-102;                                             |                    |
| Matches 523;          | Conservative 19;                                                                                                                                                                                                                                                                                                                                                                                                                                | Mismatches 42;                                                  | Indels 15; Gaps    |
| OY                    | 1                                                                                                                                                                                                                                                                                                                                                                                                                                               | MNKIRITMNSALNMAMVVSELTNRNHTKRASATVAATLATLLSATVQANATDDEDEL       | 60                 |
| Dd                    | 1                                                                                                                                                                                                                                                                                                                                                                                                                                               | MNKIRITMNSALNMAMVVSELTRNHTKRASATVAATLATLLPFTVQANAD-DDDLXL       | 59                 |
| OY                    | 61                                                                                                                                                                                                                                                                                                                                                                                                                                              | ESVASALVLOPMIDKEGNEGETSGDIGMSIYYDDHNLHGATVTLKAGNDLIKQSK         | 120                |
| Dd                    | 60                                                                                                                                                                                                                                                                                                                                                                                                                                              | EPOVORTAVVLSPRSDEGTEGEKETSDSWMAYFPFKRLKGATTLKAGNDLIKQNTN        | 119                |
| OY                    | 121                                                                                                                                                                                                                                                                                                                                                                                                                                             | D-----FTYSLKELMDLTVEFEKLSPFGANGKNVNTTSPTKGLNFPAKETAQTG          | 170                |
| Dd                    | 120                                                                                                                                                                                                                                                                                                                                                                                                                                             | EVTNENTNDSSFTYSLKLDLTDLTVEFEKLSFGANGKNVNTTSPTKGLNFAKETAQTG      | 179                |
| OY                    | 171                                                                                                                                                                                                                                                                                                                                                                                                                                             | DPVTALNGISGTFDTLAGSSASHVDAGNOST--HYTRASIKDYLNAGMNTKGVKTST       | 228                |
| Dd                    | 180                                                                                                                                                                                                                                                                                                                                                                                                                                             | DPVTALNGISGTFDTLANTGATVTNDVTDDEKKRAASKDVLMAGMNTKGVKPGTT         | 239                |
| OY                    | 229                                                                                                                                                                                                                                                                                                                                                                                                                                             | TGQSENVDVFRTYTVEFLSADFKTTTYVNVESKDKNGKRTVKIGAKTVSIKERDGKLYTG    | 288                |
| Dd                    | 240                                                                                                                                                                                                                                                                                                                                                                                                                                             | A--SDNVGFVRTYDFVEFLSADTKTTTYVNVESKDNGKTEVKIGAKTVSIKERDGKLYTG    | 297                |
| OY                    | 289                                                                                                                                                                                                                                                                                                                                                                                                                                             | KGGKNGSGSTDGEBELVRAKEYIDAIVNKAAGMKTTTANGOTGOADKFETVYSGTKVTPA    | 348                |

| DB | Accession | Score | Length | DB 2 | Length | DB 3 | Length | DB 4 | Length | DB 5 | Length | DB 6 | Length | DB 7 | Length | DB 8 | Length | DB 9 | Length | DB 10 | Length | DB 11 | Length | DB 12 | Length | DB 13 | Length | DB 14 | Length | DB 15 | Length | DB 16 | Length | DB 17 | Length | DB 18 | Length | DB 19 | Length | DB 20 | Length | DB 21 | Length | DB 22 | Length | DB 23 | Length | DB 24 | Length | DB 25 | Length | DB 26 | Length | DB 27 | Length | DB 28 | Length | DB 29 | Length | DB 30 | Length | DB 31 | Length | DB 32 | Length | DB 33 | Length | DB 34 | Length | DB 35 | Length | DB 36 | Length | DB 37 | Length | DB 38 | Length | DB 39 | Length | DB 40 | Length | DB 41 | Length | DB 42 | Length | DB 43 | Length | DB 44 | Length | DB 45 | Length | DB 46 | Length | DB 47 | Length | DB 48 | Length | DB 49 | Length | DB 50 | Length | DB 51 | Length | DB 52 | Length | DB 53 | Length | DB 54 | Length | DB 55 | Length | DB 56 | Length | DB 57 | Length | DB 58 | Length | DB 59 | Length | DB 60 | Length | DB 61 | Length | DB 62 | Length | DB 63 | Length | DB 64 | Length | DB 65 | Length | DB 66 | Length | DB 67 | Length | DB 68 | Length | DB 69 | Length | DB 70 | Length | DB 71 | Length | DB 72 | Length | DB 73 | Length | DB 74 | Length | DB 75 | Length | DB 76 | Length | DB 77 | Length | DB 78 | Length | DB 79 | Length | DB 80 | Length | DB 81 | Length | DB 82 | Length | DB 83 | Length | DB 84 | Length | DB 85 | Length | DB 86 | Length | DB 87 | Length | DB 88 | Length | DB 89 | Length | DB 90 | Length | DB 91 | Length | DB 92 | Length | DB 93 | Length | DB 94 | Length | DB 95 | Length | DB 96 | Length | DB 97 | Length | DB 98 | Length | DB 99 | Length | DB 100 | Length | DB 101 | Length | DB 102 | Length | DB 103 | Length | DB 104 | Length | DB 105 | Length | DB 106 | Length | DB 107 | Length | DB 108 | Length | DB 109 | Length | DB 110 | Length | DB 111 | Length | DB 112 | Length | DB 113 | Length | DB 114 | Length | DB 115 | Length | DB 116 | Length | DB 117 | Length | DB 118 | Length | DB 119 | Length | DB 120 | Length | DB 121 | Length | DB 122 | Length | DB 123 | Length | DB 124 | Length | DB 125 | Length | DB 126 | Length | DB 127 | Length | DB 128 | Length | DB 129 | Length | DB 130 | Length | DB 131 | Length | DB 132 | Length | DB 133 | Length | DB 134 | Length | DB 135 | Length | DB 136 | Length | DB 137 | Length | DB 138 | Length | DB 139 | Length | DB 140 | Length | DB 141 | Length | DB 142 | Length | DB 143 | Length | DB 144 | Length | DB 145 | Length | DB 146 | Length | DB 147 | Length | DB 148 | Length | DB 149 | Length | DB 150 | Length | DB 151 | Length | DB 152 | Length | DB 153 | Length | DB 154 | Length | DB 155 | Length | DB 156 | Length | DB 157 | Length | DB 158 | Length | DB 159 | Length | DB 160 | Length | DB 161 | Length | DB 162 | Length | DB 163 | Length | DB 164 | Length | DB 165 | Length | DB 166 | Length | DB 167 | Length | DB 168 | Length | DB 169 | Length | DB 170 | Length | DB 171 | Length | DB 172 | Length | DB 173 | Length | DB 174 | Length | DB 175 | Length | DB 176 | Length | DB 177 | Length | DB 178 | Length | DB 179 | Length | DB 180 | Length | DB 181 | Length | DB 182 | Length | DB 183 | Length | DB 184 | Length | DB 185 | Length | DB 186 | Length | DB 187 | Length | DB 188 | Length | DB 189 | Length | DB 190 | Length | DB 191 | Length | DB 192 | Length | DB 193 | Length | DB 194 | Length | DB 195 | Length | DB 196 | Length | DB 197 | Length | DB 198 | Length | DB 199 | Length | DB 200 | Length | DB 201 | Length | DB 202 | Length | DB 203 | Length | DB 204 | Length | DB 205 | Length | DB 206 | Length | DB 207 | Length | DB 208 | Length | DB 209 | Length | DB 210 | Length | DB 211 | Length | DB 212 | Length | DB 213 | Length | DB 214 | Length | DB 215 | Length | DB 216 | Length | DB 217 | Length | DB 218 | Length | DB 219 | Length | DB 220 | Length | DB 221 | Length | DB 222 | Length | DB 223 | Length | DB 224 | Length | DB 225 | Length | DB 226 | Length | DB 227 | Length | DB 228 | Length | DB 229 | Length | DB 230 | Length | DB 231 | Length | DB 232 | Length | DB 233 | Length | DB 234 | Length | DB 235 | Length | DB 236 | Length | DB 237 | Length | DB 238 | Length | DB 239 | Length | DB 240 | Length | DB 241 | Length | DB 242 | Length | DB 243 | Length | DB 244 | Length | DB 245 | Length | DB 246 | Length | DB 247 | Length | DB 248 | Length | DB 249 | Length | DB 250 | Length | DB 251 | Length | DB 252 | Length | DB 253 | Length | DB 254 | Length | DB 255 | Length | DB 256 | Length | DB 257 | Length | DB 258 | Length | DB 259 | Length | DB 260 | Length | DB 261 | Length | DB 2 |
|----|-----------|-------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|------|
|----|-----------|-------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|------|

[illegible]

| Q9JPR9 | 13                                                                    | RESULT       |
|--------|-----------------------------------------------------------------------|--------------|
| ID     | Q9JPR9                                                                | PRELIMINARY; |
| AC     | Q9JPR9;                                                               | PRT;         |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Created)                                  | 598 AA.      |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                     |              |
| DT     | 01-MAR-2001 (TREMBLrel. 16, Last annotation update)                   |              |
| DE     | OUTER MEMBRANE PROTEIN GNA92.                                         |              |
| GN     | GNA92.                                                                |              |
| OS     | Neisseria meningitidis.                                               |              |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |              |
| OX     | NCBI_TaxID=487;                                                       |              |
| RN     | [1]                                                                   |              |
| RP     | SEQUENCE FROM N.A.                                                    |              |
| RC     | STRAIN-NGH36;                                                         |              |
| RX     | MEDLINE=20175756; PubMed=10710308;                                    |              |
| RA     | Pizza M., Scariato V., Masiagnani V., Giuliani M.M., Arico' B.,       |              |
| RA     | Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,   |              |
| RA     | Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  |              |
| RA     | Ratti G., Santoli L., Savino S., Scarselli M., Storni E., Zuo P.,     |              |
| RA     | Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,      |              |
| RA     | Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,     |              |
| RA     | Moxon E.R., Grandi G., Rappunoli R.;                                  |              |
| RT     | "Identification of Vaccine Candidates Against Serogroup B             |              |
| RL     | Meningococcus by Whole-Genome Sequencing."                            |              |
| SR     | EMBL: AF226382; AAF42531.1; -                                         |              |
| SO     | SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;                    |              |

| Query Match           | 85.9%           | Score 2571.5                                                  | DB 2      | length 598 |
|-----------------------|-----------------|---------------------------------------------------------------|-----------|------------|
| Best Local Similarity | 86.0%           | Pred. 1.8e-100                                                |           |            |
| Matches 517           | Conservative 20 | Mismatches 49                                                 | Indels 15 | Gaps       |
| OY                    | 1               | MNKKYRIITWNSALNAAWYVSELTENRHKRSATATATVLTITLSATQAQNAATPDDEPEEL | 60        |            |
| Db                    | 1               | MNKKYRIITWNSALNAAWYVSELTENRHKRSATATATVLTITLSATQAQNAATPDDEPEEL | 59        |            |
| OY                    | 61              | ESVARSALVLOFMDIDEGNGEISTGDIQWSIYYDDHNHTLGATVTLKAGDNLIKOSG     | 120       |            |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| Db | 60  | EPVQRTAVLVFSRBDKBTGCEBCTEDBSNMAVYDEKERVILKAGAILTLKADNLIKQNTN  | 119 |
| Qy | 121 | D-----FTYSLKKEKCOLTSVTEKISFCGANGKNVITSDFRGLNPAKETAGTNG        | 170 |
| Db | 120 | ENTNENTNDSFFYTSLKKDLDLTSVELEKLSFCGANGKNVITSDFRGLNPAKETAGTNG   | 179 |
| Qy | 171 | DPTHLANGIGSTLINDTLGSSASHVDAGNGST--HYTRASIKVILNAGNNIKGVKGTST   | 228 |
| Db | 180 | DPTHLANGIGSTLINDTLGNTGATTNTVINDVNTDDEKKRRASVADVYLAAGNNIKGVKGT | 239 |
| Qy | 229 | TGQSENVDFVRTYDVEFLSADFTKTTTVNYESKDNKGRTEYKIGAKTSVIREKDKGLVYG  | 288 |
| Db | 240 | A--SDNVDFEVRTYDVEFLSADFTKTTTVNYESKDNKGRTEYKIGAKTSVIREKDKGLVYG | 297 |
| Qy | 289 | KGKGNGSSTDEGGGLYTAKEVIDAVNKKAGRMKTTTANQOTGADKFEVYTSGTATFA     | 348 |
| Db | 298 | KGKGNGSSTDEGGGLYTAKEVIDAVNKKAGRMKTTTANQOTGADKFEVYTSGTATFA     | 357 |
| Qy | 349 | SGNGTTAVTSKDDGNGITVKKVDVNVGDLANNQJONGSGMNLDSKAVVSGSGKATVSNVP  | 408 |
| Db | 358 | SGKGTATVSKDDGNGITVKKVDVNVGDLANNQJONGSGMNLDSKAVVSGSGKATVSNVP   | 417 |
| Qy | 409 | SKGKMDETVNIAGNNIEITFRNGKNIDIATVSMTPQESSVSLGACADAPTLVSDEGALNV  | 468 |
| Db | 418 | SKGKMDETVNIAGNNIEITFRNGKNIDIATVSMAPQESSVSLGACADAPTLVSDEGALNV  | 477 |
| Qy | 469 | GSKDANKRVTRITNVAAPGVKEBDVNVNOLKGVADNLNRRIDNVNGNARAGIAOIAIAGL  | 528 |
| Db | 478 | GSKDANKRVTRITNVAAPGVKEBDVNVNOLKGVADNLNRRIDNVNGNARAGIAOIAIAGL  | 537 |
| Qy | 529 | AOAYLPGKSMAGIGGGYLYGAGYAIGYSSISDTGMNVIKGTASGNSRGHFGTASAVGYO   | 588 |
| Db | 538 | VOAYLPGKSMAGIGGGYLYGAGYAIGYSSISDTGMNVIKGTASGNSRGHFGTASAVGYO   | 597 |
| Qy | 589 | W 589                                                         |     |
| Db | 598 | W 598                                                         |     |

|        | RESULT                                                                | 14           |              |
|--------|-----------------------------------------------------------------------|--------------|--------------|
| 09JPS3 |                                                                       |              |              |
| ID     | 09JPS3                                                                | PRELIMINARY: | PRT: 590 AA. |
| AC     | 09JPS3:                                                               |              |              |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Created)                                  |              |              |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                     |              |              |
| DT     | 01-MAR-2001 (TREMBLrel. 16, Last annotation update)                   |              |              |
| DE     | OUTER MEMBRANE PROTEIN GNA92.                                         |              |              |
| GN     | GNA92.                                                                |              |              |
| OS     | Neisseria meningitidis.                                               |              |              |
| OC     | Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. |              |              |
| OX     | NCBI_TaxID=487;                                                       |              |              |
| RN     | [1]                                                                   |              |              |
| RP     | SEQUENCE FROM N.A.                                                    |              |              |
| RC     | STRAIN-NGE28;                                                         |              |              |
| RX     | MEDLINE=20175756; PubMed=10710308;                                    |              |              |
| RA     | Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,         |              |              |
| RA     | Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,     |              |              |
| RA     | Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nili S.,  |              |              |
| RA     | Ratti G., Santili L., Savino S., Scarcelli M., Storni E., Zuo P.,     |              |              |
| RA     | Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,      |              |              |
| RA     | Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,     |              |              |
| RA     | Moxon E.R., Grandi G., Rappelli R.;                                   |              |              |
| RT     | "Identification of Vaccine Candidates Against Serogroup B             |              |              |
| RT     | Meningococcus by Whole-Genome Sequencing."                            |              |              |
| RL     | Science 287:1816-1820(2000).                                          |              |              |
| DR     | EMBL: AF226378; AAF42527.1; -                                         |              |              |
| SO     | SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;                    |              |              |

|                           |        |                     |           |             |
|---------------------------|--------|---------------------|-----------|-------------|
| Query Match               | 85.8%; | Score 2569.5;       | DB 2;     | Length 590; |
| Best Local Similarity     | 86.5%; | Pred. No. 2.1e-100; |           |             |
| Matches 514; Conservative | 24;    | Mismatches 47;      | Indels 9; | Gaps 4;     |

QY 1 MKKIRIINNSALNMAVYVSELTNRHTRKASATVATATLTSATVQANATDDEEL 60  
 DB 1 MKKIRIINNSALNMAVYVSELTNRHTRKASATVATATLTSATVQANADEEEDL 60  
 QY 61 ESVAASALVLOPMIDKEGENCE--IESTGIDMSIYDDHNTLHGATVTLKAGDNLIKQ 117  
 DB 61 DVQGTAVLVLYNSDKKEGKEKEVEND--WAYFNKGVLTACTITLKKAGDNLIKQ 118  
 QY 118 SCKDFTYSLKELKDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN 177  
 DB 119 NCTNFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN 178  
 QY 178 GIGSLTLDTLTLGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKGTSTGSENV 235  
 DB 179 GIGSLTLDTLTLGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKGTSTGSENV 236  
 QY 236 DEVRTYDVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSYIKEDGKLVTKGKENG 295  
 DB 237 DEVRTYDVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSYIKEDGKLVTKGKENG 296  
 QY 296 SSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFETVTSKTYTASGNGTTA 355  
 DB 297 SSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFETVTSKTYTASGNGTTA 356  
 QY 356 TYSKDDQGNITVYKVDVNGDALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKKME 415  
 DB 357 TYSKDDQGNITVYKVDVNGDALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKKME 416  
 QY 416 TVNINAGNIEITRNKNIDITATSMTPOPSSVSLGAGADAPTLSDVDEGALNVGSKDANK 475  
 DB 417 TVNINAGNIEITRNKNIDITATSMTPOPSSVSLGAGADAPTLSDVDEGALNVGSKDANK 476  
 QY 476 PVRTINVAAGVKEGDDVTNVAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLAQAYLPG 535  
 DB 477 PVRTINVAAGVKEGDDVTNVAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLAQAYLPG 536  
 QY 536 KSMMAIGGTYLGEAGYAGYSSISDGTGMWYIKGTASGNSRGHFGTSASVGYOW 589  
 DB 537 KSMMAIGGTYLGEAGYAGYSSISDGTGMWYIKGTASGNSRGHFGTSASVGYOW 590  
 RESULT 15  
 Q9JPS2 PRELIMINARY: PRT: 594 AA.  
 AC Q9JPS2: 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
 DE OTHER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGE31;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeocchi B.,  
 RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Moxon E.R., Grandi G., Saunders N.J., Granoff D.M., Venter C.,  
 RA \*Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-genome Sequencing.\*;  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226379; AAF42528.1;  
 SQ SEQUENCE 594 AA: 62114 MW: 1E2A63A78F53D256 CRC64;

Best Local Similarity 86.6%; Pred. No. 4.6e-100;  
 Matches 517; Conservative 17; Mismatches 52; Indels 11; Gaps 4;

QY 1 MKKIRIINNSALNMAVYVSELTNRHTRKASATVATATLTSATVQANATDDEEL 60  
 DB 1 MKKIRIINNSALNMAVYVSELTNRHTRKASATVATATLTSATVQANADEEEDL 60  
 QY 61 ESVAASALVLOPMIDKEGENCE--IESTGIDMSIYDDHNTLHGATVTLKAGDNLIKQ 117  
 DB 61 DVQGTAVLVLYNSDKKEGKEKEVEND--WAYFNKGVLTACTITLKKAGDNLIKQ 118  
 QY 118 SCKDFTYSLKELKDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN 177  
 DB 119 NCTNFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN 178  
 QY 178 GIGSLTLDTLTLGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKGTSTGSENV 235  
 DB 179 GIGSLTLDTLTLGSSASHVDAGNOST--HYTRAASIKDVLNAGMNIKGVKGTSTGSENV 236  
 QY 236 DEVRTYDVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSYIKEDGKLVTKGKENG 295  
 DB 237 DEVRTYDVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSYIKEDGKLVTKGKENG 296  
 QY 296 SSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFETVTSKTYTASGNGTTA 355  
 DB 297 SSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFETVTSKTYTASGNGTTA 356  
 QY 356 TYSKDDQGNITVYKVDVNGDALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKKME 415  
 DB 357 TYSKDDQGNITVYKVDVNGDALNVNOLQNSGWNLDKAVAGSSGKVISGNVSPSKKME 416  
 QY 416 TVNINAGNIEITRNKNIDITATSMTPOPSSVSLGAGADAPTLSDVDEGALNVGSKDANK 475  
 DB 417 TVNINAGNIEITRNKNIDITATSMTPOPSSVSLGAGADAPTLSDVDEGALNVGSKDANK 476  
 QY 476 PVRTINVAAGVKEGDDVTNVAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLAQAYLPG 535  
 DB 477 PVRTINVAAGVKEGDDVTNVAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLAQAYLPG 536  
 QY 536 KSMMAIGGTYLGEAGYAGYSSISDGTGMWYIKGTASGNSRGHFGTSASVGYOW 589  
 DB 537 KSMMAIGGTYLGEAGYAGYSSISDGTGMWYIKGTASGNSRGHFGTSASVGYOW 590

Search completed: July 3, 2002, 08:28:41  
 Job time: 1162 sec





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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:05 ; Search time 168.6 seconds

(without alignments)  
391.328 Million cell updates/sec

Title: US-09-771-382-4

Perfect score: 3019

Sequence: 1 MNKIVRIIMNSALNMAWAVS.....TASGNSRGHFASASVGYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_032802.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT.\*  
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23: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 3019   | 100.0       | 594    | 20    | AAV23740    |
| 2          | 3019   | 100.0       | 594    | 21    | AAV57044    |
| 3          | 3019   | 100.0       | 594    | 22    | AAU06174    |
| 4          | 2874   | 95.2        | 594    | 22    | AAV23739    |
| 5          | 2874   | 95.2        | 594    | 22    | AAU06179    |
| 6          | 2855   | 94.6        | 598    | 20    | AAI23742    |
| 7          | 2855   | 94.6        | 598    | 22    | AAU06177    |
| 8          | 2852   | 94.5        | 598    | 20    | AAV23738    |
| 9          | 2852   | 94.5        | 598    | 22    | AAU06178    |
| 10         | 2783.5 | 92.2        | 591    | 21    | AAV57045    |
| 11         | 2762.5 | 91.5        | 599    | 20    | AAV23743    |

|    |        |      |      |    |          |                    |
|----|--------|------|------|----|----------|--------------------|
| 12 | 2762.5 | 91.5 | 599  | 22 | AAU06176 | N. meningitidis H3 |
| 13 | 2758.5 | 91.4 | 591  | 20 | AAV27202 | Amino acid sequenc |
| 14 | 2758.5 | 91.4 | 591  | 20 | AAV23746 | A surface protein  |
| 15 | 2758.5 | 91.4 | 591  | 22 | AAU06171 | N. meningitidis PM |
| 16 | 2751   | 91.1 | 592  | 20 | AAI23737 | A surface protein  |
| 17 | 2739.5 | 90.7 | 591  | 20 | AAV23741 | N. meningitidis EG |
| 18 | 2739.5 | 90.7 | 591  | 22 | AAU06175 | N. meningitidis EG |
| 19 | 2636   | 87.3 | 592  | 20 | AAV23744 | A surface protein  |
| 20 | 2636   | 87.3 | 592  | 22 | AAU06172 | N. meningitidis H4 |
| 21 | 2533   | 83.9 | 592  | 22 | AAU06180 | N. meningitidis Z2 |
| 22 | 2516.5 | 83.4 | 589  | 20 | AAV23745 | A surface protein  |
| 23 | 2516.5 | 83.4 | 589  | 22 | AAU06173 | N. meningitidis P2 |
| 24 | 2504   | 82.9 | 592  | 20 | AAV27203 | Amino acid sequenc |
| 25 | 2449   | 81.1 | 512  | 22 | AAU06183 | N. meningitidis PM |
| 26 | 2409.5 | 79.8 | 513  | 22 | AAU06188 | N. meningitidis H4 |
| 27 | 2366   | 78.4 | 502  | 22 | AAU06186 | N. meningitidis PM |
| 28 | 2230   | 73.9 | 604  | 22 | AAU06181 | N. meningitidis su |
| 29 | 2032.5 | 67.3 | 433  | 22 | AAU06185 | N. meningitidis PM |
| 30 | 1887.5 | 62.5 | 407  | 22 | AAU06184 | N. meningitidis PM |
| 31 | 1328.5 | 44.0 | 2353 | 17 | AAV99393 | Haemophilus adhesi |
| 32 | 1292.5 | 42.8 | 2411 | 21 | AAV23860 | Haemophilus influe |
| 33 | 1055   | 34.9 | 1094 | 21 | AAV23858 | Haemophilus influe |
| 34 | 1050   | 34.8 | 245  | 20 | AAV27201 | Amino acid sequenc |
| 35 | 1030   | 34.1 | 1098 | 17 | AAV99392 | Haemophilus adhesi |
| 36 | 978.5  | 32.4 | 679  | 17 | AAV99394 | Haemophilus influe |
| 37 | 978.5  | 32.4 | 679  | 21 | AAV23855 | Haemophilus influe |
| 38 | 741    | 24.5 | 1004 | 21 | AAV23857 | Haemophilus influe |
| 39 | 727    | 24.1 | 1002 | 21 | AAV23854 | Haemophilus influe |
| 40 | 689    | 22.8 | 1104 | 21 | AAV23859 | Haemophilus influe |
| 41 | 689    | 22.8 | 1104 | 21 | AAV23859 | Haemophilus influe |
| 42 | 595    | 19.7 | 116  | 21 | AAV37832 | Neisseria consensu |
| 43 | 394.5  | 13.1 | 2314 | 22 | AAV69136 | M. catarrhalis les |
| 44 | 393.5  | 13.0 | 1992 | 17 | AAU04505 | M. catarrhalis str |
| 45 | 393.5  | 13.0 | 1992 | 22 | AAV69133 | M. catarrhalis str |

#### ALIGNMENTS

|                                                                   |                                     |
|-------------------------------------------------------------------|-------------------------------------|
| RESULT 1                                                          |                                     |
| ID AAV23740                                                       | AAV23740 standard; Protein: 594 AA. |
| XX                                                                |                                     |
| AC AAV23740:                                                      |                                     |
| XX                                                                |                                     |
| DT 08-SEP-1999                                                    | (first entry)                       |
| XX                                                                |                                     |
| DE A surface protein of Neisseria meningitidis.                   |                                     |
| XX                                                                |                                     |
| KW Surface protein; surface glycoprotein; infection; vaccine;     |                                     |
| KW Immunoreactive peptide.                                        |                                     |
| XX                                                                |                                     |
| OS Neisseria meningitidis.                                        |                                     |
| XX                                                                |                                     |
| PN W09931132-AI.                                                  |                                     |
| XX                                                                |                                     |
| PD 24-JUN-1999.                                                   |                                     |
| XX                                                                |                                     |
| PF 14-DEC-1998:                                                   | 98MO-AU01031.                       |
| XX                                                                |                                     |
| PR 12-DEC-1997:                                                   | 97GB-0026398.                       |
| XX                                                                |                                     |
| PA (ISIS-) ISIS INNOVATION LTD.                                   |                                     |
| PA (UYOU ) UNIV QUEENSLAND.                                       |                                     |
| XX                                                                |                                     |
| PI Jennings MP, Moxon ER, Peak IRA;                               |                                     |
| XX                                                                |                                     |
| DR WPI, 1999-418754/35.                                           |                                     |
| XX                                                                |                                     |
| PT N-PSDB; AAX85792.                                              |                                     |
| XX                                                                |                                     |
| PT Neisseria meningitidis surface proteins useful for treating N. |                                     |
| PT meningitidis infections                                        |                                     |

PS Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA:

Query Match 100.0%; Score 3019; DB 20; Length 594;  
Best Local Similarity 100.0%; Pred. No. 5.1e-173;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKKIRIINWSALNMAVAVSELTRNHTKRASATVATVATLLEFATVQASTTDDDDLYLE 60  
DB 1 mkiyriinwsalnawavseltrnhktrasatvatavlatllfatvgastdddddlyle 60  
QY 61 PVQRTAVVLSFSDKEGEGKEVTEDSNMGVYFDKKGVLTACTITLKAGDNLIKQNTNE 120  
DB 61 pvgrtavvlsfsgdgegkegtevedsnmgvyfdkkgvltactitlkagdnlikqntne 120  
QY 121 NFNASSFYSLSKKDLTDLTSVGTETKLSFANSKNVITSDTGKLNFAKTAETNGDTTVH 180  
DB 121 nfnassfyslskdltdltsvgteklfsansknvitsdtkglnfaktaetngdtlvh 180  
QY 181 LNGIGSTLTLTLNLTGATTNTNDVTDDEKKRAASVSKVDVLNAGNNIKVKGPTASDNV 240  
DB 181 lngigstltdltnltgattntndvtddekkraasvskvdvlnagnnikvgkptasdnv 240  
QY 241 DFRVRYDYVEFSADPTKTTTVAVESKDKGKREVKIGAKTSYIKKDGKLVTKGDKGEND 300  
DB 241 dfrvrydyvefsadptktttvaveskdkgkrevkigaktsyikkdgkylvtkgdkgend 300  
QY 301 SSTDGEGLVTAKEVIDAVNKAQWMTTANGOTGOADKEFTVNSGTVTFASGKGTTA 360  
DB 301 sstdgeglvtakevidavnkaqwmmttanganotgoadkeftvnsctvtfasgkgtta 360  
QY 361 TVSKDQGNITVAVDYNVGDALNVQNLNSGWNLDLSKAVAGSSGKVISGNSPSPKGMDE 420  
DB 361 tvskdognitvavdvnvgdnlvnqnlngsgwnldlskavagssgkvisgnspskgmde 420  
QY 421 TVNINAGNNIETTRNGKNIDIAFSMTPOFSSVSLGAGADAPTLVSDDGALNVGSKDANK 480  
DB 421 tvninagnniettrngknidiafsmtpofssvslgagadaptlvsddgalnvsgkdank 480  
QY 481 PVRINNVAVGVEGVTNVAAOLKGYAONLNHIDNVGNAARAGIQAITAGLYOAYLPG 540  
DB 481 pvrlnnvavgvegtvnvaqlkgyaonlnhldnvvgnaaragiqaitaglyoaylpg 540  
QY 541 KSMMAIGGCTYRGEAGYAIGSYISDGMNIIKTASGNSRCHFGASASVGYQW 594  
DB 541 ksmmaiggctyrgeagyalgysisdgmgniikgtasgnsrghfgasasvgyqw 594

RESULT 2  
ID AAY57044 standard; Protein: 594 AA.

XX AAY57044;

XX 21-FEB-2000 (first entry)

XX BASB029 amino acid sequence from *N. meningitidis* strain ATCC13090.

XX BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;  
KM infection; treatment; prevent; antibacterial drug.

OS *Neisseria meningitidis*.

XX Key Location/Qualifiers

FT Misc-difference 104 /note= "Encoded by AATC"

XX WO958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI: 2000-053103/04.

XX N-PSDB; AA239864.

PT New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
PS Claim 4; Fig 2; 74pp; English.

CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and  
CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with *Neisseria*  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes.  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.

XX Sequence 594 AA:

Query Match 100.0%; Score 3019; DB 21; Length 594;  
Best Local Similarity 100.0%; Pred. No. 5.1e-173;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKKIRIINWSALNMAVAVSELTRNHTKRASATVATVATLLEFATVQASTTDDDDLYLE 60  
DB 1 mkiyriinwsalnawavseltrnhktrasatvatavlatllfatvgastdddddlyle 60  
QY 61 PVQRTAVVLSFSDKEGEGKEVTEDSNMGVYFDKKGVLTACTITLKAGDNLIKQNTNE 120  
DB 61 pvgrtavvlsfsgdgegkegtevedsnmgvyfdkkgvltactitlkagdnlikqntne 120  
QY 121 NFNASSFYSLSKKDLTDLTSVGTETKLSFANSKNVITSDTGKLNFAKTAETNGDTTVH 180  
DB 121 nfnassfyslskdltdltsvgteklfsansknvitsdtkglnfaktaetngdtlvh 180  
QY 181 LNGIGSTLTLTLNLTGATTNTNDVTDDEKKRAASVSKVDVLNAGNNIKVKGPTASDNV 240  
DB 181 lngigstltdltnltgattntndvtddekkraasvskvdvlnagnnikvgkptasdnv 240  
QY 241 DFRVRYDYVEFSADPTKTTTVAVESKDKGKREVKIGAKTSYIKKDGKLVTKGDKGEND 300  
DB 241 dfrvrydyvefsadptktttvaveskdkgkrevkigaktsyikkdgkylvtkgdkgend 300

```
OY 301 SSTDKGEGLYTAKEVIDAVNKAQKRMKTTTANGOTGADKFEFVTSNTVFASGKGT 360
DB 301 SSTDKGEGLYTAKEVIDAVNKAQKRMKTTTANGOTGADKFEFVTSNTVFASGKGT 360
OY 361 TVSKDOGNITVWVDVNGDALNVNOLONGSNWMLDSKAVAGSSGKYISGNVSPSKGKMD 420
DB 361 TVSKDOGNITVWVDVNGDALNVNOLONGSNWMLDSKAVAGSSGKYISGNVSPSKGKMD 420
OY 421 TVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSKDANK 480
DB 421 TVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSKDANK 480
OY 481 PVKITVAVPGVKEGVDYTNVAQLKGVANLNHNDVNGNARAGIAQAIATAGLVQATLP 540
DB 481 PVKITVAVPGVKEGVDYTNVAQLKGVANLNHNDVNGNARAGIAQAIATAGLVQATLP 540
OY 541 KSMMAIGGTGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 594
DB 541 KSMMAIGGTGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 594

RESULT 3
AAU06174
ID AAU06174 standard; Protein: 594 AA.
XX
AC AAU06174;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.
XX
KM Surface antigen Nhma; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key
FT Location/Qualifiers
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..126
FT /label= V2
FT /note= "Variable region 2"
FT 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT 191..212
FT /label= V3
FT /note= "Variable region 3"
FT 213..231
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FT 232..238
FT /label= V4
FT /note= "Variable region 4"
FT 239..594
FT /label= C5
FT /note= "Conserved region 5"
XX
XX WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
```

```
PA (UYU ) UNIV QUEENSLAND.
PI Peak IRA, Jennings MP;
XX
DR MPI: 2001-488774/53.
XX
PS N-PSDB: AAS09164.
XX
PT New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9: Fig 1: 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA;
```

Query Match 100.0%; Score 3019; DB 22; Length 594;  
Best Local Similarity 100.0%; Pred. No. 5,1e-173;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNKIYRIINSAIINAWVAASELFRNHTKRASAVATVATLLEAFYQASTDDDDLYLE 60
DB 1 MNKIYRIINSAIINAWVAASELFRNHTKRASAVATVATLLEAFYQASTDDDDLYLE 60
OY 61 PVORTAVLISFRSDKEGTGKEVTEDSNMGVFEDKKGVLTAGTITLKAGDNLIKONTNE 120
DB 61 PVORTAVLISFRSDKEGTGKEVTEDSNMGVFEDKKGVLTAGTITLKAGDNLIKONTNE 120
OY 121 NPNASFTTSLKRDLDLDSVGTBKLSFSANSKNVITSPFKGINPAKKAETNGDTTVH 180
DB 121 NPNASFTTSLKRDLDLDSVGTBKLSFSANSKNVITSPFKGINPAKKAETNGDTTVH 180
OY 121 ntassfitylkkdltcltvsgeklisfsansknvltstcltqjnfaktaetngdtlvh 180
DB 121 ntassfitylkkdltcltvsgeklisfsansknvltstcltqjnfaktaetngdtlvh 180
OY 181 LNCIGSTLPTLNTGATTTWTDNDVTDDEKRAASVKDVLNNGWNTKGVKPGTTASDNV 240
DB 181 LNCIGSTLPTLNTGATTTWTDNDVTDDEKRAASVKDVLNNGWNTKGVKPGTTASDNV 240
OY 241 DFVRYTDFEFLSADRTKTTTVNVESSKDNKRETEKIGAKTSVIREKDKLVTEGKEND 300
DB 241 DFVRYTDFEFLSADRTKTTTVNVESSKDNKRETEKIGAKTSVIREKDKLVTEGKEND 300
OY 301 SSTDKGEGLYTAKEVIDAVNKAQKRMKTTTANGOTGADKFEFVTSNTVFASGKGT 360
DB 301 SSTDKGEGLYTAKEVIDAVNKAQKRMKTTTANGOTGADKFEFVTSNTVFASGKGT 360
OY 361 TVSKDOGNITVWVDVNGDALNVNOLONGSNWMLDSKAVAGSSGKYISGNVSPSKGKMD 420
DB 361 TVSKDOGNITVWVDVNGDALNVNOLONGSNWMLDSKAVAGSSGKYISGNVSPSKGKMD 420
OY 421 TVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSKDANK 480
DB 421 TVNINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSKDANK 480
OY 481 PVKITVAVPGVKEGVDYTNVAQLKGVANLNHNDVNGNARAGIAQAIATAGLVQATLP 540
DB 481 PVKITVAVPGVKEGVDYTNVAQLKGVANLNHNDVNGNARAGIAQAIATAGLVQATLP 540
OY 541 KSMMAIGGTGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 594
DB 541 KSMMAIGGTGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 594
```

Db 541 ksmmaigdytgeagyaigysisdggnwiklgtasgnsrghfgasasvgyw 594

RESULT 4  
ID AAY23739 standard; Protein; 594 AA.  
XX AAY23739;  
AC AAY23739;  
DF 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KM Surface protein; surface glycoprotein; infection; vaccine;  
KM immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
DR N-PSDB; AAX85791.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 95-97; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 594 AA;

Query Match 95.2%; Score 2874; DB 20; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.5e-164;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

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DB 121 ntndassfyslkkdljdltsveteklsfnganknitsdtkglnfaketaetngdptvh 180  
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DB 181 lngisstltdpltnngattnvdnvddekkrrasvxdvlnagwnlkygvkpgtllasdmv 240  
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DB 241 dfvrytvefplsadtktttvnveskdnkgttevkigaktvliekdglvtgkdgend 300  
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OY 361 TVSKDDGQNTVMYDVNVSDALNVLNOLNSGWNLDLSKAVAGSSGKVIISGNVSPSKGKME 420  
DB 361 tvskddgqntvmydvnvsdalnvlnlolnsgwnldlskavagssgkvissnvspskgkme 420  
OY 421 TVNINAGNNIEITRNGKNIDATFMTPOFSSVSLGAGADAPRLSVDDGALNVGSKDANK 480  
DB 421 tvninagnnieitrngknidatfsmtpofssvslgagadaprlsvddgalnvsgkdank 480  
OY 481 PVRITNVAPGVKEGVTNVAOLKGVAONLNHIDNVDGARAGIAOATATAGTVOATYLP 540  
DB 481 pvriltnvapgvkegvtvnvaolkgyaonlnhldnvdgaraiaoaatatagtlvagaylp 540  
OY 541 KSMMAIGGTYRGEAGYAIGYSSISDGNMIRIKGTASGNSRGHFGASASVGYQW 594  
DB 541 ksmmaigdytgeagyaigysisdggnwiklgtasgnsrghfgasasvgyw 594

RESULT 5  
ID AAU06179 standard; Protein; 594 AA.  
XX AAU06179;  
AC AAU06179;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis BZ198 surface antigen Nhma polypeptide sequence.  
XX  
KM Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain BZ198.  
XX  
FH Key  
FH Location/Qualifiers  
FT 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..104  
FT /label= V1  
FT /note= "Variable region 1"  
FT 105..116  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 117..126  
FT /label= V2  
FT /note= "Variable region 2"  
FT 127..190  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 191..212  
FT /label= V3  
FT /note= "Variable region 3"  
FT 213..231  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 232..238  
FT /label= V4  
FT /note= "Variable region 4"  
FT 239..594  
FT /label= C5  
FT /note= "Conserved region 5"  
XX  
XX WO200155182-A1.  
XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-AU00069.

PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
P1 Peak IRA, Jennings MP;  
XX  
DR WPI: 2001-488774/53.  
DR N-PSDB: AAS09169.  
XX  
PT New Nhma surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp: English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhma  
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhma  
CC from N. meningitidis strain 82198 is 1 of 10 Nhma polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 594 AA:  
  
Query Match 95.2%; Score 2874; DB 22; Length 594;  
Best Local Similarity 95.6%; Pred. No. 2.5e-164;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;  
  
OY 1 MKKIRIIMNSALNMAVAVSELIRNHTKRASATVATFATVQASTDDDDLYLE 60  
DB 1 mkkirylimnsalnmaavselirnhtrkrasatvatatllfatvganaddddllyle 60  
OY 61 PVQRTAVVLSFSDKEGTEKEVEDSNMGVYFDKKGVLTAGTITLKADNLIKONTNE 120  
DB 61 pvrtravvlsfsdkegtekegedsnmavfydekrvylkagaaitlkagdnlikqnthe 120  
OY 121 NTNASSFTYSLKKDLTDLTSLVGTETKLSFSANSKNVITSDFKGLNFAKKTAAFTNGDTTVAH 180  
DB 121 ntndssftyslkkdltdltsveteklsfngankvnitsdtkglntfaketaingdptvh 180  
OY 181 LMGISTLTDLTLNLTGATTNTNDVNTDEKRRASVSKVDVLAAGNNIKVKGTTASDNV 240  
DB 181 lngistltdltnlgtatnvnndvntddekrkrasvskvdlagwnlkgvkgpttasdnv 240  
OY 241 DEVRTYDVEFLTADTKTTTNNVESKDNKRTEVRKIGAKTSYIKEDGGLVYKDKGEND 300  
DB 241 divrtydvefltsadtktttnvveskdnkrtevrkigaktsyikekgylvgkykdeng 300  
OY 301 SSTDKGEGLVTAKEVYIDAVNKAQWTKTTTANGQTQADKFETVTSGTIVTFASGKTGA 360  
DB 301 sstdegeglvtakevldavnkagwtktttangqtsqadkfetvtsqtnvtfassgqta 360  
OY 361 TYSKDDGCTITMYDVNVGDALNVNOLNSGNLDSKAVAGSSGKYSINNVSPSKGME 420  
DB 361 tyskddgctitmydvnvgdalnvnglqnswnldskavagssgkysinvspskyme 420  
OY 421 TVNINAGNNIETTRNGKNIDIASMTPOSSVSLGAGADAPLTVDDEGALNVGSDANK 480  
DB 421 tvninagnniettrngknidiasmtpossvslgagadapltvsddegainvgsdtk 480  
OY 481 PVRITNVAQVKEGDTNVAQLKGAQNLNHIIDNVGNARAGIAQALITAGLVQAYLPG 540  
DB 481 pvriltvnaqvkegdtnvaqlkgaqnlhnridnvgnaragialagltvqaylpg 540

OY 541 KSMMAIGGCTYRGAGYAIGYSSISDGNWIIKTPASNGSRGHFGASASVGYQW 594  
DB 541 ksmmaigdctyrgeayiaigyssisdgwniiktpasngsrghfgasasvgyqw 594  
  
RESULT 6  
AAV23742  
ID AAV23742 standard; Protein; 598 AA.  
XX  
AC AAV23742;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN W09931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98MO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI: 1999-418754/35.  
DR N-PSDB: AAX85794.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 108-110; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 598 AA:  
  
Query Match 94.6%; Score 2855; DB 20; Length 598;  
Best Local Similarity 94.6%; Pred. No. 3.4e-163;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
  
OY 1 MKKIRIIMNSALNMAVAVSELIRNHTKRASATVATFATVQASTDDDDLYLE 60  
DB 1 mkkirylimnsalnmaavselirnhtrkrasatvatatllfatvganaddddllyle 60  
OY 61 PVQRTAVVLSFSDKEGTEKEVEDSNMGVYFDKKGVLTAGTITLKADNLIKONTNE 120  
DB 61 pvrtravvlsfsdkegtekegedsnmavfydekrvylkagaaitlkagdnlikqnthe 120  
OY 121 NTNASSFTYSLKKDLTDLTSLVGTETKLSFSANSKNVITSDFKGLNFAKKTAAFTNGD 176  
DB 121 ntndssftyslkkdltdltsveteklsfngankvnitsdtkglntfaketaingd 180  
OY 177 TVNINAGNNIETTRNGKNIDIASMTPOSSVSLGAGADAPLTVDDEGALNVGSDANK 236  
DB 177 tvninagnniettrngknidiasmtpossvslgagadapltvsddegainvgsdtk 240

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OY 237 SDNVDFVRYDVEFLSADTKTTTVNESKDNKRETEVKIGAKTSVIKERDGLVTKDK 296
PR |||||||
DB 241 sdnvdfvrydveflsadtktttvneskdnkrektevkigaktsvikekdglvtgkx 300
OY 297 GENDSTDKGEGLVTAKEVIDAVNKAQWKRKTTTANGOTGADKEFTVTSNTNTFASGK 356
PR |||||||
DB 301 dengsstdegeglvtakevidavnkagwrmtttangqtgqadkfetvtsgtklvfafasn 360
OY 357 GTTATVSKDOGNITVWVDVNGDALNVNOLONGSMNLSKAVGSSGKXVSGVSPSKG 416
PR |||||||
DB 361 gttatvskdognitlvvngdavnngalnvnglqnsqwmldskavagssgkvxsgvspskg 420
OY 417 KMDETVINAGNIEITRNKNIDIAATSMTPQESSVSLGAGADAPTLSDVDEGALNVGSK 476
PR |||||||
DB 421 kmdeitvinagnieitrnknidiatstmpqfsvslgagadaptlsvddegalnvgsk 480
OY 477 DANKPVRITNAPGVKGDVTVNAOLKGVANLNHNDVNGNARAGIAQAIATAGLVQA 536
PR |||||||
DB 481 dankpvrtnvapvkgdvtvnvaqlkvagvnlhndvngnaraqiaqaiataglaq 540
OY 537 YLPQSKMMAIGGCTYRGEAGYATGYSISDQGNMIIKTGASGNSRGHFGASASVGYQM 594
PR |||||||
DB 541 ylpqskmmaiggytgyeagyaigysistdgnvwlkgtasgnsrghfgasasvgyqm 598

RESULT 7
AAU06177
ID AAU06177 standard; Protein; 598 AA.
XX
AC AAU06177;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H15 surface antigen Nhma polypeptide sequence.
XX
KM Surface antigen Nhma; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H15.
XX
XX Location/Qualifiers
PH 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..130
FT /label= V2
FT /note= "Variable region 2"
FT 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT 195..216
FT /label= V3
FT /note= "Variable region 3"
FT 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT 236..242
FT /label= V4
FT /note= "Variable region 4"
FT 243..598
FT /label= C5
FT /note= "Conserved region 5"
XX
XX NO200155182-A1.
XX
XX 02-AUG-2001.

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PF 25-JAN-2001; 2001MO-AU00069.
XX
XX 25-JAN-2000; 2000US-017917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX
XX DR N-PSDB; AAS09167.
XX
XX New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX Sequence 598 AA;
SQ
Query Match 94.6%; Score 2855; DB 22; Length 598;
Best Local Similarly 94.6%; Pred. No. 3,4e-163;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;
OY 1 MNKTYRIINWALNAAVAVSELNRHNRASATVATVLAATLPAVQAOSTDDDDLYLE 60
DB 1 mnktyrilwmsalawavselnrhnrkrasatvatvlatlpaavqatdddddlyle 60
OY 61 PVORTAVLSRSDKEGTEGEKVEDSNMGVYFDKGLVAGTTTLKAGDNLKIKONTNE 120
DB 61 pvortavlrsrdsdkegtegekedsnmgyfydkglvagtlttlkagdnllkikontne 120
OY 121 NTNA-----SSEFTYSLKKDLDDLRVSGTEKLSFSANSKNVNTSPTKGLNFAKKTAEFNGD 176
DB 121 ntntndssftyslkkdldlrvtsekteklsfgangknvntsdtkglnfaketaingnd 180
OY 177 TTVHLNGIGSTLDTLNTGATVTWNTDNDVDEKKRAASVYKDVNLNGWNTKGVKPGTTA 236
DB 177 ttvhlngigstldtlnltgattvntdndvdekkraasvkdvnlngwnvtnkgykpgtta 240
OY 237 SDNVDFVRYDVEFLSADTKTTTVNESKDNKRETEVKIGAKTSVIKERDGLVTKDK 296
DB 237 sdnvdfvrydveflsadtktttvneskdnkrektevkigaktsvikekdglvtgkx 300
OY 241 sdnvdfvrydveflsadtktttvneskdnkrektevkigaktsvikekdglvtgkx 300
OY 297 GENDSTDKGEGLVTAKEVIDAVNKAQWKRKTTTANGOTGADKEFTVTSNTNTFASGK 356
DB 297 gendstdkgeglvtakevidavnkagwrmtttangqtgqadkfetvtsgtklvfafasn 360
OY 357 GTTATVSKDOGNITVWVDVNGDALNVNOLONGSMNLSKAVGSSGKXVSGVSPSKG 416
DB 357 gttatvskdognitlvvngdavnngalnvnglqnsqwmldskavagssgkvxsgvspskg 420
OY 417 KMDETVINAGNIEITRNKNIDIAATSMTPQESSVSLGAGADAPTLSDVDEGALNVGSK 476
DB 417 kmdeitvinagnieitrnknidiatstmpqfsvslgagadaptlsvddegalnvgsk 480
OY 477 DANKPVRITNAPGVKGDVTVNAOLKGVANLNHNDVNGNARAGIAQAIATAGLVQA 536
DB 477 dankpvrtnvapvkgdvtvnvaqlkvagvnlhndvngnaraqiaqaiataglaq 540

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Db 481 dankpvrilnvapgykegdtvnaqllkyvaqnlmrldhvdgnaraglaqataglaqa 540

QY 537 YLPGRSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594

Db 541 ylpgrsmma1gg9gtyrgeagyaigysisdgnwv1kgtasgnsrghfgasasvgyqw 598

RESULT 8  
AA023738  
ID AA023738 standard; Protein: 598 AA.

XX  
AC AA023738;  
XX  
DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.  
XX  
XX Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
XX  
XX PN W09931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PE 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX (UYOU) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI: 1999-418754/35.  
DR N-PSDB: AAX85790.  
XX  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX  
PS Claim 1: Page 91-93; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
XX meningitidis which is approximately 62 kDa. The N. meningitidis  
XX surface glycoproteins, nucleic acids, the primers and optionally  
XX a thermostable polymerase, or antibodies are useful in a kit for  
XX the detection or diagnosis of N. meningitidis infection in humans.  
XX The N. meningitidis surface glycoproteins can also be used to  
XX prevent or treat N. meningitidis infection in humans, especially  
XX in the form of vaccines. The proteins and antibodies can also  
XX be used to identify immunoreactive peptides.  
XX  
SQ Sequence 598 AA:

Query Match 94.5%; Score 2852; DB 20; Length 598;  
Best Local Similarity 94.6%; Pred. No. 5, 2e-163;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNIIYRIWNSALNMAWVAVELRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60

Db 1 mniiyriwnsalnavvvelcrnhkrasatvataatlifavqanaddddllyle 60

QY 61 PVORTAVLSPRSDEKTEGEVTEDESNMGVYFDKKGVLTAAGTITLKAGDNLIKONTNE 120

Db 61 pvgtravlsfrsdekgtgkedsnmgvyfdkkrvltagatitlkagdnlikqntne 120

QY 121 NTNA-----SFTYSLKKDLTLTSGTEKLSFSANSKVNITSPTDKGLNFAKKTAEETNGD 176

Db 121 ntentndsfstyslkkdltltsveteklsfgangknitsdtkglnfaketaetngd 180

QY 177 TTVHLNGIGSTLDTLNTGATNTVTDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236

Db 181 ptvhlngigstltdlntgatcnvndvtddekkraasvkdvlnaqwnikgvkpgtta 240

QY 237 SDNVDVRYRTDYIEFLSADPKRTTVAWNSKDNKRFEVKGATSVYKEDGKLYTGKDK 236

Db 241 sdndvryrtdyieflsadtktttvawnskdngkrfevkgatksvylkedgklytgkdk 300

QY 297 GENDSSTDKGEGLVTAKEVIDAVNKKAGMRKTTTANGOTGAOKFEVTSCTVNTFASGK 356

Db 301 genssstdegeglvtakevidavnkagwrmktltangqgqadkfevtsgtvtflasgn 360

QY 357 GTTATVSKDDGNIITWYDVNVDALNVNOLQNSGMWIDSKAAVAGSSGKVISGNVSPSK 416

Db 361 gttatvskddggnitvdyvndaldnvnlqnsqmwidskavagsgkvisgnvpsk 420

QY 417 KMDETVYNINAGNIEITRNKNIDTATSWTPQSSVSLGADAPLISVDEGALNVGSK 476

Db 421 kmdevtninagnietrknidiatstmpqfssvslgagadapltsvddegalnvgsk 480

QY 477 DANKPVRITNVAPGVKEGDTVNAOLKGVANLNNHTDNTVGNARAGITAOAIVTAGLVQA 536

Db 481 dankpvrilnvapgykegdtvnaqllkyvaqnlmrldhvdgnaraglaqataglaqa 540

QY 537 YLPGRSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594

Db 541 ylpgrsmma1gg9gtyrgeagyaigysisdgnwv1kgtasgnsrghfgasasvgyqw 598

RESULT 9  
AAU06178  
ID AAU06178 standard; Protein: 598 AA.

XX  
XX AAU06178;  
XX  
XX 24-OCT-2001 (first entry)

XX N. meningitidis B210 surface antigen Noha polypeptide sequence.  
XX  
XX DE N. meningitidis B210 surface antigen Noha polypeptide sequence.  
XX  
XX KM Surface antigen Noha; meningococcal disease; meningitis vaccine.  
XX  
XX OS Neisseria meningitidis strain B210.  
XX  
XX FH Key  
XX Location/Qualifiers  
XX  
XX FT 1..50  
XX /label= C1  
XX /note= "Conserved region 1"  
XX FT 51..104  
XX /label= V1  
XX /note= "Variable region 1"  
XX FT 105..116  
XX /label= C2  
XX /note= "Conserved region 2"  
XX FT 117..130  
XX /label= V2  
XX /note= "Variable region 2"  
XX FT 131..194  
XX /label= C3  
XX /note= "Conserved region 3"  
XX FT 195..216  
XX /label= V3  
XX /note= "Variable region 3"  
XX FT 217..235  
XX /label= C4  
XX /note= "Conserved region 4"  
XX FT 236..242  
XX /label= V4  
XX /note= "Variable region 4"  
XX FT 243..598  
XX /label= C5  
XX /note= "Conserved region 5"  
XX  
XX MO200155182-A1.

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PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX PA
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX DR
XX N-PSDB; AAS09168.
XX
XX New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain B210 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX Sequence 598 AA:
SQ
Query Match 94.5%; Score 2852; DB 22; Length 598;
Best Local Similarity 94.6%; Pred. No. 5,2e-163;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

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QY 477 DANKPVRITNVAPGVKEGDDVTNVAQLKGYAQNINNHIDNVGNARAGIAQAATAGLYOA 536
DB 481 dankepriltnvapgvykegdtvtnvaqlkgyaqpnlmrldvngnareglagataglaqa 540
QY 537 YLPGKSMAAIGGCTYRGEAGTAIGTSSISDGGNMIITKGTASGNSRGHRCASASVGYOW 594
DB 541 ylpgksmaaiaggctyrgeagtaigyssisdgtgnwvikgtsasgrhfgtsasvgyow 598

RESULT 10
AAV57045
ID AAV57045 standard; Protein; 591 AA.
XX
XX AAV57045;
AC
XX
XX 21-FEB-2000 (first entry)
DT
XX
XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
XX BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
XX infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
XX
XX Key Location/Qualifiers
FH Misc-difference 90
FT Misc-difference 92 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by AAG"
FT Misc-difference 389 /note= "Encoded by CGT"
XX
XX WO9598683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI: 2000-053103/04.
XX DR
XX N-PSDB; AAZ39865.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal -
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Nisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-AZ39865) and
CC polypeptide sequences (AAV57044-AV57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the

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CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BAs029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.

XX Sequence 591 AA:

Query Match 92.2%; Score 2783.5; DB 21; Length 591;  
 Best Local Similarity 93.3%; Pred. No. 6, 5e-159;  
 Matches 558; Conservative 9; Mismatches 20; Indels 11; Gaps 4;

QY 1 MKKIRITNNSALNMAVAVSELTRNHTKRASATVATVATLTLFAVVOASTD---DDDL 57  
 DB 1 mkkiriliwnsalnawavseltrnhtkrasatvkaavlalilfatvgasanneegeeel 60  
 QY 58 YLEPQRTAVVLSFRDEKGTGEKE-VTEDSNMGVYFEDKGVLTACTITLTKAGDNLKIKO 116  
 DB 61 YLDPQRTAVVLSFRDEKGTGEKEVEDSMNAVYFDEKGVLTARELTAKAGDNLIKQ 120  
 QY 117 NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNYITSDTKGLNFAKTAETNGD 176  
 DB 121 -----ngsnfyslkkdltdltsvteklsfsangknkntsdctglnfaketaetngd 174  
 QY 177 TTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVSKVDYLNAGNINIKVPRGTTA 236  
 DB 175 tlvhngisltldtltnlgtatnvdndvtddekkraasvskvdlnagwnikvprgta 234  
 QY 237 SDNVDFVRTYDVEELSDTKTTTVNESKDNKREVEKIGATSVIKERDKLVTKGDK 296  
 DB 235 sdnvdfvrtydveelisdtktttvneskdngkrtlevkigatsvikekdglvtgkdx 294  
 QY 297 GENDSSTDKEGLVTAKEYIDAVNKAQMRKTTTANGOTGOADKFEVTYSGTNTVTFASGK 356  
 DB 295 gendstdegeglvtakeyidavnkagvrmkttaangtqgqadkfetysgntvtfasgk 354  
 QY 357 GTTATVSKDDGNTITWYVNVGDALNVNQLNSGNMDSKAVAGSSGKAVISGNVSPSKG 416  
 DB 355 gtatvskddgntitwvnyvgdalinvgqlnsgwnldskavagssgkvlsngvpskx 414  
 QY 417 KMDETVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPLTVSDEBALVWGSK 476  
 DB 415 kmdeetvinagnniettrngknidatmtptqfssvslgagadapltvsygd-almvsgk 473  
 QY 477 DANRPVRIINVAAPVKEGCVTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGLVQA 536  
 DB 474 danrpvritnvapvkegcvtnvaqlkgyaqnlmridvndgnaraglaqalaglvqa 533  
 QY 537 YLPKSMMAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 594  
 DB 534 ylpksmmaigggtyrgeagvtaigyssisdgnmwlikgtasgnsrghfgasasvgyqw 591

RESULT 11  
 AAY23743  
 ID AAY23743 standard; Protein: 599 AA.

XX AAY23743;  
 AC 08-SEP-1999 (first entry)  
 DT  
 XX A surface protein of Neisseria meningitidis.  
 DE  
 XX Surface protein: surface glycoprotein; Infection: vaccine;  
 KM immunoreactive peptide.  
 XX Neisseria meningitidis.  
 OS  
 XX WO9931132-A1.  
 PN  
 XX

PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYOU) UNIT QUEENSLAND.  
 XX  
 PI Jennings MP, Moxon ER, Peak IRA;  
 PI  
 DR WPI: 1999-418754/35.  
 DR N-PSDB: AAX85795.  
 XX  
 PT Neisseria meningitidis surface proteins useful for treating N.  
 PT meningitidis infections

Claim 1; Page 114-115; 132pp; English.

The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

Sequence 599 AA:

Query Match 91.5%; Score 2762.5; DB 20; Length 599;  
 Best Local Similarity 91.7%; Pred. No. 1, 2e-157;  
 Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MKKIRITNNSALNMAVAVSELTRNHTKRASATVATVATLTLFAVVOASTD---DDDL 59  
 DB 1 mkkiriliwnsalnawavseltrnhtkrasatvkaavlalilfatvganatedegeeel 60  
 QY 60 EPVQRTAVVLSFRDEKGTGEKEVEEDSMNAVYFDEKGVLTACTITLTKAGDNLIKQ 116  
 DB 61 epvqrtavvlsfrdekgtegeevtedsmnavyfdkrgvltactitltkagdnlikqntn 120  
 QY 117 -NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNYITSDTKGLNFAKTAETNG 175  
 DB 121 knlentndssfyslkkdltdltsvteklsfsangknkntsdctglnfaketaetng 180  
 QY 176 DTTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVSKVDYLNAGNINIKVPRGTT 235  
 DB 181 dttvhngisltldtltnlgtatnvdndvtddekkraasvskvdlnagwnikvprgpt 240  
 QY 236 ASDNVDFVRTYDVEELSDTKTTTVNESKDNKREVEKIGATSVIKERDKLVTKGD 295  
 DB 241 asdnvdfvrtydveelisdtktttvneskdngkrtlevkigatsvikekdglvtgkx 300  
 QY 296 KGENDSSTDKEGLVTAKEYIDAVNKAQMRKTTTANGOTGOADKFEVTYSGTNTVTFASG 355  
 DB 301 kgensstdegeglvtakeyidavnkagvrmkttaangtqgqadkfetysgntvtfasg 360  
 QY 356 KGTATVSKDDGNTITWYVNVGDALNVNQLNSGNMDSKAVAGSSGKAVISGNVSPSK 415  
 DB 361 kgatavskddgntitwvnyvgdalinvgqlnsgwnldskavagssgkvlsngvpsk 420  
 QY 416 GKMDETVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPLTVSDEBALVWGS 475  
 DB 421 gkmdetvinagnniettrngknidatmtptqfssvslgagadapltvsdkgalnvgs 480  
 QY 476 KDANKPVRIINVAAPVKEGCVTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGLVQ 535  
 DB 481 kdankpvritnvapvkegcvtnvaqlkgyaqnlmridvndgnaraglaqalaglvq 540  
 QY 536 AYLPKSMMAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 594

|||||  
Db 541 aylpgkmma19gtyrgaagya1gys1sdggnwlkgtasgnsrgnftgasasvgyqw 599  
RESULT 12  
AAU06176  
ID AAU06176 standard; Protein: 599 AA.  
XX  
AC AAU06176;  
XX  
DE 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis H38 surface antigen Noha polypeptide sequence.  
XX  
KW Surface antigen Noha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain H38.  
XX  
FH Key  
FT Location/Qualifiers  
FT 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..105  
FT /label= V1  
FT /note= "Variable region 1"  
FT 106..117  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 118..131  
FT /label= V2  
FT /note= "Variable region 2"  
FT 132..195  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 196..217  
FT /label= V3  
FT /note= "Variable region 3"  
FT 218..236  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 237..243  
FT /label= V4  
FT /note= "Variable region 4"  
FT 244..599  
FT /label= C5  
FT /note= "Conserved region 5"  
XX  
PN W0200155182-A1.  
XX  
PD 02-AUG-2001.  
XX  
PE 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 20000US-0177917.  
XX  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
DR WPI: 2001-488774/53.  
DR N-PSDB; AAS09166.  
XX  
PT New Noha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 91pp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Noha  
CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Noha  
CC from N. meningitidis strain H38 is 1 of 10 Noha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 599 AA:  
Query Match 91.5%; Score 2762.5; DB 22; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.2e-157;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
OY 1 MNKIRIIMNSALNANWAVSELTNRNHRKASATVATVATLLEFATVASTTD--DDLLYL 59  
DB 1 mkiyriilmsalnwavseltrnhktrasatvtavlatillfatqanadedeeel 60  
OY 60 EPVORTAVVLSRSDKEGTEGEKVEDSNMGVYRDKKGVLRAGCTTTKAGDNLKTKO--- 116  
DB 61 epvrsalvlgimdkegeneneslgnlgsylgdnhtlmgatvllkagdnlkikqntn 120  
OY 117 -NTNENTNASSFTYSILKRDLDLDTSVGTEKLSFNSANKVNTSPDKLNFPAKKTAEING 175  
DB 121 knntentndstfysikkldldlsveteklsfngnqkvntstcklnfkakeagang 180  
OY 176 DTTVHLNGIGSTLTDPLNTGATVNTDNDVTDDEKKRAASVKDVLNAGWNIKVKPGCTT 235  
DB 181 dtvhlnglgslltdlcllntgatlntvndvldckkkaasvkdvlngwmlkvgkpgct 240  
OY 226 ASDNDFRTYDTEVFEISADPTTNTVNESKONGKRETVKIGAKSVYKKEKGRKVTGKD 295  
DB 241 asdnvdfvtydtevelisadcltctvnveskongkrtevkigaksvikexdgkrlvtgk 300  
OY 296 KGENDSTDKGEGLVTAREVIDAVNKAQRMTTANGOTGQADKFEVTSGTNTTTFASG 355  
DB 301 kgenssstdegeglvtakevidavnkagvrmtktlangqgqadkfervtsgntvtfasg 360  
OY 356 KGTATVSKDDOGNITVYDVNVGDALNVNOLNSGWLDSKAVAGSSGKVIISGNVSPSK 415  
DB 361 kgtatvskddogntlvtydvngdalnvnglqnsqwnldskavagssgkvlsngvpsk 420  
OY 416 GKMDETVINAGNNTETRRNGKNIDIASMPQESSVSLGAGADAPTSVYDEGLANGS 475  
DB 421 gkmdetvlnagnnlctlrngknidlatsmpqissvslgagadapltsvddkglainvgs 480  
OY 476 KDANKPVRITVYAPGVKEDVTNNVQLKGVAQNLNHIDNDVGNARAGIAQAIATAGLVQ 535  
DB 481 kdankpvriltvnyapgvkgedvtnnvqllkgvagnlnrldndvgnaragiataglvq 540  
OY 536 AYLPGKSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 594  
DB 541 aylpgkmma19gtyrgaagya1gys1sdggnwlkgtasgnsrgnftgasasvgyqw 599  
RESULT 13  
AAV27202  
ID AAV27202 standard; Protein: 591 AA.  
XX  
AC AAV27202;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of N. meningitidis protein ORF40-1.  
XX  
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;  
XX bacterial infection; treatment.  
OS Neisseria meningitidis.  
XX

PN W0936544-A2.  
XX  
PD 22-JUL-1999.  
XX  
PF 14-JAN-1999; 99WO-IB00103.  
XX  
PR 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX  
PA (CHIR-) CHIRON SPA.  
PI Grandi G, Masignani V, Pizzo M, Rappuoli R, Scarlato V;  
XX  
XX  
DR MPI: 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX  
XX  
PT New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing *Neisseria*  
PT meningitidis infections  
XX  
XX  
PS Claim 1; Page 62; 123pp; English.  
XX  
XX  
CC The invention provides proteins (AA27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AA29123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX  
XX  
SQ Sequence 591 AA:

Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
QY 1 MNKTYRIIMNSALNANAVASELFRNHTKRASATVATVLTLLFATVQASTTD---DDDL 57  
DB 1 mnktyrilmsalnawvseltrnhktrasatvlatllfatvqaasannegeedl 60  
QY 58 YLEPVQRTAVVLSFRSDKEGTEKE-VTEDSNMGVYFDKKGVLTAQTITTKAGDNLKIKQ 116  
DB 61 yldpvqrtavvllvnsdkegtekeveensdwaavyfnekyvltareitlkagdnllkikq 120  
QY 117 NTNENTNASSFTYSLKRDLDLTLSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEFTNGD 176  
DB 121 -----ngtnfyisllkklldltsvgteklsfsangknvntsdtkglnfaketaingnd 174  
QY 177 TTVHLNGIGSTLTDLTLLNTGATTNTVNDNTVDDEKKRAASVKDVLNAGWNIKGVKPGCTTA 236  
DB 175 tlvhlngigstltdltnlntgatntvndntvnddtkkrraasvkdvlnagwnikgvkpgtta 234  
QY 237 SDNWDFFRTDYVEFLSADPKTTTNNVESKDNKRTPEVKIGATSVYKKEGDGLVNTGDKD 296  
DB 235 sdnwdffrtydveflsadtkttnvneskdngkrtpevkigatsvikekdglvntgdkd 294  
QY 297 GENDSSTDKEGGLVTAKEVIDAVNKAQWRMKTATTANGQTQADKFETVTSCTNVTFAASK 356  
DB 295 gendsstdegeglvtakevldavnkagwrmtktattangqtqadkfetvtsctnvtfask 354  
QY 357 GTTATYSKDDQGNITWYDVNVDALNVLNOLNSGNWLSKAYAGSSGKAYISGNVSPSKG 416  
DB 355 gttatyskddqgnitwmydvnvdaalnvgllqnsywnlsgkayagsgkayisgnvpskg 414  
QY 417 KMDETVINAGNNIEITRNKNIDITASMTPOFSSVSLAGADAPATLSVDEGALNKGSK 476  
DB 415 kmdeyvinagnnieitrnknidiatstmpofssvslagadapltsvgd- alnvgsk 473  
QY 477 DANKPVRITNVAQVKEGDTNVAQLKGAQNLNHNIDVNGNARACIAQAIATAGLVQA 536  
DB 474 dknkpvriltvavpkyegdvtnvaqlkvaqnlhnridvngnaraglaqaiataglvqa 533

QY 537 YLPKSMIAIGGGYRGEAGYATGYSISIDGNNIIRKGTASGNSRGHFGASASVGYOM 594  
DB 534 ylpksmiaigggtyrgeagyaigyssidgnniirkgtsngsrghfgasasvgyom 591  
RESULT 14  
AA23746  
ID AAY23746 standard; protein; 591 AA.  
XX  
XX  
AC AAY23746;  
XX  
XX  
DT 08-SEP-1999 (first entry)  
XX  
XX  
DE A surface protein of *Neisseria meningitidis*.  
XX  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
XX  
OS *Neisseria meningitidis*.  
XX  
XX  
PN W0931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEBENS LAND.  
XX  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX  
DR MPI: 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
XX  
PT *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT meningitidis infections  
XX  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
XX  
CC The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX  
SQ Sequence 591 AA;  
QY  
Query Match 91.4%; Score 2758.5; DB 20; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2e-157;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;  
QY 1 MNKTYRIIMNSALNANAVASELFRNHTKRASATVATVLTLLFATVQASTTD---DDDL 57  
DB 1 mnktyrilmsalnawvseltrnhktrasatvlatllfatvqaasannegeedl 60  
QY 58 YLEPVQRTAVVLSFRSDKEGTEKE-VTEDSNMGVYFDKKGVLTAQTITTKAGDNLKIKQ 116  
DB 61 yldpvqrtavvllvnsdkegtekeveensdwaavyfnekyvltareitlkagdnllkikq 120  
QY 117 NTNENTNASSFTYSLKRDLDLTLSVGTSEKLSFSANSKNVNTSDTKGLNFAKKTAEFTNGD 176  
DB 121 -----ngtnfyisllkklldltsvgteklsfsangknvntsdtkglnfaketaingnd 174  
QY 177 TTVHLNGIGSTLTDLTLLNTGATTNTVNDNTVDDEKKRAASVKDVLNAGWNIKGVKPGCTTA 236  
DB 175 tlvhlngigstltdltnlntgatntvndntvnddtkkrraasvkdvlnagwnikgvkpgtta 236



Qy 417 KMDEFYNINAGNNIETTRNGKNIDIASMTPOSSYSIGAGADAPTLSDDEGALNVGSK 476  
Db 415 kmdeIvnlagnnlelItrngknIdlatsmtpqfssvslgagadapCLsvdgd-alnvgsk 473  
Qy 477 DANKPYRITNVAFVGEQDVTVNAQLKGYAQNINHNHIDNVDCGNARAGIAQAIAITAGLVOA 536  
Db 474 kdnkpyritcnvappvkegdvtlnvaqlkyvaqnlmnrIdnvdgnaragiagaIataglvgd 533  
Qy 537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGCNMIIKGTASGNSRGHFGASASVGYQW 594  
Db 534 ylpqksmmaIgggtyrgeagyaIgyssIsdggmwlkgtasgnsrgHfgasasvgyqw 591

Search completed: July 3, 2002, 08:09:07  
Job time: 493 sec

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| Query Match | Similarity | 100.0%;                                                         | Score 3019;         | DB 4;      | Length 594; |
|-------------|------------|-----------------------------------------------------------------|---------------------|------------|-------------|
| Best Local  | Similarity | 100.0%;                                                         | Pred. No. 1.5e-226; |            |             |
| Matches     | 594;       | Conservative                                                    | 0;                  | Mismatches | 0;          |
|             |            |                                                                 |                     | Indels     | 0;          |
|             |            |                                                                 |                     | Gaps       | 0           |
| Qy          | 1          | NNKIRRIINWSALNLMVAVSELTNRNHTKASATVAVATLTLFATVQASTDDDDLYLE       | 60                  |            |             |
| Db          | 1          | NNKIRRIINWSALNLMVAVSELTNRNHTKASATVAVATLTLFATVQASTDDDDLYLE       | 60                  |            |             |
| Qy          | 61         | PVORTAVVLSEFSRSDKEGTEKEVTEDEDSNMGVYFDKKGVLTACTITLKAGDNLKIKONTNE | 120                 |            |             |
| Db          | 61         | PVQRTAVVLSEFSRSDKEGTEKEVTEDEDSNMGVYFDKKGVLTACTITLKAGDNLKIKONTNE | 120                 |            |             |
| Qy          | 121        | NNNASSFYISLKKDLDTLTSVGTETKLSFANSNKVNIISDTQGLNRAAKTAETNGTYYH     | 180                 |            |             |
| Db          | 121        | NNNASSFYISLKKDLDTLTSVGTETKLSFANSNKVNIISDTQGLNRAAKTAETNGTYYH     | 180                 |            |             |
| Qy          | 181        | LNGISSTLTDLTLNLTGATNTVNTDNTVDDEKKRAASVKVULNAGNIKCYKKPCTTASDNV   | 240                 |            |             |
| Db          | 181        | LNGISSTLTDLTLNLTGATNTVNTDNTVDDEKKRAASVKVULNAGNIKCYKKPCTTASDNV   | 240                 |            |             |
| Qy          | 241        | DFVRRYDVVEFLSADPTKTTTVAVSESKDNKRREVKIGACTSVYKEDGKLVYTGKDGEND    | 300                 |            |             |
| Db          | 241        | DFVRRYDVVEFLSADPTKTTTVAVSESKDNKRREVKIGACTSVYKEDGKLVYTGKDGEND    | 300                 |            |             |
| Qy          | 301        | SSTDGEGELVTAKEDIVAVNKAQMRKTTTANGCQTQADKFEETVTSIGTINVTAFASGCGTTA | 360                 |            |             |

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Db 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
Oy 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
Db 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
Oy 421 TVNINAGNNIETTRNGKNIDATSMTPQFSVSLGAGADAPLTVSDDEGALNVGSKDANK 480
Db 421 TVNINAGNNIETTRNGKNIDATSMTPQFSVSLGAGADAPLTVSDDEGALNVGSKDANK 480
Oy 481 PVRTTNVAPGVEGDVTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGLVQAYLPBG 540
Db 481 PVRTTNVAPGVEGDVTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGLVQAYLPBG 540
Oy 541 KSMAIGGTYRGEAGYAIQYSSISDGNWITKGTASGNSRHFASASVGYOW 594
Db 541 KSMAIGGTYRGEAGYAIQYSSISDGNWITKGTASGNSRHFASASVGYOW 594
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## RESULT 2

US-09-669-974-9

```
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9
```

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Query Match 100.0%; Score 3019; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-226;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 NKKIRIITNSALNMAVAVSELTNRHTRKASATVATVATLTLFATVOASTDDDDLYLE 60
Db 1 NKKIRIITNSALNMAVAVSELTNRHTRKASATVATVATLTLFATVOASTDDDDLYLE 60
Oy 61 PVORTAVVLSFRSDEKGEKEVEEDSNMGVYFDKKGVLTAAGTITLKGADNLIKIQNTNE 120
Db 61 PVORTAVVLSFRSDEKGEKEVEEDSNMGVYFDKKGVLTAAGTITLKGADNLIKIQNTNE 120
Oy 121 NTKASSFTYSLAKKDLTDLTSVTEKLSFANSNKVNITSDTKGLMFAKTAETNGDTPVH 180
Db 121 NTKASSFTYSLAKKDLTDLTSVTEKLSFANSNKVNITSDTKGLMFAKTAETNGDTPVH 180
Oy 181 LKNGISSTLDTLNTGATNTVNDVNTDDEKRRASVADVLAAGNNIKGVKGTASDNV 240
Db 181 LKNGISSTLDTLNTGATNTVNDVNTDDEKRRASVADVLAAGNNIKGVKGTASDNV 240
Oy 241 DFRVTVDFVEFLSADTKTTTVNVEKSKDNGKRTVEVIGAKTSYIKKEDKLVYTKDKGEND 300
Db 241 DFRVTVDFVEFLSADTKTTTVNVEKSKDNGKRTVEVIGAKTSYIKKEDKLVYTKDKGEND 300
Oy 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
Db 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
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Db 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
Oy 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
Db 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
Oy 421 TVNINAGNNIETTRNGKNIDATSMTPQFSVSLGAGADAPLTVSDDEGALNVGSKDANK 480
Db 421 TVNINAGNNIETTRNGKNIDATSMTPQFSVSLGAGADAPLTVSDDEGALNVGSKDANK 480
Oy 481 PVRTTNVAPGVEGDVTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGLVQAYLPBG 540
Db 481 PVRTTNVAPGVEGDVTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGLVQAYLPBG 540
Oy 541 KSMAIGGTYRGEAGYAIQYSSISDGNWITKGTASGNSRHFASASVGYOW 594
Db 541 KSMAIGGTYRGEAGYAIQYSSISDGNWITKGTASGNSRHFASASVGYOW 594
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## RESULT 3

US-09-377-155-7

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; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7
```

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Query Match 95.2%; Score 2874; DB 4; Length 594;
Best Local Similarity 95.6%; Pred. No. 2.8e-215;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
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Oy 1 NKKIRIITNSALNMAVAVSELTNRHTRKASATVATVATLTLFATVOASTDDDDLYLE 60
Db 1 NKKIRIITNSALNMAVAVSELTNRHTRKASATVATVATLTLFATVOASTDDDDLYLE 60
Oy 61 PVORTAVVLSFRSDEKGEKEVEEDSNMGVYFDKKGVLTAAGTITLKGADNLIKIQNTNE 120
Db 61 PVORTAVVLSFRSDEKGEKEVEEDSNMGVYFDKKGVLTAAGTITLKGADNLIKIQNTNE 120
Oy 121 NTKASSFTYSLAKKDLTDLTSVTEKLSFANSNKVNITSDTKGLMFAKTAETNGDTPVH 180
Db 121 NTKASSFTYSLAKKDLTDLTSVTEKLSFANSNKVNITSDTKGLMFAKTAETNGDTPVH 180
Oy 181 LKNGISSTLDTLNTGATNTVNDVNTDDEKRRASVADVLAAGNNIKGVKGTASDNV 240
Db 181 LKNGISSTLDTLNTGATNTVNDVNTDDEKRRASVADVLAAGNNIKGVKGTASDNV 240
Oy 241 DFRVTVDFVEFLSADTKTTTVNVEKSKDNGKRTVEVIGAKTSYIKKEDKLVYTKDKGEND 300
Db 241 DFRVTVDFVEFLSADTKTTTVNVEKSKDNGKRTVEVIGAKTSYIKKEDKLVYTKDKGEND 300
Oy 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
Db 301 SSTDKGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKEETVTSNTVTFASGKGTGA 360
Oy 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
Db 361 TVSKDQDGNITVMYVNGDALNVQNLQNSGWNLDKSKAVAGSSGKVGISGNSPSKGMDE 420
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Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKKMD 420
QY 421 TVINAGNNIETIRNKNKNDIATSMTPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
Db 421 TVINAGNNIETIRNKNKNDIATSMAPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
QY 481 PVKITVAPGKGGDYTNVAOLKGVNOLNHNIDNDGNARAGIAOAIATAGLVQAYLP 540
Db 481 PVKITVAPGKGGDYTNVAOLKGVNOLNHNIDNDGNARAGIAOAIATAGLVQAYLP 540
QY 541 KSMMAIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 594
Db 541 KSMMAIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 594
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RESULT 4
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-669-974-7
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Query Match 95.2%; Score 2874; DB 4; Length 594;
Best Local Similarity 95.6%; Pred. No. 2.8e-215;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
Db 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKEVTEDSNMGVYFDKKGVLTAAGTTTLKAGNLIKONTNE 120
Db 61 PVORTAVVLSFRSDKEGTGEKEVTEDSNMGVYFDKKGVLTAAGTTTLKAGNLIKONTNE 120
QY 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
Db 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
QY 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
Db 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
QY 181 LMGISGLTDLTLNLTGATTNVTNDVTDDEKRRASVYKDVNLNAGWNIIKGVKPGTASDNV 240
Db 181 LMGISGLTDLTLNLTGATTNVTNDVTDDEKRRASVYKDVNLNAGWNIIKGVKPGTASDNV 240
QY 241 DFRVTDVTEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVIREKDGKLVYTKDGEN 300
Db 241 DFRVTDVTEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVIREKDGKLVYTKDGEN 300
QY 301 SSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKTTA 360
Db 301 SSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKTTA 360
QY 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKKMD 420
Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKKMD 420
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Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSKKMD 420
QY 421 TVINAGNNIETIRNKNKNDIATSMTPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
Db 421 TVINAGNNIETIRNKNKNDIATSMAPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
QY 481 PVKITVAPGKGGDYTNVAOLKGVNOLNHNIDNDGNARAGIAOAIATAGLVQAYLP 540
Db 481 PVKITVAPGKGGDYTNVAOLKGVNOLNHNIDNDGNARAGIAOAIATAGLVQAYLP 540
QY 541 KSMMAIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 594
Db 541 KSMMAIGGTYRGEAGYALGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 594
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RESULT 5
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-377-155-13
```

```
Query Match 94.6%; Score 2855; DB 4; Length 598;
Best Local Similarity 94.6%; Pred. No. 8.5e-214;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
Db 1 MNKIRIIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKEVTEDSNMGVYFDKKGVLTAAGTTTLKAGNLIKONTNE 120
Db 61 PVORTAVVLSFRSDKEGTGEKEVTEDSNMGVYFDKKGVLTAAGTTTLKAGNLIKONTNE 120
QY 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
Db 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
QY 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
Db 121 NTRASSFTYSLKDLTDLTSLVTEKLSFSSANSKNVITSDTKGLNPAKKTAEFTNGDTYH 180
QY 177 TVVHLNGISGLTDLTLNLTGATTNVTNDVTDDEKRRASVYKDVNLNAGWNIIKGVKPGT 236
Db 177 TVVHLNGISGLTDLTLNLTGATTNVTNDVTDDEKRRASVYKDVNLNAGWNIIKGVKPGT 236
QY 237 SDNVDFRITDYVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVIREKDGKLVYTKD 296
Db 237 SDNVDFRITDYVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVIREKDGKLVYTKD 296
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFAS 356
Db 297 GENDSSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFAS 356
QY 301 DENGSSSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFAS 360
Db 301 DENGSSSTDKGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFAS 360
QY 357 GTTATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSK 416
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVIISGNVSPSK 416
QY 417 KMDPTVNIAGNNIETIRNKNKNDIATSMTPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
Db 417 KMDPTVNIAGNNIETIRNKNKNDIATSMTPQSSVSLGAGADAPTLISVDEGALNVSNDANK 480
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Db 421 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 480  
Oy 477 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 536  
Db 481 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 540  
Oy 537 YLPGKSMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 594  
Db 541 YLPGKSMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 598

## RESULT 6

US-09-669-974-13  
: Sequence 13, Application US/09669974  
: Patent No. 6333173  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/669,974  
: CURRENT FILING DATE: 2000-09-26  
: PRIOR APPLICATION NUMBER: US 09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: PRIOR FILING DATE: 1997-12-12  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: Patentin Ver. 2.0  
: SEQ ID NO 13  
: LENGTH: 598  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
: US-09-669-974-13

Query Match 94.6%; Score 2855; DB 4; Length 598;

Best Local Similarity 94.6%; Pred. No. 8.5e-214;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Oy 1 MNKIYRIIWSALNMAVAVSELTNRHTRKASATVATLTLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNMAVAVSELTNRHTRKASATVATLTLFATVQASTDDDDLYLE 60  
Oy 61 PVQRTAVVLSFRSDKEGEGEKEGTEDSMWAYYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGEGEKEGTEDSMWAYYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Oy 121 NTNA-----SFTYSLKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKKAETNGD 176  
Db 121 NTNENTNDSSFTYSLKDLTDLTSVTEKLSFGANGNKVNITSDTKGLNFAKKAETNGD 180  
Oy 177 TTVHLNGIGSTLTDLTLTGATNTVNDVTDDEKKRAASVADVNAAGMNKIGVPGTTA 236  
Db 181 PTVHLNGIGSTLTDLTLTGATNTVNDVTDDEKKRAASVADVNAAGMNKIGVPGTTA 240  
Oy 237 SDNVDFVRTPDVEFLSADFTKTTTVNVEKDKGRTEVYKIGAKTSVIREKDGKLVTKGDK 296  
Db 241 SDNVDFVRTPDVEFLSADFTKTTTVNVEKDKGRTEVYKIGAKTSVIREKDGKLVTKGDK 300  
Oy 297 GENDSSTDKGEGLVYAKAEVIAVNAKGRMKTTPANGOTGADKFEYVTSCTNVTFAAGK 356  
Db 301 DENGSSTDEGEGLVYAKAEVIAVNAKGRMKTTPANGOTGADKFEYVTSCTNVTFAAGN 360  
Oy 357 GTTATVSKDDGCGNITVMVDVNGDALNVNOJLONSGMNLDSKRAVAGSSGKVIISGNVSPSKG 416  
Db 361 GTTATVSKDDGCGNITVMVDVNGDALNVNOJLONSGMNLDSKRAVAGSSGKVIISGNVSPSKG 420  
Oy 417 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 476  
Db 421 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 480

Db 421 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 480  
Oy 477 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 536  
Db 481 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 540  
Oy 537 YLPGKSMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 594  
Db 541 YLPGKSMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 598

## RESULT 7

US-09-377-155-5  
: Sequence 5, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/377,155  
: CURRENT FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: PRIOR FILING DATE: 1997-12-12  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: Patentin Ver. 2.0  
: SEQ ID NO 5  
: LENGTH: 598  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
: US-09-377-155-5

Query Match 94.5%; Score 2852; DB 4; Length 598;

Best Local Similarity 94.6%; Pred. No. 1.5e-213;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

Oy 1 MNKIYRIIWSALNMAVAVSELTNRHTRKASATVATLTLFATVQASTDDDDLYLE 60  
Db 1 MNKIYRIIWSALNMAVAVSELTNRHTRKASATVATLTLFATVQASTDDDDLYLE 60  
Oy 61 PVQRTAVVLSFRSDKEGEGEKEGTEDSMWAYYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGEGEKEGTEDSMWAYYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Oy 121 NTNA-----SFTYSLKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKKAETNGD 176  
Db 121 NTNENTNDSSFTYSLKDLTDLTSVTEKLSFGANGNKVNITSDTKGLNFAKKAETNGD 180  
Oy 177 TTVHLNGIGSTLTDLTLTGATNTVNDVTDDEKKRAASVADVNAAGMNKIGVPGTTA 236  
Db 181 PTVHLNGIGSTLTDLTLTGATNTVNDVTDDEKKRAASVADVNAAGMNKIGVPGTTA 240  
Oy 237 SDNVDFVRTPDVEFLSADFTKTTTVNVEKDKGRTEVYKIGAKTSVIREKDGKLVTKGDK 296  
Db 241 SDNVDFVRTPDVEFLSADFTKTTTVNVEKDKGRTEVYKIGAKTSVIREKDGKLVTKGDK 300  
Oy 297 GENDSSTDKGEGLVYAKAEVIAVNAKGRMKTTPANGOTGADKFEYVTSCTNVTFAAGK 356  
Db 301 DENGSSTDEGEGLVYAKAEVIAVNAKGRMKTTPANGOTGADKFEYVTSCTNVTFAAGN 360  
Oy 357 GTTATVSKDDGCGNITVMVDVNGDALNVNOJLONSGMNLDSKRAVAGSSGKVIISGNVSPSKG 416  
Db 361 GTTATVSKDDGCGNITVMVDVNGDALNVNOJLONSGMNLDSKRAVAGSSGKVIISGNVSPSKG 420  
Oy 417 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 476  
Db 421 KMDFTVNINAGNNIEITFRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVEGALNVGSK 480  
Oy 477 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 536  
Db 481 DANKPVRITTNVAPGVKEGDDVTNVQOLKGYAONLNHINDVGNARAGIAQAIATAGLVQA 540

Db 481 DANKPVRITNAPGVEGDVTNVAOLKGYAQNLRNDVNDGNARAGIAQAIAATAGLAQA 540  
QY 537 YLPKSMMAIGGTYRGEAGYAGYSSISDGGWIIKGTASGNSRGHFGASASVGYOW 594  
Db 541 YLPKSMMAIGGTYRGEAGYAGYSSISDGTGMWIKGTASGNSRGHFGTSASVGYOW 598

## RESULT 8

US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 94.5%; Score 2852; DB 4; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.5e-213;

Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIRIINMSALNANVAASELNRNHTKRASATVAVATLTLFATVQASTDDDDLYLE 60  
Db 1 MNKIRIINMSALNANVAASELNRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTEKEVTEDESNMGVYFDEKKGVLTAAGTITLKAGDNLIKONTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTEKEVTEDESNMAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
QY 121 NTVA-----SFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNPAKTAETNGD 176  
Db 121 NTNENNTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKNVNTSDTKGLNPAKTAETNGD 180  
QY 177 TTVHLNGIGSTLTDLTLNLTGATTNTNDVNTDDEKRRASVSKDVLNAGNNIKGVKPGTTA 236  
Db 181 PTYHLNGIGSTLTDLTLNLTGATTNTNDVNTDDEKRRASVSKDVLNAGNNIKGVKPGTTA 240  
QY 237 SDNVDEVRITDYVEFLSADTKTTTVNVESEKDNKRTVEVIGAKTSYIKEDGKLVYTKGK 236  
Db 241 SDNVDEVRITDYVEFLSADTKTTTVNVESEKDNKRTVEVIGAKTSYIKEDGKLVYTKGK 300  
QY 297 GENDSSTDGEGELVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSVGTNVTFAAGK 356  
Db 301 GENGSSSTDGEGELVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSVGTNVTFAAGK 360  
QY 357 GTTATVSKDDQGNITVYDVNVGDALNVNOLONGSNGLDSKAVAGSSGKVISGNVSPSKG 416  
Db 361 GTTATVSKDDQGNITVYDVNVGDALNVNOLONGSNGLDSKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVNIAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 421 KMDETVNIAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DANKPVRITNAPGVEGDVTNVAOLKGYAQNLRNDVNDGNARAGIAQAIAATAGLAQA 536  
Db 481 DANKPVRITNAPGVEGDVTNVAOLKGYAQNLRNDVNDGNARAGIAQAIAATAGLAQA 540

## RESULT 9

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 91.5%; Score 2762.5; DB 4; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.3e-206;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MNKIRIINMSALNANVAASELNRNHTKRASATVAVATLTLFATVQASTDDDDLYLE 59  
Db 1 MNKIRIINMSALNANVAASELNRNHTKRASATVAVATLTLFATVQANATDEDEEEL 60  
QY 60 EPQRTAVVLSFRSDKEGTEKEVTEDESNMGVYFDEKKGVLTAAGTITLKAGDNLIKONTNE 116  
Db 61 EPVRSALVLFQMDIDKNGENENSTGNIGSIYYDHNHTLHAGATVTLKAGDNLIKONTNE 120  
QY 117 -NTNENNTNDSSFTYSLKKDLTDLTSVGTSEKLSFSAANSKNVNTSDTKGLNPAKTAETNG 175  
Db 121 KNTNENNTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKNVNTSDTKGLNPAKTAETNG 180  
QY 176 DTVHLNGIGSTLTDLTLNLTGATTNTNDVNTDDEKRRASVSKDVLNAGNNIKGVKPGTT 235  
Db 181 DTVHLNGIGSTLTDLTLNLTGATTNTNDVNTDDEKRRASVSKDVLNAGNNIKGVKPGTT 240  
QY 236 ASDNVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTVEVIGAKTSYIKEDGKLVYTKGK 295  
Db 241 ASDNVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTVEVIGAKTSYIKEDGKLVYTKGK 300  
QY 296 KGENSSTDGEGELVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSVGTNVTFAAGK 355  
Db 301 KGENSSTDGEGELVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSVGTNVTFAAGK 360  
QY 356 KGTATVSKDDQGNITVYDVNVGDALNVNOLONGSNGLDSKAVAGSSGKVISGNVSPSKG 415  
Db 361 KGTATVSKDDQGNITVYDVNVGDALNVNOLONGSNGLDSKAVAGSSGKVISGNVSPSKG 420  
QY 416 GKMDETVNIAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSK 475  
Db 421 GKMDETVNIAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 476 KMDPVRITNAPGVEGDVTNVAOLKGYAQNLRNDVNDGNARAGIAQAIAATAGLAQA 535  
Db 481 KMDPVRITNAPGVEGDVTNVAOLKGYAQNLRNDVNDGNARAGIAQAIAATAGLAQA 540  
QY 536 AYLPKSMMAIGGTYRGEAGYAGYSSISDGGWIIKGTASGNSRGHFGASASVGYOW 594  
Db 541 AYLPKSMMAIGGTYRGEAGYAGYSSISDGGWIIKGTASGNSRGHFGASASVGYOW 598

Db 541 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 599

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RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15
```

Query Match 91.5%; Score 2762.5; DB 4; Length 599;  
Best Local Similarity 91.7%; Pred. No. 1.3e-206;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

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OY 1 MNKIRIITNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTD--DDIYL 59
DB 1 MNKIRIITNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTDDEEEL 60
OY 60 BPVOPTAVVLSFRSDEKGEKEVTEDSNMGVYFDKGVLTAGTITLAKAGDLKIKO--- 116
DB 61 BPVVSALVLQMDKEGENESSTGNIGWSIYDHNHTLHGATVTLAKAGDLKIKONTN 120
OY 117 -NTNENTNASSFTYSLKDLTDLTSVTEKLSFSANSKNVNTSDTKGLNFAKKTAEING 175
DB 121 KTNENTNDSFTYSLKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKKTAEING 180
OY 176 DTTVHLNGIGSTLDTLLNTGATVNTVDNVTDDKKRAASVADVLMAGMNIKGVKPGTT 235
DB 181 DTTVHLNGIGSTLDTLLNTGATVNTVDNVTDDKKRAASVADVLMAGMNIKGVKPGTT 240
OY 236 ASDNDFEVRTYDVEFLSADTKTTVNVESSKNGKRTVEKIGAKTSVIREKDGKLVGTGD 295
DB 241 ASDNDFEVRTYDVEFLSADTKTTVNVESSKNGKRTVEKIGAKTSVIREKDGKLVGTGD 300
OY 296 KGENSDSTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEYTSCTNTYFASG 355
DB 301 KGENSSSTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEYTSCTNTYFASG 360
OY 361 KGTATVSKDDOGNITVMTDVNVDGALNVNOJONGSGMNLDSKRAVAGSSGKVISGNVSPSK 415
DB 361 KGTATVSKDDOGNITVMTDVNVDGALNVNOJONGSGMNLDSKRAVAGSSGKVISGNVSPSK 420
OY 416 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSIGAGADAPTLISVDEGALNVGSK 475
DB 421 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSIGAGADAPTLISVDEGALNVGSK 480
OY 476 KDANKPVRTITNAPGVKESGDVTNVAOLKGAONLNHIDNVGNARAGIAQAIATAGLVQ 535
DB 481 KDANKPVRTITNAPGVKESGDVTNVAOLKGAONLNHIDNVGNARAGIAQAIATAGLVQ 540
OY 536 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 594
DB 536 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 594
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Db 541 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 599

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RESULT 11
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
```

Query Match 91.4%; Score 2758.5; DB 4; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2.6e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

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OY 1 MNKIRIITNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTD--DDIYL 57
DB 1 MNKIRIITNSALNMAVAVSELTRNHTKRASATVATVATLTLFATVOASTDDEEEL 60
OY 58 YLEPVORTAVVLSFRSDEKGEKEK-VTEDSNMGVYFDKGVLTAGTITLAKAGDLKIKO 116
DB 61 YLDPQRTAVVLSFRSDEKGEKEKVEENSDMAYYFENKGVLTARELTLLAKAGDLKIKO 120
OY 117 NTNENTNASSFTYSLKDLTDLTSVTEKLSFSANSKNVNTSDTKGLNFAKKTAEING 176
DB 121 -----NGTNFTYSLKDLTDLTSVTEKLSFSANGKNVNTSDTKGLNFAKKTAEING 174
OY 177 TTVHLNGIGSTLDTLLNTGATVNTVDNVTDDKKRAASVADVLMAGMNIKGVKPGTTA 236
DB 175 TTVHLNGIGSTLDTLLNTGATVNTVDNVTDDKKRAASVADVLMAGMNIKGVKPGTTA 234
OY 237 SDNDFEVRTYDVEFLSADTKTTVNVESSKNGKRTVEKIGAKTSVIREKDGKLVGTGD 296
DB 235 SDNDFEVRTYDVEFLSADTKTTVNVESSKNGKRTVEKIGAKTSVIREKDGKLVGTGD 294
OY 297 KGENSDSTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEYTSCTNTYFASG 356
DB 295 KGENSSSTDEGEGLVTAKEVIDAVNKAQRMTTANGOTGOADKFEYTSCTNTYFASG 354
OY 357 GTTATVSKDDOGNITVMTDVNVDGALNVNOJONGSGMNLDSKRAVAGSSGKVISGNVSPSK 416
DB 355 GTTATVSKDDOGNITVMTDVNVDGALNVNOJONGSGMNLDSKRAVAGSSGKVISGNVSPSK 414
OY 417 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSIGAGADAPTLISVDEGALNVGSK 476
DB 415 KMDETVNIAGNNIEITRNGKNIDIASMTPOFSSVSIGAGADAPTLISVDEGALNVGSK 473
OY 477 KDANKPVRTITNAPGVKESGDVTNVAOLKGAONLNHIDNVGNARAGIAQAIATAGLVQ 536
DB 474 KDANKPVRTITNAPGVKESGDVTNVAOLKGAONLNHIDNVGNARAGIAQAIATAGLVQ 533
OY 537 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 594
DB 534 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOM 591
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RESULT 12  
US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 91.4%; Score 2758.5; DB 4; Length 591;  
Best Local Similarity 92.3%; Pred. No. 2.6e-206;  
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

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QY 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFATVQASTDD---DDDL 57
Db 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFATVQASANNRERPKD 60
QY 58 YLEPYQRTAVVLSFRSDKEGEGEKE-VTEDSNMGVYFEDKKGYLTAAGTITLAKGDNLIK 116
Db 61 YLDPQRTAVVAVLVNSDKGEGEKEVEENSDWAYFENEKGYLTAETITLAKGDNLIK 120
QY 117 NNENNTNASSFTYSLKKDLTDLTSGTEKLSFSAANSKNVNTSDTKGLNFAKTAETNGD 176
Db 121 -----NGTNFTYSLKKDLTDLTSGTEKLSFSAANSKNVNTSDTKGLNFAKTAETNGD 174
QY 177 TTVHLNGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVQDVNLNAGNINIGVPRGTTA 236
Db 175 TTVHLNGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVQDVNLNAGNINIGVPRGTTA 234
QY 237 SDNVDVFRITVDVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSYIKEDGKLVTKGDK 296
Db 235 SDNVDVFRITVDVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSYIKEDGKLVTKGDK 294
QY 297 GENDSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGQADKREFTVSGTNVTFASG 356
Db 295 GENDSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGQADKREFTVSGTNVTFASG 354
QY 357 GTTATVSKDDGNTITVMDVNVGDLNVNQLNSGMNLSKAVAGSSGKVISGNVSPSG 416
Db 355 GTTATVSKDDGNTITVMDVNVGDLNVNQLNSGMNLSKAVAGSSGKVISGNVSPSG 414
QY 417 KMDDEVININAGNNIETIRNGKNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 415 KMDDEVININAGNNIETIRNGKNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 473
QY 477 DANKPVRTITNVAQVKEGSDVTVNVAOLKGYAQNLNHNHIDNVGNARAGIAQAIATAGLVQ 536
Db 474 KDNKPVRTITNVAQVKEGSDVTVNVAOLKGYAQNLNHNHIDNVGNARAGIAQAIATAGLVQ 533
QY 537 YLPKGSMAIIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 594
Db 534 YLPKGSMAIIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 591
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RESULT 13

US-09-377-155-2  
; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 91.1%; Score 2751; DB 4; Length 592;  
Best Local Similarity 92.0%; Pred. No. 1e-205;  
Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;

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QY 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFATVQASTDD---DD 56
Db 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFATVQASANNRERPKD 60
QY 57 YLEPYQRTAVVLSFRSDKEGEGEKE-VTEDSNMGVYFEDKKGYLTAAGTITLAKGDNLIK 115
Db 61 YLDPQRTAVVAVLVNSDKGEGEKEVEENSDWAYFENEKGYLTAETITLAKGDNLIK 120
QY 116 ONTNTNASSFTYSLKKDLTDLTSGTEKLSFSAANSKNVNTSDTKGLNFAKTAETNG 175
Db 121 Q-----NGTNFTYSLKKDLTDLTSGTEKLSFSAANSKNVNTSDTKGLNFAKTAETNG 174
QY 176 TTVHLNGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVQDVNLNAGNINIGVPRGTT 235
Db 175 TTVHLNGIGSLTDLTLNTGATTNTNDVTDDEKKRAASVQDVNLNAGNINIGVPRGTT 234
QY 236 ASDNDVFRITVDVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSYIKEDGKLVTKGDK 295
Db 235 ASDNDVFRITVDVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSYIKEDGKLVTKGDK 294
QY 296 KGENSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGQADKREFTVSGTNVTFASG 355
Db 295 KGENSSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGQADKREFTVSGTNVTFASG 354
QY 356 KGTATVSKDDGNTITVMDVNVGDLNVNQLNSGMNLSKAVAGSSGKVISGNVSPSG 415
Db 355 KGTATVSKDDGNTITVMDVNVGDLNVNQLNSGMNLSKAVAGSSGKVISGNVSPSG 414
QY 416 KMDDEVININAGNNIETIRNGKNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 475
Db 415 KMDDEVININAGNNIETIRNGKNIDATSMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 473
QY 476 KDNKPVRTITNVAQVKEGSDVTVNVAOLKGYAQNLNHNHIDNVGNARAGIAQAIATAGLVQ 535
Db 474 KDNKPVRTITNVAQVKEGSDVTVNVAOLKGYAQNLNHNHIDNVGNARAGIAQAIATAGLVQ 533
QY 536 AYLPKGSMAIIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 594
Db 534 AYLPKGSMAIIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 592
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RESULT 14  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173

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: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: PRIORITY FILING DATE: 2000-09-26
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 976398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 592
: TYPE: PRN
: ORGANISM: Neisseria meningitidis
: US-09-669-974-2

```

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? APPLICANT: PEAK, Ian Richard Anselm
? APPLICANT: JENNINGS, Michael Paul
? APPLICANT: MOXON, E. Richard
? TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
? FILE REFERENCE: 065064/0128
? CURRENT APPLICATION NUMBER: US/09/377.155
? CURRENT FILING DATE: 1999-08-19
? PRIOR APPLICATION NUMBER: PCT/AU98/01031
? PRIOR FILING DATE: 1998-12-14
? PRIOR APPLICATION NUMBER: GB 9726398.2
? PRIOR FILING DATE: 1997-12-12
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 11
? LENGTH: 591
? TYPE: PRT
? ORGANISM: Neisseria meningitidis
US-09-377-155-11

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:12 ; Search time 95.27 Seconds  
(without alignments)  
599.108 Million cell updates/sec

Title: US-09-771-382-4

Perfect score: 3019

Sequence: 1 MKKIRIINNSALNMAVAVS.....TASGSRGHFGASASVGYQM 594

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR-71:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description         |
|------------|--------|-------------|--------|-------|---------------------|
| 1          | 2758.5 | 91.4        | 591    | 2     | adhesin NMB0992 [i  |
| 2          | 2533   | 83.9        | 592    | 2     | probable surface f  |
| 3          | 620    | 20.5        | 298    | 2     | adhesin homolog HI  |
| 4          | 398.5  | 13.2        | 2059   | 2     | surface protein XF  |
| 5          | 384.5  | 12.7        | 1190   | 2     | surface protein XF  |
| 6          | 375.5  | 12.4        | 1107   | 2     | probable autotrans  |
| 7          | 368.5  | 12.2        | 1588   | 2     | probable adhesin Z  |
| 8          | 368.5  | 12.2        | 1588   | 2     | probable adhesin E  |
| 9          | 331.5  | 11.0        | 658    | 2     | probable surface p  |
| 10         | 244    | 8.1         | 1091   | 2     | hypothetical prote  |
| 11         | 239    | 7.9         | 1004   | 2     | hypothetical prote  |
| 12         | 224    | 7.4         | 2249   | 2     | 190k surface anti   |
| 13         | 222    | 7.4         | 1018   | 2     | probable adhesin p  |
| 14         | 220    | 7.3         | 1536   | 2     | high-molecular-we   |
| 15         | 219    | 7.3         | 1286   | 2     | adhesin AIDA-I pre  |
| 16         | 219    | 7.3         | 4919   | 2     | hypothetical prote  |
| 17         | 216.5  | 7.2         | 1325   | 2     | yeast protein - Esc |
| 18         | 216    | 7.2         | 1487   | 2     | hypothetical prote  |
| 19         | 214.5  | 7.1         | 949    | 2     | hypothetical prote  |
| 20         | 214.5  | 7.1         | 1005   | 2     | AIDA-I adhesin-lik  |
| 21         | 213    | 7.1         | 3705   | 2     | probable autotrans  |
| 22         | 211.5  | 7.0         | 1477   | 2     | high-molecular-we   |
| 23         | 209.5  | 6.9         | 1910   | 2     | probable adhesin h  |
| 24         | 209    | 6.9         | 5188   | 2     | probable RTX famli  |
| 25         | 209    | 6.9         | 5291   | 2     | hypothetical prote  |
| 26         | 208    | 6.9         | 1327   | 2     | AIDA-I adhesin-lik  |
| 27         | 208    | 6.9         | 1349   | 2     | probable beta-bar   |
| 28         | 205.5  | 6.8         | 936    | 2     | SABP protein - Cam  |
| 29         | 204.5  | 6.8         | 1577   | 2     | hemolysin A precu   |

|    |       |     |      |   |                    |
|----|-------|-----|------|---|--------------------|
| 30 | 203.5 | 6.7 | 1343 | 2 | hypothetical prote |
| 31 | 203   | 6.7 | 1608 | 2 | hemolysin A - Ser  |
| 32 | 203   | 6.7 | 4936 | 2 | hypothetical prote |
| 33 | 201.5 | 6.7 | 1109 | 2 | surface-array prot |
| 34 | 200.5 | 6.6 | 1343 | 2 | hypothetical prote |
| 35 | 200   | 6.6 | 980  | 2 | probable flagellin |
| 36 | 200   | 6.6 | 980  | 2 | probable structure |
| 37 | 200   | 6.6 | 3013 | 2 | probable invasiv   |
| 38 | 198   | 6.6 | 2020 | 2 | ABC-type transport |
| 39 | 197   | 6.5 | 2551 | 2 | hypothetical prote |
| 40 | 197   | 6.5 | 3029 | 2 | hypothetical prote |
| 41 | 195   | 6.5 | 1029 | 2 | outer membrane pro |
| 42 | 195   | 6.5 | 1417 | 2 | hypothetical prote |
| 43 | 194.5 | 6.4 | 4152 | 2 | filamentous hemag  |
| 44 | 194   | 6.4 | 920  | 2 | surface array prot |
| 45 | 194   | 6.4 | 2468 | 2 | hypothetical prote |

## ALIGNMENTS

|                                                                                                                                                                                                                                                                                                     |                                                                               |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|
| RESULT 1                                                                                                                                                                                                                                                                                            |                                                                               |
| G81133                                                                                                                                                                                                                                                                                              | adhesin NMB0992 [Imported] - Neisseria meningitidis (strain MC58 serogroup B) |
| C:Species: Neisseria meningitidis                                                                                                                                                                                                                                                                   |                                                                               |
| C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001                                                                                                                                                                                                                         |                                                                               |
| C:Accession: G81133                                                                                                                                                                                                                                                                                 |                                                                               |
| R:Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al.; H.; Qin, H.; Yamathavan, J.; Gill, J.; Scariato, V.; Masiugnani, V.; Piazza, M. Science 287, 1809-1815, 2000 |                                                                               |
| A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moron, E.R.; Rappunli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755                                                                                |                                                                               |
| A:Accession: G81133                                                                                                                                                                                                                                                                                 |                                                                               |
| A:Molecule type: DNA                                                                                                                                                                                                                                                                                |                                                                               |
| A:Status: preliminary                                                                                                                                                                                                                                                                               |                                                                               |
| A:Reference: A81000; MUID:20175755                                                                                                                                                                                                                                                                  |                                                                               |
| A:Residues: 1-591 <TEP>                                                                                                                                                                                                                                                                             |                                                                               |
| A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAFA1395.1; PID:g722                                                                                                                                                                                                               |                                                                               |
| A:Experimental source: serogroup B, strain MC58                                                                                                                                                                                                                                                     |                                                                               |
| C:Genetics:                                                                                                                                                                                                                                                                                         |                                                                               |
| A:Gene: NMB0992                                                                                                                                                                                                                                                                                     |                                                                               |
| Query Match                                                                                                                                                                                                                                                                                         | 91.4%; Score 2758.5; DB 2; Length 591;                                        |
| Best Local Similarity                                                                                                                                                                                                                                                                               | 92.3%; Pred. No. 1.5e-131;                                                    |
| Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;                                                                                                                                                                                                                                     |                                                                               |
| 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFAVQASTD---DDDL 57                                                                                                                                                                                                                                          |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 1 MKKIRIINNSALNMAVAVSELTRNHTKRASATVATLTLFAVQASTD---DDDL 60                                                                                                                                                                                                                                          |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 58 YLEPVQRTAVVLSFSDKEGTEKE-VTEDSNMGVYFDKGVLTAGTTLKAGDNLKIKO 116                                                                                                                                                                                                                                     |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 61 YLDPQRTAVVAVLVNSDKGTEKEKEVEENSDMAYVFNKGVLFAREITLLKAGDNLKIKO 120                                                                                                                                                                                                                                  |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 117 NTNENMNASFTYSIKKDLTDTSVGTEKLSANSKNKNTISDPKGLNFAKKTAEATND 176                                                                                                                                                                                                                                    |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 121 -----NGTFNFTYSIKKDLTDTSVGTEKLSANSKNKNTISDPKGLNFAKKTAEATND 174                                                                                                                                                                                                                                   |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 177 TTVHLNGISGLTDLTLNMGATTNTNDVTDDEKKRAASVDVNLNAGNIGVKGRTGA 236                                                                                                                                                                                                                                     |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 175 TTVHLNGISGLTDLTLNMGATTNTNDVTDDEKKRAASVDVNLNAGNIGVKGRTGA 234                                                                                                                                                                                                                                     |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 237 SDNVDFVTRTYDVEFLSADTKTTTVNVESEKDKGRTKRTSVIKRDKGLVTGKDK 296                                                                                                                                                                                                                                      |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 235 SDNVDFVTRTYDVEFLSADTKTTTVNVESEKDKGRTKRTSVIKRDKGLVTGKDK 294                                                                                                                                                                                                                                      |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 297 GENDSTDKGELVTAKEYIDAVNKAAGPMKTTTANGOTGQADKREFTVSGTNVFPASGK 356                                                                                                                                                                                                                                  |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 295 GNGSSTDEGELVTAKEYIDAVNKAAGPMKTTTANGOTGQADKREFTVSGTNVFPASGK 354                                                                                                                                                                                                                                  |                                                                               |
|                                                                                                                                                                                                                                                                                                     |                                                                               |
| 357 GTTATVSKDQDGNITVMTVDVNVGDLNVLNQLNSGNLDSKAVAGSSGKIVISGNVSPSKG 416                                                                                                                                                                                                                                |                                                                               |

|||||  
Db 355 GTTATATSKDQGGNTTAVYDVAVNGALNVNQLQNSGMWLDLSAAVAGSSGKYISGVNPSK 414  
QY 417 KMDETVAINAGNNIEITRNKKNIDIASMTPOFSSVSLGAGADAPTLVSDDEGALNYSK 476  
|||||  
Db 415 KMDETVAINAGNNIEITRNKKNIDIASMTPOFSSVSLGAGADAPTLVSDDEGALNYSK 473  
QY 477 DANKPVRITNAPGVKEDVYTNVAQLKGVANLNHNDVNGNARAGIAQAIAATAGLVOA 536  
|||||  
Db 474 KDKPVRITNAPGVKEDVYTNVAQLKGVANLNHNDVNGNARAGIAQAIAATAGLVOA 533  
QY 537 YLPKSMMAIGGGTYRGEAGYALGYSSISDPGMMIIGKTASGNSRGHFGASASVGY 594  
534 YLPKSMMAIGGGTYRGEAGYALGYSSISDPGMMIIGKTASGNSRGHFGASASVGY 591

RESULT 2  
A81888  
Probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain Z249)  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
; Holtroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL62755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match 83.9%; Score 2533; DB 2; Length 592;  
Best Local Similarity 86.4%; Pred. No. 3.2e-120;  
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

QY 1 MNKTYRIINMSALNAAVAVSELTRNHRKRSATVATVATLTLFATVQASTD-DDDLYLE 59  
|||||  
Db 1 MNKTYRIINMSALNAAVAVSELTRNHRKRSATVATVATLTLFATVQASTDDEDEBEL 60  
QY 60 EPVORTAVVLSFRSDKEGTEGKE-----VTEDSNMGVYFPKKGVLTAAGTTLKAGDNLKI 114  
|||||  
Db 61 ESVOR-SVAGSISQASMGSGELETLISLMTNDS-----KEFYDPYIIVYTLKAGDNLKI 112  
QY 115 KONTNENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVNTSDTKGLNFAKKAETN 174  
|||||  
Db 113 KONTNENTNASSFTYSLKKDLTGLINTEKLSFGANGKKNILISDTKGLNFAKKAETN 172  
QY 175 GDTTVHNLNGISLTLDLTLNLTGATTNTNDVNTDEKKRAASVDVYNAGNITKGVPRGT 234  
|||||  
Db 173 GDTTVHNLNGISLTLDLTLNLTGATTNTNDVNTDEKKRAASVDVYNAGNITKGVPRGT 230  
QY 235 TA--SDNVDEVRTYDYEFLSADTKTTTVNVESSKNGKRTVEKIGAKTSVYKEDGKLYT 292  
|||||  
Db 231 TTGQSEKVDVRYTDYEFELSAADTKTTTVNVESSKNGKRTVEKIGAKTSVYKEDGKLYT 290  
QY 293 GKQGENDSSTDKGEGIVTAKEVIDAVNKAQWRKTTTANGQGTQADKFEETVTSQNTVF 352  
|||||  
Db 291 GKQGENDSSTDKGEGIVTAKEVIDAVNKAQWRKTTTANGQGTQADKFEETVTSQNTVF 350  
QY 353 ASGKGTATATSKDQGGNTTAVYDVAVNGALNVNQLQNSGMWLDLSAAVAGSSGKYISGVN 412  
|||||  
Db 351 ASGKGTATATSKDQGGNTTAVYDVAVNGALNVNQLQNSGMWLDLSAAVAGSSGKYISGVN 410  
QY 413 PSKGMDETVAINAGNNIEITRNKKNIDIASMTPOFSSVSLGAGADAPTLVSDDEGALN 472  
|||||  
Db 411 PSKGMDETVAINAGNNIEITRNKKNIDIASMTPOFSSVSLGAGADAPTLVSDDEGALN 470

QY 473 VGSKDNKPVKITNAPGVKEDVYTNVAQLKGVANLNHNDVNGNARAGIAQAIAATAG 532  
|||||  
Db 471 VGSKDNKPVKITNAPGVKEDVYTNVAQLKGVANLNHNDVNGNARAGIAQAIAATAG 530  
QY 533 LVQAYLPGKSMMAIGGGTYRGEAGYALGYSSISDPGMMIIGKTASGNSRGHFGASASVGY 592  
|||||  
Db 531 LVQAYLPGKSMMAIGGGTYRGEAGYALGYSSISDPGMMIIGKTASGNSRGHFGASASVGY 590  
QY 593 QW 594  
591 QW 592

RESULT 3  
I64138  
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Feilichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman,  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Yente  
A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:032846; GB:I42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 20.5%; Score 620; DB 2; Length 298;  
Best Local Similarity 46.6%; Pred. No. 2e-24;  
Matches 145; Conservative 41; Mismatches 91; Indels 34; Gaps 7;

QY 1 MNKTYRIINMSALNAAVAVSELTRNHRKRSATVATVATLTLFATVQASTD-DDDLYLE 60  
|||||  
Db 1 MNKTYRIINMSALNAAVAVSELTRNHRKRSATVATVATLTLFATVQASTDDEDEBEL 60  
QY 61 EPVORTAVVLSFRSDKEGTEGKE-----VTEDSNMGVYFPKKGVLTAAGTTLKAGDNLKI 119  
|||||  
Db 50 -INDAGTFVVVQSTPEDIEDSAAKTDN-----KNQALKAGDTLTLKAKKNLAKL--- 99  
QY 120 ENTNASSFTYSLKKDLTDLTSVTEKLSFSAN-----SNKVNITSDTKGLNFAKKAETN 172  
|||||  
Db 100 -DQGGKSVTFLAKDLVYTAKEVIDAVNKAQWRKTTTANGQGTQADKFEETVTSQNTVF 155  
QY 173 TNGDTTVHNLNGISLTLDLTLNLTGATTNTNDVNTDEKKRAASVDVYNAGNITKGVPRGT 232  
|||||  
Db 156 TNGDTTVHNLNGISLTLDLTLNLTGATTNTNDVNTDEKKRAASVDVYNAGNITKGVPRGT 214  
QY 233 GTTASDNDVRYTDYEFELSAADTKTTTVNVESSKNGKRTVEKIGAKTSVYKEDGKLYT 292  
|||||  
Db 215 AGGTFENVLDVAGDNEFTTGDKNTLDVLTAKENKTEVEKTPKTSVIXNNKGLT 274  
QY 293 GKQGENDSST 303  
275 GKQKDKANTGT 285

RESULT 4  
D82671  
surface protein Xf1529 [Imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20355717  
A>Note: for a complete list of authors see reference number A59328 below



Db 1003 F-----VKVNSLNN-----SATPIAGVDTAIGVATGASGDSI 1037  
Qy 461 -----PTLSVDEGAL-----NVGSKDANKPVRTINVAPEGKEDVTNVAOLK 503  
Db 1038 AMGNKASADNAVAIGNHNSVADBRANTVSVGSASGR--QVINVAGAGTADTDVAVNSQAN 1095  
Qy 504 GVAQNLNHNHIDVNGNAR---AGIAQAIATATAGLVOAYLPKGSMAIIGGTYRGEAGVAI 559  
Db 1096 OGILITAKQYTDGVGSLRBDTDGVAALATATANLPQATYIPGRGMTSVGSVSRGSAIAY 1155  
Qy 560 GYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594  
Db 1156 GVSVSSESGRWYKFGSGSANTRSQVYIGAGVGYOW 1190  
  
RESULT 6  
AC0976  
probable autotransporter sabb [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mole, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AC0976  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD0303.1; PID:q16504923; GSPDB:GN00176  
C:Genetics:  
A:Gene: sabb

Query Match 12.4%; Score 375.5; DB 2; Length 1107;  
Best Local Similarity 21.7%; Pred. No. 2.1e-11;  
Matches 185; Conservative 105; Mismatches 262; Indels 299; Gaps 33;  
  
Qy 27 TRKASATVATVATLLEFATVASTTD--DDLY--LEPVQRTAVLSFRSDEKGTGE 80  
Db 273 TRKASATVATVATLLEFATVASTTD--DDLY--LEPVQRTAVLSFRSDEKGTGE 80  
Qy 81 KVTEDSMNGVYFEDKKVGLACTIT--IKAGD-----LTKIKONT----- 118  
Db 333 DNLNMTTNSFSASHGSSTTKITNVAAGELSEESTDAVNGSOLFETNEKVDONTTDTA 392  
Qy 119 -----NENTNASSFTYSLKKDLTDLTSVTEKL--SFSAN--SKKVNITSDT 161  
Db 393 ANTTNTITONSTAIENLNTSVSDINTSI--TGLTDMNLLMDELDGARSANNGSSTKITTNA 451  
Qy 162 KCLNFAKKTAEFNG---DTVHLNGISGTLTDTLLNTGATTNVTNDVTDDEKKRAASV 217  
Db 452 AGALSEDSTDAVNGSOLFETNOKVDONTSAIAD--INT--SITNLGTDALSMWDEDEGAFSA 508  
Qy 218 KQVLNAGNMIKGVKPGTTASDNVDF--RTYDT-----VEFLSADPKTTTVN-- 262  
Db 509 SHGTGNTKTNVAAGELASDSTDAVNGSOLFETNMLISQYNESISOLAGDITSEYITEN 568  
Qy 263 -----VESKDNCKRTEVIGAKTSVIEKDKGLVTGKDK-----GENDSSTDG 306  
Db 569 GTGVYIIRNDNGLEGQ-----DAYATNGATAVGYTAAVAGSAGCLALGONSSSISIG 621  
Qy 307 -----EGLYV---TAKEVIDAVNKA---GRRMKTITAN 332  
Db 622 STALSGSTSNRAITGIRETSATSDGVYIGYNTDRELLGALSIGTDESYRQITNVAD 681  
Qy 333 GGTGQ-----ADKFEVITSGTNTVTFASGKGTAA---TYSKDDG-- 368  
Db 683 GSEADAVTROLONAGAVTTPTPKYHANSTEDSLAVGDSILAMGAKTIVNADAGIG 741

Qy 369 ---NITVMDVNVGDALNVN-----OLONGWMLDSK----- 397  
Db 742 IGLNLTVMADALINGIALISGNARAHNANSIANGNGSOTTRGACTDTVATVMDTPQNSVGEF 801  
Qy 398 AVAGSSKVIYSGNVSDBSKKMDETVYNINAG---NNIEITRGNKI----- 439  
Db 802 SVSEDEGGRQIINTVNAASADTDA---VNVGOLKVYDQAGSRPTQSTITNLNTOVSNLDFRV 858  
Qy 440 -----DIATSMTPQF-----SSVSLGAGADAP-----TLSVDE 468  
Db 859 TINIENGIDVTYTGSTKIFKRTTDCADANAQADSAVIGSISIAAENSVALGTSVADE 918  
Qy 469 -GALNVGSKDANKPVRTINVAPEGKEDVTNVAOLK----- 503  
Db 919 ANTVSVGSSTQGR--RITNVAAGVNNTDAVNVVAOLKASPAESVRYETNADGSVNTSVLNL 976  
Qy 504 -----GVAQ-----NUNHIDVNGNARAG 523  
Db 977 GDGSGGTRIGNVSAVNDTDAVNVVAOLKRSVEANTYTDQMKGENSKIKIGIENKMSG 1036  
Qy 524 IAOATATAGLVOAYLPKGSMAIIGGTYRGEAGVAIQYSSISDGGNWIITKTASGNSRGH 583  
Db 1037 IASAMAMGLPOATVAPGAMNTSIAGTENGESAVAIQVSMVSESGWYKLOGTSNSQGD 1096  
Qy 584 FGASASVGYOW 594  
Db 1097 YSAALGAGFGOW 1107  
  
RESULT 7  
AB6036  
probable adhesin 25029 [imported] - Escherichia coli (strain 0157:H7, substrain EDL93)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: AB6036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, J.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dinalanta, E.; Potamousis, K.; Apoda, N.  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.  
A:Reference number: AB6036; MUID:21074935; PMID:11206551  
A:Accession: AB6036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:q12518349; PIDN:AA658749.1; GSPDB:GN00145; UMGF: A:Experimental source: strain 0157:H7, substrain EDL933  
C:Genetics:  
A:Gene: 25029

Query Match 12.2%; Score 368.5; DB 2; Length 1588;  
Best Local Similarity 23.0%; Pred. No. 7.4e-11;  
Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;  
  
Qy 7 IIV-----NSALNMAVAVSELTNRHTRKASATVATVATLLEFATVASTTDDDLYLE 60  
Db 880 LLMADADAGENGAFSA-----AHGKDKTASVITNV--ANGAISAASDAVNGSOLF-- 927  
Qy 61 PVQRTAVVLSFRSDEKGEKEVTEDSMNGVYFEDKKVGLACTITL-----KAGDNLI 114  
Db 928 -----TTNKYIADALG--GDAEVNAD-----GRITAPTYIYANAEVNVNADALDA 970  
Qy 115 KONT-----NENTNASSFTY-----SLKKDLTDL--TSVTEKLTSFA 150  
Db 971 LDDNALLMDETANAGGAGVASHDGKASITTVANGSISSESDTDAVNGSOLFATNMALIEQ 1030  
Qy 151 NSKNVN-----ITSDTKGLNFAKKTAEITNGDTVHLNGI----- 184  
Db 1031 NTQIINQLAGNTDATTYIENGAGINVTNRNDGLAFNPNASAGVGATTAIGYVSAKGDSS 1090  
Qy 185 -----GSTLTDTLLNTGA--TIVNTNDN-----TDEKKRAASVAKD 219

```
Db 1091 VAIGGYSYSDVDTGIALGSSSVSRVIAKGRDTSITENGVIYGYDTTDELLGALISGD 1150
QY 220 -----VLNAGNNIKGVKRGKTTASDNVDFVRYDYEFELFASDTKTTTVAVESKDNGK --- 270
Db 1151 DCKYROIIN-----VADGSEAHDAVT--VRQLONAIGAVATTPKRYEFANSTEEDSLAV 1202
QY 271 -RTEVKAIGAKTSVIREK-----DGKLVTKGKRGEND-----SSTDKEGLVTAK 314
Db 1203 GTDLSLGMKAKTIVNGDKIGIGTGAYVDANALNGIAISNAQVIHNSIAIENGSTTTTG 1262
QY 315 V-----IDAVNKAGMRKTTTANGQ-----TGADKREFTVYSGTNTVPASGKGT 359
Db 1263 AOTNTAYNMADAPQNSVGEFVSADGQROITNVAAGSAD-----TDAVNV--GOLKVT 1315
QY 360 ATVSKDDGDNITVM-----YDVNVGDAL-----NVNQLONGSNNLDS 396
Db 1316 AOVSONTO--STINLDRVTNLDNRVTNIENGIGDIYTTGISTYKFTKNTDGVASAGKDS 1374
QY 397 KAVASSGKGVISGNVSPSKGM---DETVINAGNNIEITRN---GKNIDIATSMTPQPS 450
Db 1375 VAIGSGSTIAADNSVALGTSVATEENTISVGSSTNORRITVAAGKATDVAVNAOLKS 1434
QY 451 SVSLGAGADAPTLVSDDEGALNVGSKDANKPVRTNVAPVKEGDTVNAOLKVAQ--- 507
Db 1435 SEAGVRYDTRKADGSDIDYNTILGGNGG--TTRISNVSAVNNNDVYNAOLKQSVQETK 1493
QY 508 -----NLNHHIDNVDCNARAQIATATAGLVQATLPKGSMAIGGCTYRGEAGVAT 559
Db 1494 QYTDORWEMDKLSTKTESKLSGGIASAMAMTGLPOATYPGASMASTIGGTYNGESAV 1553
QY 560 GYSISIDGNNIITKGTASGNSRHFASASVGYOW 594
Db 1554 GYSWVSANGRWYKLOGSTNSOGEYSALGAGIOW 1588
```

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RESULT 8
H91188
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 11588 <HAY>
A:Cross-References: GB:BA000007; PIDN:BA837903.1; PID:q1363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 050952
C:Genetics:
A:Gene: ECS4480
```

```
Query Match 12.2%; Score 368.5; DB 2; Length 1588;
Best Local Similarity 23.0%; Pred. No. 7.4e-11;
Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;
QY 7 ITW-----NSLNLNMMVAVSELTRNHTKASATVATVATLTLFATVQASTDDDDLYLE 60
Db 880 LUMDADAGNCAFSA-----AHGKDKTASVITNV--ANCAISAASDAINGSQLY-- 927
QY 61 PVORTAVVLSFSDKEGTEKEVEDSNNGVYEDKKGVLTACTITL-----KAGDNLEKI 114
Db 928 -----TTKKYIADALG--GDAEVNAD-----GTTTAPTYITANENYNNVGDALDA 970
QY 115 KONT-----NENTNASSFTY-----SLKKDLTDL--TSVTEKLSFSA 150
Db 971 LDDNMLMDETANGGAGAYNASHDKASITTVANNGSISDSDTDAVNGSOLNATNMIMQ 1030
QY 151 NSNKVN-----ITSDTKGLNFAKKTACTAGTGTTHLNGI----- 184
```

```
Db 1031 NTQIINQLAGNTDARYIOENGAGINVRITNDGLAFENDASAGVATALIGNSVAKGDS 1090
QY 185 -----GSTLTDTLLNTGA--TTNVTNDNV-----TDEKKRAASVYD 219
Db 1091 VAIGGYSYSDVDTGIALGSSSVSRVIAKGRDTSITENGVIYGYDTTDELLGALISGD 1150
QY 220 -----VLNAGNNIKGVKRGKTTASDNVDFVRYDYEFELFASDTKTTTVAVESKDNGK --- 270
Db 1151 DCKYROIIN-----VADGSEAHDAVT--VRQLONAIGAVATTPKRYEFANSTEEDSLAV 1202
QY 271 -RTEVKAIGAKTSVIREK-----DGKLVTKGKRGEND-----SSTDKEGLVTAK 314
Db 1203 GTDLSLGMKAKTIVNGDKIGIGTGAYVDANALNGIAISNAQVIHNSIAIENGSTTTTG 1262
QY 315 V-----IDAVNKAGMRKTTTANGQ-----TGADKREFTVYSGTNTVPASGKGT 359
Db 1263 AOTNTAYNMADAPQNSVGEFVSADGQROITNVAAGSAD-----TDAVNV--GOLKVT 1315
QY 360 ATVSKDDGDNITVM-----YDVNVGDAL-----NVNQLONGSNNLDS 396
Db 1316 AOVSONTO--STINLDRVTNLDNRVTNIENGIGDIYTTGISTYKFTKNTDGVASAGKDS 1374
QY 397 KAVASSGKGVISGNVSPSKGM---DETVINAGNNIEITRN---GKNIDIATSMTPQPS 450
Db 1375 VAIGSGSTIAADNSVALGTSVATEENTISVGSSTNORRITVAAGKATDVAVNAOLKS 1434
QY 451 SVSLGAGADAPTLVSDDEGALNVGSKDANKPVRTNVAPVKEGDTVNAOLKVAQ--- 507
Db 1435 SEAGVRYDTRKADGSDIDYNTILGGNGG--TTRISNVSAVNNNDVYNAOLKQSVQETK 1493
QY 508 -----NLNHHIDNVDCNARAQIATATAGLVQATLPKGSMAIGGCTYRGEAGVAT 559
Db 1494 QYTDORWEMDKLSTKTESKLSGGIASAMAMTGLPOATYPGASMASTIGGTYNGESAV 1553
QY 560 GYSISIDGNNIITKGTASGNSRHFASASVGYOW 594
Db 1554 GYSWVSANGRWYKLOGSTNSOGEYSALGAGIOW 1588
```

```
RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
Jl. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1658 <KUR>
A:Cross-References: GB:AL590842; PIDN:CAC89747.1; PID:q15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902
```

```
Query Match 11.0%; Score 331.5; DB 2; Length 658;
Best Local Similarity 25.0%; Pred. No. 1.7e-09;
Matches 132; Conservative 73; Mismatches 209; Indels 113; Gaps 21;
QY 99 LFAGTTTLKAGNLKIKONTNENTNASSFTYSLKKDLDTLTSVTEKLSFSANSKNVNT 158
Db 214 LGAGAVTQA--NSTLGAASINTVGAOSSYSAYALTAPOASVGEIGITFALGNKRT-- 269
QY 159 SDTKGLNFAKKTAEITNGTTHLNGISLTLDTLNTGATTVNTN--DNVTDEKKRAAS 216
Db 270 -----GVAAGSASSDAVNVVAQLTAVGDOVOO-----TANITSIGRVTTIE---GS 313
```

```

0Y 217 VKDVLNAGNMIKVKPPTTASDNVDFTVYDTEFLSADTKTTTVNEESKGNKRT---- 272
Db 314 MASIANGG-CVKTFHANSTPDVY-----ASGTNSVAIGPASLASGNALASG 360
0Y 273 --EVKIGAKTSVIKEDGKLVTKGDKGENDSSTDKEGELVTAKEYIDAVNKKAGMRKTTT 330
Db 361 AGAVAIIG--DGAASAADGSVAIGGGSGDN-----GRGV--ENYIGKYSNA-----SMT 404
0Y 331 ANGQTQADKFEVYVSTNTNTFASGKGTATATVSKDDOGNTIYMYDVNVGDALNVLNOLNS 390
Db 405 SSG-- --TVSVGNTAT-- --GETRTVSVNADG-- --LQATDAVNLRLDLDG-- 442
0Y 391 GWNLDKAVAGSSGKVIISGVNPSFKKMDFTVINAGNANI--EITRNGKNIDI--ATSMTP 447
Db 443 -----IAASIVYENNVSGLONGTDMFOYNNSSGLAKPSATGANSATGAGGSVAS 493
0Y 448 QFSSVSLGACADAPTLUS-----VDEGALNVGSKDANKPVRITNYAPGVKEGDVTN 498
Db 494 GNNSTPAFGSCAKAPTAANSALGANSVADBRANSVSGVSGNER--QITNVAAPATQGDVAV 551
0Y 499 VAOLKGYAQNLNHNHIDVNGNAR-----AGIQAOLITAGLVCAVLPKSKMAIG 547
Db 552 FDLKLSISNOTNMYTNYRSELPKODLRKONSVLSAGIASAMASMASTOPYTSGSSMTTIG 611
0Y 548 GGYRGEAGVAYIGVYSISDGGNWTIIKGTASGNREHFGASASVGYOW 594
Db 612 AASYROOSALSLGVSSISDSGRWVSKLOASSNTQDFFELGVGVGYOW 658

```

RESULT 10  
 G64964  
 hypothetical protein b2000 - *Escherichia coli*  
 C:Species: *Escherichia coli*  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
 C:Accession: G64964  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of *Escherichia coli* K-12.  
 A:Reference number: A64720; MUID:9742617  
 A:Accession: G64964  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1091 <BLAT>  
 A:Cross-references: GB:U0000291; GB:U000096; NID:g1788298; PIDN:AACT5061.1; PID:g1788309;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Keywords: nucleotide binding; P-loop  
 F:683-690/Region: nucleotide-binding motif A (P-loop)

[illegible]

|    |     |                                                                   |     |
|----|-----|-------------------------------------------------------------------|-----|
| OY | 278 | -AKTSVIERECKKILVTGDKDGENDSSTDEGEIV-----TAKEVIDAIVRKACMRM-----     | 326 |
| Dd | 281 | TANITVVVAAGGDQIUYHGH---ALDPTTLNGGIQIYYANGGTASDIYV-VNSDGMQIKYKNGV  | 335 |
| OY | 327 | -KTTTANGOTGOADFEETVSCTNTVFASG----KGITATYSKDPOGNITYMYDVNNGDA       | 381 |
| Dd | 336 | AGNTTIVN-QKGRLL-QVDAGGTATTNTLTKGGGALIVYSTAAFTV-----               | 375 |
| OY | 382 | LNVNOLONSGMWLDSCAVAGSSGKVISCNNVSPSKMKDETYNINAGNIIEITRNKKNDI       | 441 |
| Dd | 376 | -GINRL-----CAFSVEBKADNVV-----LEMGRIHDV                            | 403 |
| OY | 442 | ATSMPPOESSVSLGA-----GADAPLTSVDEGLANTSGDKANKPRITTNAVAPVKRGCD       | 495 |
| Dd | 404 | IITHGRTATRIRDGDTLPDRNGTGATTYSMCGVGILLDSGAAVSGTRSDKAPSISGGQ        | 463 |
| OY | 496 | VTVNAQLMGVAONLNHNHIIDNVDSNARAGIAQA IATFAGLVQAYLPQKSMAAIIGGGTYRGEA | 555 |
| Dd | 464 | ADALLMEKGSSEFTLL-----AGDPATDTT-----VNGGLETFARG                    | 497 |
| OY | 556 | GYAIGYSSIDSDDGNWIIRKTASGN                                         | 579 |
| Dd | 498 | CTLACTTTLINNGAILLTLSGKYNN                                         | 521 |

RESULT 11  
c82672  
surface-exposed outer membrane protein Xrl516 [imported] - *Xylella fastidiosa* (strain  
C:Species: *Xylella fastidiosa*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: C82672  
R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
A:Reference number: A82515; MUID:20365717  
A>Note: For a complete list of authors see reference number A59328 below  
A:Accession: C82672  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:Cross-references: GB:AF003981; GH:AE003849; NID:9106543; PIDN:AF84325.1; GSPDB:GNP8  
A:Experimental source: strain 965C  
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
B:Jones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facinolan, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Jungstetter, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Krumae, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Autores: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: Xrl516

|                       | Query Match                                                   | Similarity | Score        | DB 239; | Length | 1004;        |
|-----------------------|---------------------------------------------------------------|------------|--------------|---------|--------|--------------|
| Best Local Similarity | 22.0%;                                                        | Pred.      | No. 0.00013; |         |        |              |
| Matches               | 158; Conservative                                             | 96;        | Mismatches   | 293;    | Indels | 172; Gaps 33 |
| QY                    | 2 NKIYRIINSAIANAWAVASELITRN-----HTKASATVATAVLTLFEATVOASTPT    | 52         |              |         |        |              |
| Db                    | 4 NOIYRKFMULSIGSWSVASHMTINDGCCDYLHSHGVRRKRSLAIGALTYSVTHAQSVK  | 63         |              |         |        |              |
| QY                    | 53 DDDDLLELPVORTA---VVISFRDSKEGTGGEKEVEDS-----NMGV-----       | 91         |              |         |        |              |
| Db                    | 64 -----SPAMTAKCVVAHYADSOYNRPADRPLPTDGSELMTIHMLDMKKFPECGNNSTA | 116        |              |         |        |              |

```

0Y 92 --YFPKKNVLTAAGTITLTAAGNLKIKONTN-----EWTNASSFTY-----SLKDKLTD 137
Db 117 ICFEFKAPAPNA-----IALGYNSSYTQSANNGVALGNSJTYGYNVALGASMASELNV 172
0Y 138 LTSVGETKLSFSANSKNVNTSDTKGLNFAKKTAEETNGDITJHLNGISGTLTDLTLMTGA 197
Db 173 ISVGGGDVGTGPAYRRIYV--GDGIGNNDVANKSQLGD--VYASVNDVAASXTIAL----- 226
0Y 198 TTNVTNDVNTDDEKKRAASVDVNLACNNITGKPGCTIASDNVDFVRYDYVEFLSADT- 256
Db 227 TNOVTGSSVA-----SASGKESTAIGSGAQAADVNTVAFGRAIANAVG--ASALGFDSH 279
0Y 257 ----KTTIVNESKD-----NGKREYVIGAKTSYIKKDKKILYTKRD-- 295
Db 280 AKGINSTIVTGHQSVSLGOGGVSLGTNSFVGESENGLALGNSJLVLLQGVDSVALGSGSM 339
0Y 296 -KGENDSSTDKEGL--VTAKEVI-----DAVNACAGRMKTTTANGOTGADKPEET 343
Db 340 ASEPRVSVSGGDGRGPAVRRIYVGDGICINNDVANKSQLDGYTASVNDVVAASVKNTAG 399
0Y 344 V--TSGTNTVTAAGCKGTTAT--VSKDDOGNITVMTDVNVGDALNVNQLONSGMND----- 395
Db 400 AIOLITGSGVASVSGDDSTAAAGASQAQAADSSIA-----LGARSRAINAIGSSALGDVGHALG 455
0Y 396 --SKRAVASSSGKVIISGNVSPSKGKMDIEYVNIACNNIETTKGNKNIIDATISMTQFSSVS 453
Db 456 ANSTLALGGOSTPAISEGGSILG---YNSFVGOSATNGIALGNS-----AIVSGVNSVA 504
0Y 454 LGAGADAPTLVSDEGALNVGSKD--ANKPV--RITNVPAVPEKEGDPVTVAOLDKGAQNLN 510
Db 505 LGAGSVASBELNV-----ISVGGGDVGTGPAYRRIYVNDGDIIGNNDVANKSQLDGYTASVN 559
0Y 511 N---HIDNVGNGAR--AGIAQAT--ATAGLVOAYLFGKSMMAIG----- 547
Db 560 DVAAASVKKIVTQITGSGVASAIGKIDSTAMGASQAQAADSSVALGTRATANAIGSSVLG 619
0Y 548 -----GTYRGAGVAGIYSSISDGCNNIIR-----GTASGNSRBFHGA--SASVGY 592
Db 620 VDSRARGINSTALGHOSNAIGDGVSLGFSFNVRGSEGHGVALGIDAVVSCRDKSTALCY 678

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RESULT 12
A:14177
190K surface antigen precursor - Rickettsia rickettsii
C:Species: Rickettsia rickettsii
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999
C:Accession: A41477
R:Anderson, B. E.; McDonald, G. A.; Jones, D. C.; Regnery, R. L.
Infect. Immun. 58, 2760-2769, 1990
A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, ne
A:Reference number: A41477; MUID:90354033
A:Accession: A41477
A:Molecule type: DNA
A:Residues: 1-2249 <AND>
A:Cross-references: CB:M1227; MID:g152465; PID:AAA26380.1; PID:g152466
A>Note: The authors translated the codon GAT for residue 430 as Gly, and CAA for residue
C:Keywords: surface antigen; tandem repeat
F:1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>

Query Match 7.4% Score 224; DB 2; Length 2249;
Best Local Similarity 24.2%, Pred. No. 0.0021;
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

QY 13 LNAWVAEELFPN--HTKRASATVATLTLPTVQASTDDDDL-----YLEPQRT 65
| | : : : : : : : | | | | : : : : : | | |
Db 640 LNLGALSOVGDIGENTSLATISVAGTATLGGAVIKATTTKTTNNAVSAVKFNPPVVT 699

QY 66 AVVLFSRSDKEG---TGEKEVTEDSNMGVYEDKKGVLT---AGTITLKAGDNLKIKON 117
| : : : | | | | | | : : : : : | | |
Db 700 GAlDSTGNANNGIYVFTGNSVYTGDIG-----NTNALATVNWAGATATL---GGAVIKAT 751

QY 118 TNENTMASSFTYSLKKDLTLDSVGETKLSFSAANSKNYNTSDTKGLNFAKTAETNGDT 177

```

[illegible]

```

RESULT      13
H83135
Probable adhesis PA04082 [imported] - Pseudomonas aeruginosa (strain PA01)
C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: H83135
R.Stover, C.K.; Plam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A.Reference number: AB2950; MUID:2043737
A.Accession: H83135
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-1018 <SNO>
A.Cross-references: GB:AE004824; GB:AE004091; NID:9950277; PIDN:AAG07469.1; GSPDB:GN
C.Experimental source: Strain PA01
C.Genetics:
A.Gene: PA04082

Query Match          7.4% Score 222; DB 2; Length 1018;
Best Local Similarity 22.5%; Pred. No. 0.00097;
Matches 148; Conservative 82; Mismatches 233; Indels 196; Gaps 28;

QY      1 MNKRIIRIWSNALNWAVASELITRNHTKRASATATATATLATILFAVQAOSTDDDDLYLE 60
        |||::||: | ||: | | | : | | | |
DB       1 MNKCALVMWNSQGCMWNVSEGSRRGRPKAPAKAAIASVLALLGATALAPA-----YAL 54

QY      61 PQQRATVVLSPRSDKEGGEKEVEDSNMGGYVPFKGVLTAGCTITLKAQNDLKIKONTNE 120
        |||::||: | ||: | | | : | | | |
DB       55 PGGGIV-----GGANGELTHLSGGLNSLVNQKVKK 85

```



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OY 121 -NTNASEFTSLKKDLDTDLTSGTEKLSF-----SANSNKVITSDPKGLFEAKTLETNDG 176
Db 86 LIAMWDEFSVA-----AGERVITFNPQSSSIALNRVIGTKASDIQGR-IDANQ 133
OY 177 T-TYHLNGISGTLDTLTLTGATTNV-----TNDNVYDDE-----KKRAASYKDVLN 222
Db 134 VELNPNRGV-----LEGRGAQVNNVGGVLAASLDLTDLDEFNGNSRRYRFTGPSTNGVILN 186
OY 223 AGMNIKVCYKPGTFA-----SDNVDFVRYDYVEFLSADAKRTTIVNYESKDNCKPFEVIG 277
Db 187 HGCALITAEEGSIALLCGAQVDNKGVTYLAQMGVGLGASDILL-----NPDGKKLLDIRVD 242
OY 278 AKTSVIEKQDKLVYTKGDKGENSDTJGEGVL--TAKEVIDAVNKKAGMRKTTTANGQ 334
Db 243 AGVANALASNGGL-----KADGGVFLMAARTALNLTIVNSOGALTEARSLRGK 292
OY 335 TGO-----ADKFEFTVSGTNVTFASGKGTATVSKDDCGNTIVMYDVVAGALVWNLQ 388
Db 293 NGRVYLDGGPDKVMVGGALSANLNGPHGIVTEYRGA-----VEVALCTQNTLTA 345
OY 389 NSGNN-----LDSKAVAGSSGKVI-----SGNVS--PSKG--KMETVWIN 425
Db 346 SNGLNGTWIKIADKIDVPSAVSDGYVHADTLRSNLASTNIELVSTKQDLDLDSGVMA 405
OY 426 AGNNI-----EITRNRCKNIDIASMTPOSSVSLGAGADAPILSLVDDGALNVGSK--- 476
Db 406 SGNRLGAGSADLTLLNR-----LNASGAKAGLEIKAGALIDINDKIVL 449
OY 477 -----DANKFVRL-----TNVAPGVKBEQDYTNVNOALGVQVNNLNHID 514
Db 450 GGAGSALAMLDGEGHRYNGTASVSLAGANTVYSGGYTTVVQNLOAIKRNKNDG-LY 508
OY 515 NVNDNARAGIAQIATATAGLYQVAILPGKSMATIG--CYTRGE--AGYALIGVSSIDSG 568
Db 509 VLAGGILLAGSYCTA-----LQSDIGAPGVSGTLDGIGNSIGMLSTSNRG 554

```

RESULT 14  
A:Accession: A43855  
high-molecular-weight surface-exposed protein HKM1 - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A43855  
R:Barenkamp, S.-J.; Leininger, E.  
Infect. Immun. 60, 1302-1313, 1992  
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nonypeable Haemophilus pertussis.  
A:Reference number: A43855; MUID:92192797  
A:Accession: A43855  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1536 <BAR>  
A:Cross-references: GB:U08876; GB:M84616; NID:g475770; PIRN:AAA20527.1; PID:g475771  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)

Query March 7.3% Score 220; DB 2; Length 1536;  
Best Local Similarity 22.7%; Pred No. 0.0021;  
Matches 130; Conservative .88; Mismatches 210; Indels 144; Gaps 30;

QY 98 VLTACTITLKAGDNLKIKONTNENTNASSFTYSLEKKDLT-----DLTSV---GTEKLSE 148  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db YINSKYFNVSSTSSLRFTSGSTKG----FSIEEKDLNTMGGITLLQVEGTGMIG 820

OY 149 SANSKRVIVITSPTKLNPAKTTA--ETNGDTVLHLG---IGSLT-----TDPL 192  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 821 KGIYAKKNITEGGINITEGSRKAVTEIEBVTINNANVTLLIGSDFDHQKEPLTIKKDI 880

OY 193 INTGATG---INTN--DNVTDEKKRAASVKVLNAGNIKV-----KPGTT 235  
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 881 INSGMLTMAGNIVYNLAGNLTVESN---ANFKAITPTFPWGVGLFDNKGSNSIATGGAR 937

QY 236 ASD-----WVDPRYDYEFELFADPTKTTVYVESKONGKRTVEIGAKTSVIREK 286  
Db 938 FKIDNSKNLSITTTNSSSYIRKTIISNTLNKMGDLNITNE--GSDBEQIGDVS---QK 992  
QY 287 DGKLVYCKDK-----GENDSSTDKGEGLYTAK---EVIDAANKAGRMK 328  
Db 993 EGNLTJISDKINITKQITKAGDVGENSDPTANNANLITKRELKLQDNLINGENKAE 10522  
QY 329 TTAN-----GQTGAADKFEYVTSIN---VTFASGKTATFVKDDQGNITVYVDV 378  
Db 1053 ITAADGSDLTIGMTNSAD-----GTNAKKYTFQOVKQSKISA---DGHVYTLISKVET 1102  
QY 379 GDALNVNQ-----LQNSGMWLDNSKRAVAGSSGKVIISGNVPSFKMDETVINAGNNIETLRN 435  
Db 1103 SGNNSNTEFSDSNMAGLTIDAKV-----TVNNNTISRK-----AVSISATSGEITTK 1151  
QY 436 GKNIADIAT--SMTPOFSSVSLAGADAPLTVD--DEGALNVGSKDANKPVRIITNVABV 491  
Db 1152 GTTINATGTAVGVELTAQGTGSLIGIESSGCVLTLTEGALAIVANSIGN-----TVVYTA 1205  
QY 492 KEGDYVNAV--QLKV-AQNLNHNHDVDCNARAGIAQAIATAGVQATLPEKSSMAIIG 548  
Db 1206 NSGALTITLAASTIKGTESVYTSQSOSGDIGTISGGEVYKATRESLTT-----QNSNKIKA 1260  
QY 549 GTYNGEAGVAGVSSISDGMNITKTSAGNS 580  
Db 1261 TT--GEANVTSAITGIG-----GTISGNT 1282

RESULT 15

adhesin AIDA-I precursor - Escherichia coli plasmid pIB6  
S28634

C:Species: Escherichia coli  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Oct-1999  
C:Accession: S28634; S22680; S28881; S72657  
R:Benz, I.  
submitted to the EMBL Data Library, March 1992

A:Reference number: S28634

A:Accession: S28634

A:Molecule type: DNA

A:Residues: 1-1286 <BEN>

A:Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA6156.1; PID:g42255  
R:Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 6, 1539-1546, 1992

A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Esch.  
A:Reference number: S22680; MUID:92326638

A:Accession: S22680

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 839-1286 <BE2>

A:Cross-references: EMBL:X65022

A:Experimental source: strain 2787

A:Accession: S28881

A:Molecule type: protein

A:Residues: 50-56 <BE3>

A:Experimental source: strain 2787  
R:Suhr, M.; Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 22, 31-42, 1996

A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the outflow  
A:Reference number: S72657; MUID:97055419

A:Accession: S72657

A:Molecule type: protein

A:Residues: 847-856 <SUH>

A:Experimental source: DAEC strain 2787

C:Genetics:

A:Genome: Plasmid pIB6

C:Keywords: membrane protein

F:1-49/Domain: signal sequence #status predicted <SIG>  
F:50-1286/Product: adhesin AIDA-I #status predicted <AMT>

|             |                                     |
|-------------|-------------------------------------|
| Query Match | 7.3%; Score 219; DB 2; Length 1286; |
|-------------|-------------------------------------|





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:29:54 ; Search time 48.34 Seconds

(without alignments)  
475.784 Million cell updates/sec

Title: US-09-771-382-4

Perfect score: 3019

Sequence: 1 MNKIRIIMNSALNMAWAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 244   | 8.1         | 1039   | 1 AG43_ECOLI | P39180 escherichia  |
| 2          | 224   | 7.4         | 2249   | 1 OMPA_RICRI | P15921 rickettsia   |
| 3          | 219   | 7.3         | 1286   | 1 AIDA_ECOLI | Q03155 escherichia  |
| 4          | 216.5 | 7.2         | 1325   | 1 YDEK_ECOLI | P32051 escherichia  |
| 5          | 204.5 | 6.8         | 1577   | 1 HLVA_PROMI | P16466 proteus mir  |
| 6          | 203   | 6.7         | 1608   | 1 HLVA_SERMA | P15320 serratia ma  |
| 7          | 198   | 6.6         | 2003   | 1 YDBA_ECOLI | P33666 escherichia  |
| 8          | 195   | 6.5         | 1654   | 1 OMPB_RICRI | Q53947 r outer mem  |
| 9          | 195   | 6.5         | 1953   | 1 BIGA_SALTY | P25927 salmonella   |
| 10         | 194.5 | 6.4         | 933    | 1 SLAP_CAMEF | P35827 campylobact  |
| 11         | 193   | 6.4         | 2021   | 1 OMPA_RICCN | Q52857 rickettsia   |
| 12         | 192.5 | 6.4         | 1645   | 1 OMPB_RICRY | P96989 r outer mem  |
| 13         | 192.5 | 6.4         | 1655   | 1 OMPB_RICCN | Q9K833 r outer mem  |
| 14         | 190   | 6.3         | 2334   | 1 WAPA_BACSU | Q07833 bacillus su  |
| 15         | 187   | 6.2         | 1569   | 1 YPTA_ECOLI | P52143 escherichia  |
| 16         | 180.5 | 6.0         | 918    | 1 YMTB_CAEEL | P34487 caenorhabdi  |
| 17         | 176   | 5.8         | 1228   | 1 SLAP_BACST | P35825 bacillus st  |
| 18         | 173   | 5.7         | 1300   | 1 I20K_RICRI | P14914 rickettsia   |
| 19         | 172.5 | 5.7         | 1567   | 1 ICEN_XANCT | P18127 xanthomonas  |
| 20         | 172.5 | 5.7         | 3591   | 1 FHAB_BORPE | P12255 bordetella   |
| 21         | 171.5 | 5.7         | 1861   | 1 APUB_THETU | P38536 t amylopull  |
| 22         | 170.5 | 5.6         | 917    | 1 HXA3_HAEIN | P45355 haemophilus  |
| 23         | 170.5 | 5.6         | 1656   | 1 OMPB_RICJA | Q06653 r outer mem  |
| 24         | 169   | 5.6         | 1770   | 1 PMPC_CHLTA | O84419 chlamydia t  |
| 25         | 167   | 5.5         | 1643   | 1 OMPB_RICPR | Q53020 r outer mem  |
| 26         | 165.5 | 5.5         | 1036   | 1 HP12_DEIRA | P13126 delonococcus |
| 27         | 165   | 5.5         | 642    | 1 FLUD_CAMEJ | Q9PHW6 campylobact  |
| 28         | 165   | 5.5         | 928    | 1 HXA2_HAEIN | P45354 haemophilus  |
| 29         | 165   | 5.5         | 928    | 1 PM10_CHLPP | Q9T065 chlamydia p  |
| 30         | 165   | 5.5         | 1007   | 1 Y741_CHLUM | Q9PJ16 chlamydia m  |
| 31         | 164.5 | 5.4         | 1025   | 1 SLAP_CAUCR | P35828 caulobacter  |
| 32         | 163.5 | 5.4         | 1276   | 1 PMPE_CHLPP | Q9Z899 chlamydia p  |
| 33         | 162.5 | 5.4         | 1167   | 1 CAGA_HELPJ | Q9Z1T1 helicobacte  |

|    |       |     |      |               |                    |
|----|-------|-----|------|---------------|--------------------|
| 34 | 161   | 5.3 | 1848 | 1 CBPA_CLOCL  | P38058 clostridium |
| 35 | 160.5 | 5.3 | 671  | 1 AAYS_ENTFA  | P37710 enterococcu |
| 36 | 160.5 | 5.3 | 1310 | 1 VAC3_HELPY  | Q48253 helicobacte |
| 37 | 160.5 | 5.3 | 2476 | 1 ATRK_MOUSE  | Q61687 mus musculu |
| 38 | 159.5 | 5.3 | 2329 | 1 YS89_CAEEL  | Q09624 caenorhabdi |
| 39 | 159   | 5.3 | 550  | 1 FLIC_SHIFTL | Q08860 shigella fl |
| 40 | 158.5 | 5.3 | 1291 | 1 VAC4_HELPY  | Q48258 helicobacte |
| 41 | 158   | 5.2 | 497  | 1 FLIC_ECOLI  | P04949 escherichia |
| 42 | 158   | 5.2 | 730  | 1 GIN3_YEAST  | P18494 saccharomyc |
| 43 | 157.5 | 5.2 | 524  | 1 P60_LISIV   | Q01837 listeria iv |
| 44 | 156.5 | 5.2 | 862  | 1 SLA2_BACAN  | P94217 bacillus an |
| 45 | 155.5 | 5.2 | 1902 | 1 PIP_LACIC   | P16271 lactococcus |

## ALIGNMENTS

RESULT 1  
ID AG43\_ECOLI STANDARD: PRT: 1039 AA.  
AC P39180; P76360; P75614; P97241; Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Flufluff protein).  
GN F1U OR B2000.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426517; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Kasai H., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
RA Sasayandaram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horichi T.;  
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ML 308-225;  
RA Henderson I.R., Owen P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN-ML 308-225;  
RX MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN-K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded

RT In the genome of Escherichia coli K-12.  
RL Electrophoresis 18:1259-1313(1997).  
RN [6]  
RP GENE NAME:  
RX MEDLINE-97257509; PubMed-9103983;  
RA Henderson I.R., Mehan M., Owen P.;  
RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
RT determines colony morphology and autoaggregation in Escherichia coli  
RT K-12."  
RT FEMS Microbiol. Lett. 149:115-120(1997).  
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY  
CC FUNCTION AS AN ADHESIN.  
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
CC CHAIN).  
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.  
CC -1- SIMILARITY: TO ADHESIN AIDA-1 AND TO BORDETELLA PERTACTIN.  
CC  
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CC  
DR EMBL; AEO00291; AAC7061.1; ALT INIT.  
DR EMBL; D90838; BAA15825.1; ALT INIT.  
DR EMBL; D90839; BAA15832.1; ALT INIT.  
DR EMBL; U24429; ABA47869.1; -.  
DR Ecogene; EGI2686; flu.  
KW Outer membrane; signal; Complete proteome.  
FT SIGNAL 1 52  
FT CHAIN 53 551  
FT CHAIN 552 1039  
FT VARIANT 2 2  
FT VARIANT 41 42  
FT VARIANT 46 46  
FT VARIANT 157 157  
FT VARIANT 188 188  
FT VARIANT 303 305  
FT VARIANT 320 320  
FT VARIANT 372 372  
FT VARIANT 493 493  
FT VARIANT 497 497  
FT VARIANT 585 585  
FT VARIANT 709 709  
FT VARIANT 721 721  
FT VARIANT 751 753  
FT VARIANT 803 803  
FT VARIANT 815 815  
FT VARIANT 824 824  
FT VARIANT 829 835  
FT VARIANT 845 847  
FT VARIANT 855 855  
FT VARIANT 888 888  
FT VARIANT 1025 1025  
FT CONFLICT 61 63  
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEEB0 CRC64;  
Query Match 8.1%; Score 244; DB 1; Length 1039;  
Best Local Similarity 22.6%; Pred. No. 4.6e-05;  
Matches 141; Conservative 64; Mismatches 215; Indels 204; Gaps 28;  
QY 1 MNKIRIIMNSALNMAVAVSELFRNHRKASAFVAVATLTLFAVQASTDDDLYLE 60  
DB 5 LNTCYRLVNMHTGAFVAVSELARARKGVAVALSLAAVSLPVLAA-----DIYVH 58  
QY 61 PVQRAVAVLSRSDEKGEKEVEDSNWGVYFDKKGVLTACTITLKAGDNLIKQNTNE 120  
DB 59 P-----GE-----TVNGGTLANHDNOIVEGTNG 82

QY 121 NTNASFYSLKDLTDLTSYTERKLSFNSANSKNVITSDTKGNFAKKAETNGDTVA 180  
DB MTISTGLEYPDNE-----ANTGGQWVDGGGTANKTTVTSG--GLQRYPGGSVS-DFVIS 135  
QY 181 LINGISL-----DTPLNTG-----ATTNTNDNVTDDEKRAASVADYNAGNI 227  
DB 136 AGG-GOSLQGRVAVNTPLNGGQWMEGAIAATGYIIND-----GMQV 176  
QY 228 KGVPRGTASNDVFEVFT-----YDFEFLSADTKTTVNVESKDNKRETVIG 277  
DB 177 --VPRGYATDTV--VNTGAGCGDAENGDTGQVGRGAVTTIN--KNGRQVRAEG 228  
QY 278 -AKTSVIEKDKLVTKGDKGENDSSTDGEGLV--TAKVIDAVKAKGRM----- 326  
DB 229 TANTTVYVAGDDQVYHGH--ALDTLLNGGYOYHNGSTADTV--VNSDMQAIKNGV 283  
QY 327 -KTTTANQGTQADKFEVYTSNTVFSG---KGTATVSKDQGNITVYMDVNVDA 381  
DB 284 AGNTTVN-QKGR-L-QVDAAGTATVTLKQGALVTSTAFVY----- 323  
QY 382 LNVNQLNSGNLSDSKAVAGSSGKVISGNVSPSKMDFTVINAGNIEITRNKNIDI 441  
DB 324 -GINRL-----GAFSVECKADNVY-----LENGRILDV 351  
QY 442 ATSMTPQFSVSLGA-----GADAPLTVDEGALNVGSKDANKPVRTVNAPEVKEGD 495  
DB 352 LTGHATATVTRVDDGTLDRNGGTATVSMNGGVLLADSGAAVSGTRSDKAFSIGGQ 411  
QY 496 VTNVAOLKGVANQNNHNDVNDGNARAGIAQIAATAGLVQAVLPKSMMAIGGCTYRGEA 555  
DB 412 ADALMLERKSSPTLN-----AGDTATDTT-----VNGGLFTARG 445  
QY 556 GVAIGYSSISDGNMIKGTASGN 579  
DB 446 GTLAGTTLLNNGAILTLGKTYNN 469  
RESULT 2  
ID OMPA\_RICRI STANDARD; PRT; 2249 AA.  
AC PLS921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
DE antigen) (ompA) (comp A).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
CX NCBI\_TaxID=783;  
RN [1]  
RE SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RT repeated, near-identical sequences."  
RL Infect. Immun. 58:2760-2769(1990).  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
CC  
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CC -----
DR EMBL: M31227; AAA26380.1; -
DR PIR: A41477; A41477.
DR InterPro: IPR003858; rompa_rompb.
DR Pfam: PF02708; rompa_rompb.1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT CHAIN 1 28
FT SIGNAL 1 28
FT DOMAIN 29 2249
FT REPEAT 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 287 358 A (TYPE I).
FT REPEAT 359 430 B (TYPE II).
FT REPEAT 431 505 C (TYPE II).
FT REPEAT 506 577 D (TYPE II).
FT REPEAT 578 652 E (TYPE II).
FT REPEAT 653 724 F (TYPE II).
FT REPEAT 725 799 G (TYPE II).
FT REPEAT 800 874 H (TYPE I).
FT REPEAT 875 949 I (TYPE I).
FT REPEAT 950 1021 J (TYPE I).
FT REPEAT 1022 1093 K (TYPE II).
FT REPEAT 1094 1165 L (TYPE II).
FT REPEAT 1166 1180 M (TYPE II).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 7.4%; Score 224; DB 1; Length 2249;
Best Local Similarity 24.2%; Pred. No. 0.0011;
Matches 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34;

OY 13 LNAWAVSELTRN--HTKRASATVATVATLLEATVQASTDDDL-----YLEPQRT 65
DB 640 LNLNGLSLQVTDIGTNSLATISVAGATATLGAVIKATTTKITNAVASAKFTNPPVYT 699
OY 66 AVVLSFRSDKEG---TGEKVEDSNMGVYFDKKGVL---AGTITLKAGDNLIKON 117
DB 700 GAIDSTGNANNGIVFTGNSVTGDI-----NTNALATVNGAGTATL---CGAVIKAT 751
OY 118 TNENNTNASSFTYSLKKDLIDLSVGEKISFSPANSKVNITSPTKLNPAKKAETNGDT 177
DB 752 TTKLTNMAASVL---TLTNAVAVLGAIDNTGTGDNVGV---LNLNGLSLQVTDG- 799
OY 178 TVHLNGLSTLDTLTNTGATNTVNDV---TDDEKRRASAKVDVNLGNMKGVKPGT 224
DB 800 -----IGTNSLATISVAGATATLGAVIKATTTKITNAVASVLTLTNAVAVLTVGAVNDT 853
OY 235 TASDNDVFRYTDVEFLSADTKTTTVNVEKSKDNGKRTVEKIGAKT-----SVIKEDKG 289
DB 854 TGGDNVGVNLNGLSLQVTDIGNT-----NSLAT--ISVAGATATLGAVIKATTTTK 904
OY 290 L-----VTGKKGENDSSTDKGEG 309
DB 905 LTNAAASVLTLTNAVAVLGAIDNTGTGDNVGVNLNGLSLQVTVG-DIGTNSLATISVAG 963
OY 310 VTA-----KEYIDAVNKGAMKTTTANGOTGQADKFEYVSGTNFASGKGTTATV 362
DB 964 GATATLGAVIKATTTKITLPAASAVKFTNPPVYVTAIDNTGNANNGI-VFTGNSVTGAV 1022
OY 363 SKDDGQNTVMTDVNGDALNVNQLNSGMNLSKAVASSGKVISGANSPSKGNDETV 422
DB 1023 -----GNTNALATVNGAGT--LVQGGVYKANTINLTJNAAVFTNPPVYVTAIDNTG 1075
OY 423 NINAG-----NNEITRNGKNIDIATSKTPQSSSVSLGAG-----ADAPLISVDDG 469
DB 1076 NANNGVFTGTSTVANGN-----TNALATVNGAGTLLQVGGVYKANTINLTJNAA 1128
OY 470 ALNVGSKDANKPRITNVAPGVKEGDTVNAQLKGAVALNHIIDVNDGNARA-----GTA 525
DB 1129 S-----AVTFTN--PVYVTAIDNTG-----NANNGIYFTGNSVTGIDGNT 1169
OY 526 QAIAT---AGL-VQAYLPGRKSMMA-----IGGCTYRDEAGVAGIY---561
DB 1170 NALATVNGAGTITGA---GSLAANNIDFGARSTLEFNGPLDGG-----GAIPIYPR 1220
```

```
OY 562 SSISDGNMTRK-----GTASGNSRGH---FGASASVG 591
DB 1221 GAIANNMNAIILNVNTKLTATSHLTIGTVAEINIGAGNLTFTIDASVG 1266

RESULT 3
AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC 003155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aida-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "Aida-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is synthesized via a precursor molecule.";
RT Mol. Microbiol. 6:1539-1546(1992).
CC - FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI TO EPITHELIAL CELLS.
CC - SUBCELLULAR LOCATION: Outer membrane.
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CC DR EMBL: X65022; CAA46156.1; -
DR PIR: S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 1286
FT PROPEP 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 7.3%; Score 219; DB 1; Length 1286;
Best Local Similarity 20.9%; Pred. No. 0.001;
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps 30;

OY 1 MNKIRIINMSALNAVAVSELTRN-----TKRASATVATA--VLATLEPATQAST 51
DB 1 MNKAYSIIMSHSRQAMIVASLARGHGVLAKTLLVLAVALSTGNAFAVNIGTVSSGG 60
OY 52 TDDDDLYLEPVQRTAVLSPRSDKEGTGEKEVEDSNMGVYFPKKGVLATGTTLKAGDN 111
DB 61 TVSSG-----ETQIYVS-----GRGNSNATVNSGCTIYVNNGGTTFATTVNSSSQN 107
OY 112 L-----KIKONTNENTNASSFTYSLK----- 132
DB 108 VGTSGATITSTVNSGIIQVRSSGCVASATNLSCGAQNI--YNLGHASNTVIFSGNGTIFS 166
OY 133 ---KDLTDLTSVGTETKLSFANSKNXVNIISDTGGLNPAKKTATETNGDTVHLN----- 182
DB 167 GGTIDSTNISSGQQRVSSGCVASNTTINS-----SGAQNILSEGAISTHISSGNGYI 221
OY 183 GIGSTLDTLNTGATNTVNDVTDDEKRRASVAVDLNAGNNIRGVKGTASDNDVF 242
DB 183 GIGSTLDTLNTGATNTVNDVTDDEKRRASVAVDLNAGNNIRGVKGTASDNDVF 242
```

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Dh 222 SAGANAEITVNSGCFORVNSG-----AVATGTVLSGG--TQVSSGGSAISrsvy 270
Qy 243 VRrTDYIEFLADPrKtTtTVNVEsDNKREvKIGATsYIKEDDKLVTKDKGErDSS 302
Dh 271 NSGVOYV-FACATVTDtTVN--SGGNONISSGIGVSEITTVNStGTONIYSG--GSALSA 324
Qy 303 TDKGEGLVTAKEVIDAVNKAQRKtTtTANG-----OTGADKREYtTSGNVTfAG-- 355
Dh 325 NIKSOT-----VNSEtAINTLVSDGQYHINNGIGLAsTtYINOGsYVNISSGtY 375
Qy 356 -----KGtTAtVSKDQGNITVMyD--VNvGD-ALNVNOLONGsWNL-----DSK 397
Dh 376 AESTIINSGGLrVrLSDIGYARGtTILNNSGRENVsNGSVYNAminTGNOIYIDSGEAT 435
Qy 398 AVAASSG--KVISONsPSPSKGMDEYtVINAGN--NIETIRNOKtN-----DIA 442
Dh 436 AIVTSGtGQRINSNGtAPVONsVYVtTVrTSSAKPFDAEYSGKQrTVYrLmGIWISnFL 495
Qy 443 TSMTPOESSVSLGADAPtLVSDDEGALN-----vG 474
Dh 496 TAVVSMFPGTSSGA-----NVNLSGRILNfAGNVYtGLINDEGRrOYVtSGATATStVG 548
Qy 475 SKDANKPVRITNVAPYKKEGDVtVNAOLKGYAQNLNHNIDNVGNARA-----GIAQAI 529
Dh 549 NNBEREYV-----LSGGITIDGTVLNSGLQAVSSG-----GKAATVINEGAQfVY 595
Qy 530 TAGLVQAVtLPKsSMALIGCGrYrREAGrVAlCYSISIDSGN 569
Dh 596 DGGOV-----tGTnIK--NGGtYrVDSQASALINtALtSSGn 629

```

| RESULT | 4                                                                     |
|--------|-----------------------------------------------------------------------|
| ID     | YDKE_ECOLI                                                            |
| AC     | P32051; P76140; p71768;                                               |
| DT     | 01-OCT-1993 (Rel. 27, Created)                                        |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)                           |
| DT     | 16-OCT-2001 (Rel. 40, Last annotation update)                         |
| DE     | Hypothetical lipoprotein ydek precursor (ORF1).                       |
| GN     | YDKE OR ORF1 OR B1510.                                                |
| OS     | Escherichia coli.                                                     |
| OC     | Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;      |
| OX     | NCBI_TaxID=562;                                                       |
| RN     | [1]                                                                   |
| RP     | SEQUENCE FROM N.A.                                                    |
| RC     | STRAIN=K12 / MG1655;                                                  |
| RX     | MEDLINE=97426617; PubMed=9278503;                                     |
| RA     | Blahtner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,   |
| RA     | Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,     |
| RA     | Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,      |
| RA     | Mau B., Shao Y.;                                                      |
| RT     | "The complete genome sequence of Escherichia coli K-12.";             |
| RL     | Science 277:1453-1474(1997).                                          |
| RN     | [2]                                                                   |
| RP     | SEQUENCE FROM N.A.                                                    |
| RC     | STRAIN=K12;                                                           |
| RX     | MEDLINE=97251357; PubMed=9097039;                                     |
| RA     | Alba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,           |
| RA     | Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,          |
| RA     | Makino K., Miki T., Mizubuchi K., Mori H., Mori T., Motomura K.,      |
| RA     | Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., |
| RA     | Sampel G., Seki Y., Sivasubram S., Tagami H., Takada J.,              |
| RA     | Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;           |
| RT     | "A 570-kb DNA sequence of the Escherichia coli K-12 genome            |
| RT     | corresponding to the 28.0-40.1 mln region on the linkage map.";       |
| RL     | DNA Res. 3:363-377(1996).                                             |
| RN     | [3]                                                                   |
| RP     | SEQUENCE OF 595-1325 FROM N.A.                                        |
| RX     | MEDLINE=94100243; PubMed=8274505;                                     |
| RA     | Catwrlight P.J., Timms M.W., Litngow T., Hoej P.B., Hoogenraad N.J.;  |
| RT     | "An Escherichia coli gene showing a potential ancestral relationship  |
| RT     | to the genes for the mitochondrial import site proteins ISP42 and     |

|    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                     |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|
| RT | MOM38.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | "                                                                                   |
| RL | Biochim.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Acta 1153:345-347(1993).                                                            |
| CC | -I-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Potential).       |
| CC | -I-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SIMILARITY: TO E.COLI YFAL.                                                         |
| CC | -I-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS ISP42 AND MOM38.     |
| CC | -I-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | CUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653. |
| CC |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                     |
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| CC |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                     |
| DR | EMBL;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AEO00248; AAC74583.1; "-                                                            |
| DR | EMBL;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | D90793; BAA15190.1; ALT_INT.                                                        |
| DR | EMBL;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | D90794; BAA15197.1; ALT_INIT.                                                       |
| DR | EMBL;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | X73295; CAA51730.1; ALT_FRAME.                                                      |
| DR | PIR;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | S34315; S34315.                                                                     |
| DR | EcoGene;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | EG11780; ydek                                                                       |
| DR | ProSITE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PS00013; PROKAR_LIPOPROTEIN_1.                                                      |
| KW | Hypothetical protein; Membrane; Lipoprotein; Signal; Complete proteome.                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                     |
| FT | SIGNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1 .. 18 POTENTIAL.                                                                  |
| FT | CHAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 19 .. 1325 HYPOTHETICAL LIPOPROTEIN YDEK.                                           |
| FT | LIPID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 19 .. 1325 N-Acyl diglyceride (POTENTIAL).                                          |
| FT | CONFLICT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 884 .. 884 M -> K (in ref. 3).                                                      |
| FT | CONFLICT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 1317 .. 1317 M -> S (in ref. 3).                                                    |
| QD | SEQUENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 1325 AA; 136514 MW; 263A066FA19AD7D CRC64;                                          |

```

Query March 7.2%: Score 216.5; DB 1; Length 1325;
Best Local Similarity 23.1%: Pred. No. 0.0014;
Matches 150; Conservative 75; Mismatches 260; Indels 165; Caps
QY 1 MNKIRIITMNSALNAMAWEVSELTNRHNRKASATVAVATLTLFATVQASTDDDDLYLE 60
Db 1 MNRIRYVIMNCTTLOVFOACSELTFRRAKRTSTVNLKRKSSGLTFRSRL----- 47
QY 61 PVQRTAVLSRSPRSEKTEGKEVREDS-----NMGVYDK--KGLVLTGTLTKLAGDNLKI 114
Db 48 ----TLGGLLALSSASGASLEVDNDITINIDDAVDAYLVGNYGTGVNLTLAGGNASL 103
QY 115 KONTNENTNASSFFYSLLKDLTDLTSY--GTEKLSFSSANSNK-VNI-TSDTKGLNFAK- 169
Db 104 ----TTITTSYIGANEDSEGVNVNLGGTWRLYDGSNNARPLNVOGSGTGLTIKQKG 156
QY 170 -----TAETNGDITVHLANGISLTITDLNTGA-----TTWTVNDVNTDDEKKRAAS 216
Db 157 HVDGYYLRLGSESTGVGTVNVNEGDSVLTLEFEGISYGTGSLNIT-----DKGYVTS 210
QY 217 VKVDYLNAGMINIKGKPGCTTASDNDVFRYDVLEFLSADTKRTTVNES-----KDNKG 270
Db 211 IVALL-----GIQASNGO-----VYVEKGEMLIKRINDS 240
QY 271 RTEVKGIAKTSVIREKKDGLVTGKOKGENDSSTDGKGLVTAKEVIDAVNKAQMRKMTT 330
Db 241 SIERQIG-----NQGTGEATIREG--GLVTAETNITIGGNATG---IGT 278
QY 331 ANGOTGADKREYTSSTNTVTFASGKGTATVSKNDDGNGITVATDVAVNGALN--VNOIQ 368
Db 279 LNVV--DQDSVITVRLRYNGYFNG--TVNISNNGLLNKKEYSLVGVQDGSHEVAVNVD 333
QY 389 NSGNL-----DKAVAGSSGKYISGNVSPSKMDEYNINAGN----- 428
Db 334 KGHNNFLTGAEAFRIYITIGADGDELAVNVSBSGKVDSSIIITAG--KMET---GNGNITVK 387
QY 429 -NIETRNKNIDIAIATSMTPQSSVSLGAGADAPTLVSDDEGALNV-----GSKDANKP 481

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Db 388 DKNSVTNLGTNLGDHGEEMINISNOGLVYVSSGSSIGYGETGVGNVSTTGGMWEYKNK 447
OY 482 VRTTNAPGVKEDVTNNVAOLKGVANLNHNIDVGNARAGIAOAIATGVALP--- 539
Db 448 VYTTIGVAGVGNLISDGG--KEVSQNIIFLGGKASIGITLNLMDATSSPDYGVINGVP 505
OY 540 GKSMAGIGGTYRGEAGYAI-----GYSSISDGGNMIKCTGASNSR 581
Db 506 GSGIVANVSGATLNTSTGTFGIGNASGKIVNISTSLMNLK--TSSTMAQ 554

RESULT 5
HYA_PROMI
ID HYA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMa.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
RT J. Bacteriol. 172:1206-1216(1990).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMa REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMa MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S. MARCESCENS HEMOLYSIN (SHLA).
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CC
CC EMBL; M30186; AAA25657.1; -
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
FT SEQUENCE 1577 AA; 165869 MW; 175975E0C924BD29 CRC64;

Query Match 6.8%; Score 204.5; DB 1: Length 1577;
Best Local Similarity 22.6%; Pred. No. 0.0066;
Matches 149; Conservative 76; Mismatches 257; Indels 177; Gaps 30;
OY 22 LTRNHTKRASATVATVATLTLFATVOASTTDDDDLYLEFVORTAVAVLSFRSDEKTEGK 81
Db 317 LRTTELKGNIT-----LVASSHNQIKASDLMDGITLQADLTL-----DGKQLQOK 364
OY 82 EYVEDSNW-----GYFDDKG---VITACTITL-----KAGDNLKI 114
Db 365 ETDIDNRWEYSWKRYDTKEKQIQIQISQIDARNMNTLTATKGDVTLDAAKINAGNMLAI 424
OY 115 -----KONTNENTNASFTYSLK-----DLTDLT----- 139

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Db 425 NANKDINHNGLYEKESSENGKRNHTSRLESQWSMNSHOTETLKLAKSELATAGDGLDAQ 484
OY 140 -SVGTEKLSFANSKNKYNITSDTKGLNFAKTAETNGDTTHLN-----GIGSTLDTLL 193
Db 485 GSITAGCAKLHANNENLVNNAKDNINLNQK-----TNDKRTVTDNHVMWIGGQGNKNN 540
OY 194 NTGATTVTNDNTVDEKKAASVQVNLNAGWNK-----VPGTTASNDVDFRYDT 248
Db 541 NQOQVSHAT--QLTADQDLAADNNVNTIGSOVKQGAFAVK--TTQGDVVDNALSET 596
OY 249 VEFISAD-----TKTIVNESKDKRKREKIGAKTIVIEKD-----GKLVYGDKG 297
Db 597 ISKIDERTGAPNITKSSHNKNETNKOTSTGSELISDAQLTVSGNDVNVGLSLKSDKL 656
OY 298 ENDSSTD--KGGGLVY-----AREVIDAVNAKAGRMKTTANGOTGADK 340
Db 657 GHSIAGDINVKSAQOYVKIDEXKTSIAITGHAKREVEKQYSAGFHITHHTNKNSTFTEQ 716
OY 341 FETVTSNTVTFASGKTATVS--KDDQNTIVMYDVNVDALNVQDLNDSGNLDSKA 398
Db 717 ANSTISGANVDLQANKQVTFAGSDLKTTPAGNASITGD--NVAFVSTENKQOTD--NTDPTI 773
OY 399 VAGSSGKVISGANSPPSKKDETFYNINAGNIEITRN--GKNIDATSMPTQFSSVSLGAG 457
Db 774 SGGSF---YTGVDKVSKAADFOYD--KQHTQTEVTKRKGSOTEVAGDLTITANKDLHEG 829
OY 458 A-----DAFTLSVDE-----GALNVG-----SKDNKPRV-----IT 485
Db 830 ASHHVEGRYQESGNIHLAVNDSETSKTSLNVDIVGNLDYSGVTKPVKKAIEDGVN 889
OY 486 NVAPVKEGVTVNAOLKGVANLN--HIDNVNDAKRAI-----AQALITA 531
Db 890 TTRPG--NNTDLTKRYTARAIAIANLANSLETPVGEVIGKGGSQOSQOTSDQAVST 947

RESULT 6
HYA_SERMA
ID HYA_SERMA STANDARD; PRT; 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";
RT J. Bacteriol. 170:3177-3188(1988).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: TO P. MIRABILIS HEMOLYSIN (HPMa).
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CC

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CC EMBL; M22618; AAA50323.1; -  
 DR PIR; A28182; A28182.  
 KW Hemolysis; Toxin; Outer membrane; Signal.  
 FT SIGNAL 1 30  
 CHAIN 31 1608  
 SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.7%; Score 203; DB 1; Length 1608;  
 Best Local Similarity 22.9%; Pred. No. 0.008;  
 Matches 156; Conservative 82; Mismatches 259; Indels 184; Gaps 33;

9 W-NSALNMAVAVSELTNRH--TKRASATVAVATLTLFAVQAS--TTDDDDLYLEPV 62  
 471 WNSDESESLKASELSRSEGLTLKAGRNVSQ-----GAKVHAORDLTIDADNOIQGV 524  
 63 ORTAVVLSFRSKEGTGEKEVTEDESNMGVYFDPKGVLTAGITTLKAGNLIKQNTNENT 122  
 525 OKTANAKAVRDK-----TSW-----GIGGDN-KNNSRREIS 558  
 123 NASSFTYSLKDLTDLTSGTEKLSFSANSNKVNT-SDTKGLNPAKKTAEFTNGDTVHL 181  
 559 HAS-----ELTSGGTLRLN---GQCVTTTSGKARQKGEVTA-THGGLRID- 602  
 182 NGISFTLDTLTLTGATNTVNDVNTDEKRRASVKDVLNAGNLIKGVKPGTTASDNDV 241  
 603 NALSTTVDKIDARTGATNITSSSHKADNSYQSTASEL-----KSDTNLT 648  
 242 FVRTDYVEF-----LSADTKTTVNV-----ESKDNQ 269  
 649 LVSHKADAVIGSQVASGSELVESKSTGNINVKAAERQONIDEQKALTALVNGYAKKAGKQ 708  
 270 KTEVKI-----GAKTSYIKKEDKLYTG--KDKGENDS-----TDKGEGLYTAKEV 315  
 709 YRAGLRIRHTRSEKTTTRENSSASSLSCGSYKLAKEKDYITPSGLVADKDAVSNGKV 768  
 316 --IDAVNAGWBMKTTTANG---QTQADKFEPTVSGTNVTFASCKGTTATVSK----- 364  
 769 SFLADDKXTASTEQTKIGCGFYTGIDK---LGSVEAGEVNNK--TQAGSKAKITSGS 824  
 365 DDQGITVYVYDYNVDALNVLNOLNSGNLDSKAVAGSGKATISGNSPFSKRMDEYNI 424  
 825 DVKGNLT---INARDKLTQOGAQSISGAVQENAGVDHLAAADTASTTTTKTIVGNI 880  
 425 NAGNNIEITRNKNIDITFMTPOSSVSLGADAPLTLYVDEG-----ALNWSKD 477  
 881 -----GANVDYSAVTRPVERAVGKAKKLDL-TGVINDIGIGCAPNGLDIGAOG 928  
 478 ANKPVRIITN--VAPVKEGDV-----TNVAQLKGVQONTLNHIDNVDGNARA 522  
 929 GSSEKSSSSQAVVSSVQAGSIDINAKGEVRDQTOYQASKG-AVNLTRDSHRSEAAANR 987  
 523 GIAQALATAGL--VOAYLPKSKMAIG---GGTYRGEAGTAIGTSSISDGNW----- 570  
 988 QDEQSRDRGRSGAVVYTTTGSIDLTVADKGEGTGRSNNSSAQAVTGSIDANGINVVK 1047  
 571 ---IKGTASGNSRGHFGASA 588  
 1048 KDAITQGTALNGRGKTA VNA 1068

RESULT 7  
 YDBA\_ECOLI STANDARD. PRT: 2003 AA  
 AC P33666; P76087; P76088; P76856; P76857; P76859;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein ydba.  
 GN YDBA OR B1401/B1405.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655.  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12".  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sanpei G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map".  
 RL DNA Res. 3:363-377(1996).  
 RN [3]  
 RP SEQUENCE OF 464-2003 FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=92190338; PubMed=1665988;  
 RA Moszer I., Glaser P., Danchin A.;  
 RT "Multiple IS insertion sequences near the replication terminus in  
 Escherichia coli K-12".  
 RL Biochimie 73:1361-1374(1991).  
 CC -I- SIMILARITY: TO S.TYPHIMURUM ORF NEAR CYSG (AC P25928).  
 CC -I- CAUTION: THIS IS A CONCEPTEUAL TRANSLATION: THE GENE CODING FOR  
 THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2/IS30C ELEMENT  
 BETWEEN AMINO ACIDS 839 AND 840.  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL; AE000237; AAC74483.1; ALT\_SEQ.  
 DR EMBL; AE000237; AAC74487.1; ALT\_SEQ.  
 DR EMBL; D90778; BAA15009.1; ALT\_SEQ.  
 DR EMBL; D90778; BAA18880.1; ALT\_SEQ.  
 DR EMBL; D90779; BAA18881.1; ALT\_SEQ.  
 DR EMBL; X62680; -; NOT\_ANNOTATED\_CDS.  
 DR Ecogene: EG11307; ydba.  
 KM Hypothetical protein: Complete proteome.  
 FT CONFLICT 489 489 I -> V (IN REF. 2).  
 FT CONFLICT 495 495 I -> V (IN REF. 2).  
 FT SEQUENCE 2003 AA; 205949 MW; B83A12C8B5320EE CRC64;

Query Match 6.6%; Score 198; DB 1; Length 2003;  
 Best Local Similarity 24.7%; Pred. No. 0.018;  
 Matches 151; Conservative 74; Mismatches 229; Indels 158; Gaps 35;

32 ATVAVATLTLTFAVQASTTDD-----DDLLEPQRTAVVLSFRS 73  
 73 STGAAALITAL--AVVELNDDDDHHRRNSPLPTPPDESDDTVPTPPGDELTIPDP 130  
 74 DKEGTGEKEVTEDESNMGVYFDPK-KGVLA-----GTITLAKGDNLIKQNTNENT 120  
 131 DDTPTTPKPVSPFNN--VILDKTEKTLTRDSVFTYENADGTISLQDSNGRKATINIMQ 188  
 121 NTNASSFTYSLKDLTDLTSGTEKLSFSANSNKVNTSDTKGLNPAKKTAEFTNGDTT-V 179



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Db 189 IDEANN-TVALE---GVSADGATKWQYNHNGELV-ITGDNATVNNNGKTTVDKSDGTG 242
QY 180 HLNG-IGSLTDLTLMT---GATTNTNDNVYDDEKKRAASVDYLNAGNKGVPRTT 235
Db 243 EINGNNGKVIQDDLDVSGGGHIDITGDSATVD-NKGTMTVDPSMGQIDGDK-AIV 300
QY 236 ASDNVDFVRYDVEFLADTKTTTVNVESKONGK---PTEVIGAKTSVIREKDKL-V 291
Db 301 NNGESTITNGGIGTQINGDDATANNNGKTTVDKSDGTGTEIN-GNNGKVI-QDDLDV 357
QY 292 TGRDKG---ENDSST--DKGEGLVTAKEYID-----AVNKGMRMKTITANGOTGA 338
Db 358 SGGGHGIDITGDSATVDNKGTMVTPDESIGIQVDGDAVNNNEG---ESATINNGGTG-- 412
QY 339 DKFETSTGNTYFASGKTTATVSKDDOONTITVMDVNVGALNNQNLONGSNMNDSKA 398
Db 413 ---TQINDDDAT-ANNNGKTTVDKSDGTG-----E 439
QY 399 VAGSSGKVI-SGNVSPSKMDETVNIAGNNIEITRNKGNIDIASMT---PQSSSVSL 454
Db 440 IAGNNGKVIQDDLDVSGG-----GHGIDITGDSATVDNKGTMVTPDE---SI 485
QY 455 GAGADAPTLSDVEGALNVGSKDANKPVRTTNPAPGVEKEDVTNNVQNLKGAONLNNH-I 513
Db 486 GIQIDGDAIVNNEGEST-----ITNGGTG-----TQINGNDATANNNGSK 525
QY 514 DNVDGNARAGIAQAIATAGIQAIVLPKSMMAIGGCTGEGEAGYAIIGSSIDSGMWIIR 573
Db 526 TYVDGDSGTG-TRIAIGNIGIVN--LDG-SLTVTG-----AHGVENIGDNGTVNNK 572
QY 574 GTASGNSRGHFG 585
Db 573 GDIVSDTGSIG 584

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RESULT 8
OMP_RICRI ID OMP_RICRI STANDARD: PRT: 1654 AA.
AC 053047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (cell surface antigen 5) (Sec5) (rmpB)
DE (rmp B) [contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.

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CC -I- SIMILARITY: BELONGS TO THE RICKETTSIA OMPA/OMPB FAMILY.
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CC
DR EMBL: X16353; CAA34403.1;
DR InterPro: IPR003858; ROMP.A.OMP.B.
DR Pfam: PF02708; ROMP.A.OMP.B.1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT DOMAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.5%; Score 195; DB 1; Length 1654;
Best Local Similarity 21.3%; Pred. No. 0.02;
Matches 165; Conservative 93; Mismatches 273; Indels 244; Gaps 36;

QY 30 ASATVATAVLATLLPFTVQ-----ASTDDDLVLEPVQRAVVLSPRSDEKGTGEKE 82
Db 20 STATVASFAGSMGAIQONRTTNGAATVVDAGFQPTAAPNVGALNA-----V 71
QY 83 VTEDSNMGVYFDEK---KGLV--TAGTITLAKGDNLIKONTNENTNASSFTYSLK--K 133
Db 72 ITANANNNGINFNTPAGSFNLLNTANNLLAVTSEDTLTGFIINNVHNAISFULTNAGK 131
QY 134 DLFTDLTSVTEKLSFSANSKVI-----TSDRKGL-----NFAK 168
Db 132 TLF-ITGQGVTVNAQAATKKAQNVVVOFNNGAIDNNDLKVGRIIDGAPASTVLVNLAN 190
QY 169 KTAETN---GDPTVHLNGISLTLDP-----LLNT-----195
Db 191 PTTQKAPLLIGDNAVIANGVNGLVNTNGFTIQVSNKSEFAVKAINIADGGCITFENDANN 250
QY 196 -----GATTNVINDNTVD-----EKRRASVYKDLNA-GMNIKGVKPTGTDNDV 241
Db 251 ANTLNLAQAGTTINFTGDTGTGLVLSKHAATNFTITSLGSLKGVIEFTVVA----- 306
QY 242 EVRYDVEFLADTKTTTVN-----VESKONGK-----270
Db 307 -VDGOLTANAGANAVIGTNNAGRAAGFVAVYDNGKVAITDQVYAKDVVIOANATGQ 365
QY 271 ---RTEVKIGAK-TSVIKKEDGLVNGKDESSSTDKGEGLVTAKEYIDAV----- 319
Db 366 VNRHIVDVGADGTTAFKTAASKVTTITD--SNFGNTDFG-NLAAQIKVFNALTLGNTF 422
QY 320 -----NKAGMRMKTITANG--QTGQADKFEYVTSCTNTYFASGKGT-----TATVS 363
Db 423 GDASNPGNTNG--VTFPDAGTLESASADANVAVTNNTITAEASGAGVVLGSHAEELR 480
QY 364 KDDOQNTTMYDVNVGDALN--VNQNLONGSNMNDSKRAVAGSSGKVIISGNVSPSKGKA--- 418
Db 481 LGNAGSIFKLAD--GTVINGKVNTALVGCALAAGTITLDGSAITLDGNGAGNALQ 537
QY 419 -----DETVINNA-GNNIEITRNKNI-----DIATSMTPQFS 450
Db 538 RITLANDAKKTLTLCGANITIGAGGTTIDLOANGGTTIKLTSTQNTIVVDFDLATA-TDQ 596
QY 451 VSLSGADAPTLSDVE-----GALNVGSKD---ANKPYRTNVVAPGVKEDV 496
Db 597 VVASSLTNQTLITLNGIKTIGANNKTLGQFNIGSSKTVLSNGVAINELVIG-NDGAV 655
QY 497 -----TNVAQLGVAONLNNHIDNVGNARAGIAQAIATAGIQAIVLPK-----S 542
Db 656 QFAHRYLLRTTNAGGQGIIFNPVNVNNGTTLAAGTNLGSATNPPLAEINFGSGVAVDP 715
QY 543 MMAIGGTYGEGAGYA-----IGYSSISDGGNMIINGTASGNSRGHFGASA 588

```

Db 716 VLNVEGVNL---YATNITTTDANVGSFVFNAGTNTIVSGVGGQGNKFTVA 766

RESULT 9

BIGAL\_SALTY STANDARD: PRT: 1953 AA.

AC P25927; P25928; Q9XC03;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Putative surface-exposed virulence protein biga precursor.

CM BIGA OR STM3478.

OS Salmoneilla typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OX NCBI\_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=14028;

RA Stojilkovic I., Valentine P., Heffron F.;

RT "Salmoneilla typhimurium rhs homolog";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmoneilla enterica serovar Typhimurium

RT LT2.";

RL Nature 413:852-856(2001).

RN [3]

RP SEQUENCE OF 1-765 FROM N.A.

RC STRAIN=LT2;

RX MEDLINE=91100301; PubMed=1987123;

RA Wu J.Y., Siegel L.M., Kredich N.M.;

RT "High-level expression of Escherichia coli NADPH-sulfite reductase:

RT requirement for a cloned cygS plasmid to overcome limiting shiroheme

RT cofactor.";

RL J. Bacteriol. 173:325-333(1991).

CC -I- CAUTION: Ref.3 sequence differs from that shown due to frameshifts

CC in positions 414 and 732.

CC -----

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

DR EMBL: AF133696; AAD39458.1; -

DR EMBL: AE008859; AAL22340.1; -

DR EMBL: M64606; AAA27042.1; ALT\_FRAME.

DR EMBL: M64606; AAA27043.1; ALT\_FRAME.

DR PIR: C39200; C39200.

DR PIR: D39200; D39200.

DR StyGene; SG10437; biga.

DR Virulence; Repeat; Signal; Complete proteome.

FW SIGNAL 1 27 POTENTIAL.

FT CHAIN 28 1953 PUTATIVE SURFACE-EXPOSED VIRULENCE

FT DOMAIN 101 252 PROTEIN BIGA.

FT REPEAT 101 103 15 X 11 AA TANDEM REPEATS.

FT REPEAT 104 113 1 (INCOMPLETE).

FT REPEAT 114 122 2 (INCOMPLETE).

FT REPEAT 123 133 3 (INCOMPLETE).

FT REPEAT 134 144 4.

FT REPEAT 145 155 5.

FT REPEAT 145 155 6.

FT REPEAT 156 166 7.

FT REPEAT 167 177 8.

FT REPEAT 178 188 9.

FT REPEAT 189 199 10.

FT REPEAT 200 210 11.

FT REPEAT 211 221 12.

FT REPEAT 222 232 13.

FT REPEAT 233 243 14.

FT REPEAT 244 252 15 (INCOMPLETE).

FT CONFLICT 207 207 D -> DRGDDVTPDD (IN REF. 1).

FT CONFLICT 514 514 A -> R (IN REF. 3).

FT CONFLICT 1698 1698 D -> N (IN REF. 1).

FT CONFLICT 1795 1798 OYLE -> T (IN REF. 1).

FT CONFLICT 1836 1837 SA -> T (IN REF. 1).

SQ SEQUENCE 1953 AA; 200150 MW; 611B3FLC954D91AE CRC64;

Query Match 6.5%; Score 195; DB 1; Length 1953;

Best Local Similarity 21.7%; Pred. No. 0.025;

Matches 141; Conservative 81; Mismatches 232; Indels 196; Gaps 33;

QY 41 TELFATVASTDDDDIVLEPYQRTAVILS-FRSDKEGGEKEYE----- 85

Db 347 TVISGDDQAHNS-DRGMDISGODRTGVIISGDRVTNLTGDSSTVDGATGMVYISGDGTTN 405

QY 86 -----DSNMGVYFDRKKGYLT-----ACTITLKADNLIKIKONTNENTNASF 127

Db 406 TISGSHVDNATGALISGCTTTFAGDIAVGGGTATIIDGNMTIK-----NTGTS-- 458

QY 128 TYSKKDLTDLTSVTEKISFANSKNVITSDTGLNFAKKTAEKNGDTYHLNGIGST 187

Db 459 -----DISGAGSTGVTDGNNAVN-----NDGDMITTDGCTGCH 493

QY 188 LT-DTL--NTGATT-----NVTNDNVTDEKKRAVSKVDLNLG-NNIKGVKPGT 234

Db 494 ITGDNVITDNGSTTVSGADATALKIEGDNL-----YINGNQITSGAAGT 541

QY 235 TA-SDNVDFVRTYDVEFLADTKTTTVNESKDNKGRTEKIGAKTSYIKERDKLYTG 293

Db 542 RIDGDADHTTNGD-----IAYDGAGSAVVIINGDMSLTQA-----GDLIV- 583

QY 294 KKGENDSSTDKBEGVLVAKVEYIDAVNKAAGRMKTTTANGCGQADKPEYTSQTNVTF- 352

Db 584 -----TDGAMGIIITVGTGENEAKN-----TGNATVRDADSVGFVVAEKKRTEK 625

QY 353 -----ASGKPTTAVSKDDGNTITVYDVNVDALNVNOLNSGMNLSKRAVAGSSGV 406

Db 626 NKGDIDVSLNGTALYS-GDMSQVTLDDINV---VSVDSEGVSSSATGVSQSDSNV 681

QY 407 -TSGNVSPS-----KGMDETVINAGNNIEITRNGK-NI---DIATSMTPQFSV 452

Db 682 DITGVNVSADYGGQDLAAGAPLFGVVGNGNVTTLNGALINDNDLSATGGQYLDVY 741

QY 453 SIGAADAPTLVSDDGALNVSKDANKFVRTINAPGVKEDYVNVQAKVQAQNLNH 512

Db 742 GLSVTGDNDVDEID--GGNI--THSEDPDGT-----ADITGISVSGNSTVTLNGH 790

QY 513 IDNVGNGNRAG-----IAOAIAATAGLV-----QATLP-----GKSMAIGGTYR 552

Db 791 -STIDNTVYGGHVVLARKNNGSLILGDDSVYDVNVSIIPGYTTYNAALMADEGTSI 849

QY 553 GEAG-----YAI-----GYSSISDGMWIKGTASGNSRGHFGASASV 591

Db 850 ENKGDTISHGYSVIRADNGSEVNSGDILVYATSSNSEDBRAATRRASG 899

RESULT 10

SLAP\_CAME SLAP\_CAME STANDARD: PRT: 933 AA.

AC P35827;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DE S-layer protein (Surface array protein) (SAP).  
GN SAPA.  
OS Campylobacter fetus.  
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_TaxID=196;  
RN (1)  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN=84-32 / 23D;  
RA MEDLINE=90354448; PubMed=2387868;  
RA Blaser M.J., Gotschlich E.C.;  
RT "Surface array protein of Campylobacter fetus. Cloning and gene  
RT structure."  
RL J. Biol. Chem. 265:14529-14535(1990).  
RN [2]  
RP ERRATUM.  
RA MEDLINE=91035477; PubMed=2229082;  
RA Blaser M.J., Gotschlich E.C.;  
RL J. Biol. Chem. 265:19372-19372(1990).  
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
CC CRITICAL FOR VIRULENCE.  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: J05577; AAA23032.1; -  
KW Cell wall; S-layer.  
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match 6.4%; Score 194.5; DB 1; Length 933;  
Best Local Similarity 23.0%; Pred. No. 0.011;  
Matches 151; Conservative 87; Mismatches 238; Indels 181; Gaps 29;

OY 1 MKIRITINSLNLMVAASELIRHTRKASATVAT-----AVLATL 42  
DB 246 LNAITTAITRAALLTDQAEILITKRTNVENINISDLETSDFVFNQYKGFNVLGDI 305  
OY 43 L-FATVQASTDDDDLLLEPVORTAVVLSFRSDKESTGEKEVEDSMGVYFDKKGVLTA 101  
DB 306 VSFATDASKSVN-----VETTGITTAFTA--AGTGKVDV-----AGKISA 344  
OY 102 GTTITKAGDNKIKONTNENTNASSFT-YSLK---KDLTDLTSVTEKLSFSANSKV- 155  
DB 345 LVADRTSVNLATMDTITLTSAANAATSVNLKORQAKDAF--ITSAMQOK--YNNRRNRRIA 401  
OY 156 NITSPTKGINFAKKTAEFTNGDTTILN-GIGSTLDTL-----LNTGATTVNTMD 204  
DB 402 TTTSATAVENLTFFVKA-----TNVALNGMGMDLATVTTIDNALTAIDIKSASTLNLINS 456  
OY 205 NVTDE-----KKRAASVKDVIANAGMIKGVPGTTASDNVDFV---TYDVT 249  
DB 457 SVNGPKHLYSSKRRYCKFRRAAKYK--LNT-----TAADQYTLKANATDNL 504  
OY 250 EFLSADFTKTTVNVEKONGKFEVKGATSVIKEDKGLVTKDGENDSSTDKGEGL 309  
DB 505 EFDSTAKTTSVTASG-----SGKTLVKGAEVETLVNID----- 539  
OY 310 VTAKEVIDAVNKAGRMKTTTANGOTGADKFEYTSIGNVTFASCKGTATVSK--DDQ 367  
DB 540 TTAFNALQSV-----SFGKTGGGKF-SVKTGGDKIEFVGTTLLEGSVIAD 587  
OY 368 GNITVAYDVNVDALNVNOLONGMNLDSKAVAG---SSGKVISGNVSPSKGMDETVNI 424  
DB 588 GNDITAKMSAALTSAFTMIKINIEVAISDAYATADLSSAKRNSYITTTKEADDTTLTI 647

OY 425 MAGNIEITRNKNIDIAISMTPOFESSYLAGADAPTLSDYDEGALVNSKQDANKPVRI 484  
DB 648 NKDQVY-----NFTAADGSVKLTIVKLN--DVTALMIYKVLDAAD----- 690  
OY 485 TNVAPGVEKEDVYTNVQALGVAQNLNHNIDVNGNARAGIAQAIATAGVQAVLPKSKM 544  
DB 691 TTNALCTAADKALV-----IDTGIEITLNTSLVYKATSETTANVNNKLTPTVTSI 741  
OY 545 AIGG-----GTYRG-----EAGYALGYSISDGMWIKGTASGNS 580  
DB 742 IIDGMQITLGHAGTACTDYSKVSMIDASALKAGLTFDASAITLGANATIKGSGGADS 798

RESULT 11  
OMPA\_RICCN  
ID OMPA\_RICCN STANDARD; PRT; 2021 AA.  
AC 052657; P95591; P95592; P95593; P95594; 052667; 052668; 052669;  
AC 052670; 052674;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
DE antigen) (rompA) (romp A).  
GN OMPA OR RC1273.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=94171067; PubMed=8125327;  
RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia  
RT conorii (Malish 7 strain).";  
RL gene 140:115-119(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RX MEDLINE=97015921; PubMed=8662558;  
RA Roux V., Fournier P.E., Raoult D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and  
RT analysis of restriction fragment length polymorphism of PCR-amplified  
RT DNA of the gene encoding the protein rompA.";  
RL J. Clin. Microbiol. 34:2058-2065(1996).  
RN [4]  
RP SEQUENCE OF 953-2012 FROM N.A.  
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;  
RA Raoult D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study  
RT of the outer surface protein rompA.";  
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PTM: GLYCOSYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC -----  
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```
CC
DR EMBL; U01028; AA017405.1; -
DR EMBL; AE008674; AAL03811.1; -
DR EMBL; U03794; AAB49549.1; -
DR EMBL; U03798; AAB49550.1; -
DR EMBL; U04524; AAB49551.1; -
DR EMBL; U04524; AAB49556.1; -
DR EMBL; U04618; AAB49563.1; -
DR EMBL; U03440; AAC35176.1; -
DR EMBL; U03443; AAC35179.1; -
DR EMBL; U03448; AAC35184.1; -
DR EMBL; U03453; AAC35189.1; -
DR InterPro; IPR003858; rompa_rompb.
DR Pfam; PF02708; rompa_rompb; 1.
KM Antigen; Repeat; Signal; Cell wall; s-layer; glycoprotein;
KM Complete proteome.
FT SIGNAL 1 38
FT CHAIN 39 2021
FT DOMAIN 238 946
FT DOMAIN 1424 1528
FT VARIANT 60 60
FT VARIANT 76 76
FT VARIANT 86 137
FT VARIANT 126 133
FT VARIANT 953 954
FT VARIANT 1245 1245
FT VARIANT 1308 1308
FT VARIANT 1877 1877
FT VARIANT 10 10
FT CONFLICT 92 92
FT CONFLICT 126 126
FT CONFLICT 137 137
FT CONFLICT 157 157
FT CONFLICT 368 369
FT CONFLICT 374 388
FT CONFLICT 640 640
FT CONFLICT 669 669
FT CONFLICT 793 793
FT CONFLICT 803 804
FT CONFLICT 809 823
FT CONFLICT 898 898
FT CONFLICT 908 908
FT CONFLICT 985 985
FT CONFLICT 1009 1009
FT CONFLICT 1013 1013
FT CONFLICT 1182 1182
FT CONFLICT 1314 1314
FT CONFLICT 1451 1451
FT CONFLICT 1624 1624
FT CONFLICT 1628 1628
FT CONFLICT 1872 1872
FT CONFLICT 1875 1875
FT CONFLICT 1879 1879
FT CONFLICT 1936 1936
FT CONFLICT 1965 1970
FT CONFLICT 1997 1997
SQ SEQUENCE 2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;
```

Query Match 6.4%; Score 193; DB 1; Length 2021;  
Best Local Similarity 21.7%; Pred. No. 0.033;  
Matches 165; Conservative 90; Mismatches 269; Indels 238; Gaps 36;

OY 10 NSALNANWAVSELFRN-HTRKASATVAT-AVLATLFTVQASTDDDDLYLEPVQRTAV 67  
DB 487 NNGIVTFPGDSVTGNGTNTALATISVAGAKATLGAIITATTKTLTD-----NAS 538  
OY 68 VLSFRSDKEGTGEKEVEDSNNWG-VYFDKRGVLA-----GTITLKAG----DNLKI 114

```
DB 539 AVFTFPNPVYTGALDNGNANNGIYTFGDSVTGNGTNTALATISVAGAKATLGAI 598
OY 115 KONFENT-NASSEFTYSLKDLDTLSVTEKLSFSANSKNVITSPDKGNLFAKKAET 173
DB 599 KATTTKLTLDNASAVTFT-----NPVYTGALDNGNANNGIYTFGDSVTGNGTNT 650
OY 174 NGDFTVHLNGISLTDLTLTGATTVYNDVNDYDEKKAASVYKVDYLNAGMINKYKPG 233
DB 651 NALATVNV-GAGIATLEGAIVKATTKTLTN-----AASVLTITLVNAVLTDADN 699
OY 234 TTASDNDVFTYDTEVELSADTKT-----TVNV-----ESKNG-----KTEVKIGAKSVI 283
DB 700 TTGVNDVGNVLNGLALSGVTGNGTNTALATISVAGAKATLGAVITATTKTLTDNASAV 759
OY 284 KEKDGKLTG-----KDKGENDSTDKGELVTAK-----EVIDANKA-----GWRKKT 328
DB 760 TFTNPVYTGALDNTGNANNGIATFTGDSVTGNGTNTALATVNVAGLLRVGGVYKS 819
OY 329 TTAN-----GOTGQADK-----FETVT-----SGTN-----VTFAS 354
DB 820 NTILTDNASAVFTFPNPVYTGALDNGNANNGIYTFGDSVTGNGTNTALATISVGA 879
OY 355 GKGT-----TATVSKDOGNITVMTDVVNGALVNOLONGMNLDSKAAVAGSSGV 406
DB 880 GKATLGAIITATTKTLTDNASAVFTFPVYTGAI-----NNG-NANNNGIYTFGDS 933
OY 407 ISGNVSPSKMDFTVIVNANNIEI-----TRNGKNIDATSMTPPOFSVSLGAGADAP--- 461
DB 934 VTGNGTNTAL--ATVNGAGVTLQAGGSLDANNIDGARSTLEPNLGGGNAIPIYF 991
OY 462 --TLVDEGALVNGSK-----DANK-PVRITN----- 486
DB 992 KGALANGNNALITVNTKLTAYHLTIGTVAEINIGACNLFAIDASAGDVITLNMODIFR 1051
OY 487 -----VARGVEGV-----TVNAQLKGAVQNL 509
DB 1052 ALDSALVSLNLGVGNVNNILLAIDLAVAGVDEGTVEGNGVNLGNSVA---GAARNI 1108
OY 510 NN-----HIDVNGNARAGIAOIA--TAGLVQAVLPGRSM 544
DB 1109 GDVGNGKNTLLINNAVITTDVNLLEGIONVLINNADFTSTAFNAGTIO----- 1159
OY 545 AIGGTY-----RGAGYAIGYSSISDGMNIIKGTASGNSR 581
DB 1160 -INDATYITDANNGNLNPAGNIKFAHADQILIONSGNDR 1200
RESULT 12
ID OMPB_RICTY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein 4, precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scat) (OMPb)
DE (OMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].
GN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=94040787; PubMed=822486;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.;
RL Gene 133:129-133(1993).
RN [2]
```

RP PARTIAL SEQUENCE.  
 RC STRAIN-MILMINGTON;  
 RX MEDLINE-92114896; PubMed-1370573;  
 RA Ching W.M., Carl M., Dasch G.A.;  
 RT "Mapping of monoclonal antibody binding sites on CNBR fragments of  
 the S-layer protein antigens of Rickettsia typhi and Rickettsia  
 prowazekii.";  
 RL Mol. Immunol. 29:95-105(1992).  
 RN [3]  
 RP IDENTIFICATION OF CLEAVAGE SITE.  
 RX MEDLINE-92104668; PubMed-1729180;  
 RA Hackstadt T., Messer R., Cleplak W., Peacock M.G.;  
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
 membrane protein of rickettsiae: identification of an avirulent  
 mutant deficient in processing";  
 RL Infect. Immun. 60:158-165(1992).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 S-LAYER WITH HEXAGONAL SYMMETRY.  
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC  
 DR EMBL: L04661; AAB48987.1;  
 DR InterPro: IPR003858; OMPA\_rOmpB.  
 DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
 KW Antigen; S-layer; Transmembrane; Cell wall.  
 FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.  
 FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
 FT CONFLICT 657 657 H -> N (IN REF. 2).  
 FT CONFLICT 842 842 V -> I (IN REF. 2).  
 FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
 FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
 SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB1855EE CRC64;

Query Match 6.4%; Score 192.5; DB 1; Length 1645;  
 Best Local Similarity 21.5%; Pred. No. 0.027;  
 Matches 160; Conservative 80; Mismatches 258; Indels 247; Gaps 36;

OY 25 NHTKRSATVA-----TAVLATLFAVQASTTDDDD-----LYEPVOR 64  
 DB 40 NRTNAAATVDGAGFDQAGAVLPEATNSVITANSNAITFENPENGUNLSLELTANT 99  
 OY 65 TAVLSFRSDKCTGEKTEEDSMGVFPD-----KKGVLPTAGTTTLKAGDMLKIKOM 118  
 DB 100 LAVTIN-----ENTTIGFTYNTVKQGNFENFTIGACKSLITIGHGTTAQAATTKAONV 154  
 OY 119 NENTNASSFTYLSLKDLDTLTSVTEKLSFSA-----NSKNVITSDTKGLNFAKKTAE 173  
 DB 155 VSKVNGAAMIND-----NDLSGVGS--IDFTAPSVLENLINPTQEAFL-----T 199  
 OY 174 NGDTYHLNGISSTLTDLTLNTGATNTVNDNVTDEKKAASVKYVLNAGNWKVKRG 233  
 DB 200 LQGNNAKIVGANGIL-----NITNGFY-----KVSDFTEAG--IKTINIG 237  
 OY 234 TTSASDVDFRYDVEEFSADTKTTTVNESKD-----NGKRTVEKI-----GAK 279  
 DB 238 D--NOGLMNTPTDANALNLQGGGNTINENGSDGKLVLSKKNALFEFNVTGSLGN 295  
 OY 280 TSVIKERD-----GKL-----VTGKDKGENS-----STDKG-----EGLVTAKEV 315  
 DB 296 LKGVIEFDTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSDNCGNAATISGVYAKDI 355

OY 316 IDAVNKAQRMKTTTANGOT-----GOADKEFTVSGTNTVPSAGKGTATVSKD 365  
 DB 356 V-----IOSANAGGVTFEHLVDVGLGKTKTFKADSKYITTEMASFGST----- 400  
 OY 366 DQGNITVMYDVN-----VQDALNVNQLQNSGNMLDLSKAVAGSSGVYISGNVSPS-- 414  
 DB 401 DQGNLVAQIVVPNNKILTGNFTGDA-----KNGG--NTAGVIFENAGNLTGVSNTDPTN 453  
 OY 415 ----KKMDETVNI-----NAGNNIETRKNKIDITSMTPQFSSVSLGA 456  
 DB 454 VTNIKALIEGAGIVQLSGIHGAELRLGNAGSIFKFLA--DQTVINGVGNONPLVNNALAA 512  
 OY 457 GA---DAPLSDVD--EGALNVGSKD---ANKRVRTNVAAP---GVKRG----- 494  
 DB 513 GSIQLDGSALITTDIGNGAVNALQDITTLANDASKILITLGSANITANAGGAHFPANG 572  
 OY 495 -----DVTNVAOLKGVANQ-----LNHIDNVQGNAR-----AG 523  
 DB 573 TTIQLTSTQNNILVDFLDVTTDQTVGVDASSLNNQTLTINSGITANTKTILGRFNG 632  
 OY 524 IQAQITAGLV-----QAYLPKSMALIGGTYRGEAGYAIQYSSISD 566  
 DB 633 SSKTILNAGDVAINELVMENDGSVHLTHNTYLTITKTINANQCKIIVAADPINTDYLAD 692  
 OY 567 GGNWIIKGTASGNSRGHFGASASVG 591  
 DB 693 GTN--LGSASEPLSNHFTKANG 715

RESULT 13  
 OMPB\_RICCN  
 ID OMPB\_RICCN STANDARD; PRT; 1655 AA.  
 AC 09KRA3; 09KRA9; 09XC45;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (cell surface antigen 5) (Scd5) (rOmpB)  
 DE antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).  
 GN OMPB OR RC1085.  
 OS Rickettsia conorii.  
 OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae: Rickettsia.  
 OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Malish 7;  
 RX MEDLINE-21442074; PubMed-11557893;  
 RA Ogata H., Audie S., Renesto-Audiffren P., Fournier P.-E., Barde V.,  
 RA Samsom D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
 RL Science 293:2093-2098(2001).  
 RN [2]  
 RP SEQUENCE OF 33-1649 FROM N.A.  
 RC STRAIN-Indian lick typhus, and Malish 7;  
 RX MEDLINE-20393643; PubMed-10939649;  
 RA Roux V., Raoult D.;  
 RT "Phylogenetic analysis of members of the genus Rickettsia using the  
 gene coding the outer-membrane protein ompb (ompb).";  
 RL Int. J. Syst. Evol. Microbiol. 50:1445-1455(2000).  
 RN [3]  
 RP SEQUENCE OF 353-1655 FROM N.A.  
 RC STRAIN-Malish 7;  
 RA Steens J., Walker D.;  
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
 australis, the most divergent rickettsia of the spotted fever group.";  
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY

```
CC SIMILARITY)
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
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DR EMBL: AE008659; AAL03623.1; -
DR EMBL: AF123721; AAF34124.1; -
DR EMBL: AF123726; AAF34129.1; -
DR EMBL: AF149110; AAD39533.1; -
DR InterPro: IPR003858; OMPA_rCMPB.
DR Pfam: PF02708; OMPA_rCMPB; 1.
KM Antigen: S-layer; Cell wall; Complete proteome.
DR CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT CONFLICT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 6.48; Score 192.5; DB 1; Length 1655;
Best Local Similarity 22.48; Pred. NO. 0.027;
Matches 149; Conservative 78; Mismatches 283; Indels 155; Gaps 31;

QY 10 NSALNAAVASELTNRHTKRASATVATVATLLEFATVQASTDDDDLYLEPVORTAVVL 69
DB 211 NGTLN-----VANGFIKVSXSEFATVNVINIDGQIMNTDANNVTNLQANGAFI 263
QY 70 SFRSDKBSTGEKEVTEDSNMGVYFDKKGVLTAQTTLKAGNKL--IKONT----- 118
DB 264 TF-NCTDGTGR-----VLLSKNAAATDFVNTGLGKLIIEFTVAANGOLKA 313
QY 119 NENNTASSFTSLAKKDLDTLSVGEK-----LSFSANSNKV-----NTSDTKGLNF 166
DB 314 NAGNAA-----VIGNNAGRAGEVVSVDGKVAATIDGQYAKDMVTQS 359
QY 167 AKKTAETNGDTVHLNGIGSTLTDTLLTGATVTVNDVDEKKRAASYKD--VINA 223
DB 360 ANAYGVNFRIVDVGDTGTAFTAKSKVAITONSNGTDPFGMLAQIIVPNTMLNG 419
QY 224 GWNITGVKPGTTASDNDVFRFYD---TVEFLSADTKTTVN---VESKNG----- 269
DB 420 NPTGDASNPNGTAG-----VTFDANGTLASASADANVAVNNTITAIEASAGVQVLSGT 474
QY 270 KRTGVKAGKSVIKKEDKGLVTKDGENSDSPDKGGLVTAKVIDAVKAGRMKTT 329
DB 475 HAAELRLGNAGSVPEKLADGVINGR---VNQALVGLALAGATTLEG-----SA 521
QY 330 TANGOTGA-----DKFEVTV-----SGTNVTFASKGTATVATVSKDDO 367
DB 522 TITGDIGNAGAAALOGTITLANDATKITLLGANTIGANGGTINQANGGTIKLTS--TQ 579
QY 368 GNITVMVDV-----NVGDLANVNOIIONSGWNIDSKAVAGSSGKRVISGNVSPSKGM-D 419
```

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DB 580 NNIVDFDLAINDQTVADVASSLTNAQTLINKICTGVGANNNTIOPNIGSSKITVLS 639
QY 420 ETVNVN---AGNN---IEITRGNKNIDATSMTPD-----FSSV-----SLGADAPPLSV 465
DB 640 GDVAINELVIGNNAGVAFANHTVLTFTTNAGGKLIIFNVVNNNTLTATGTLGS-AT 698
QY 466 DDEGALVNGSKDANKPYRITNVAPGVKEGDTVNAQLKVAQNLNNHIIDVNG-NAKAGI 524
DB 699 NPLAINEFGSGAANVDVTLNVGKVMN-YATNTTTDA---NNGSEIFNAGGTIVSG- 753
QY 525 AQAATATGIVQ-----AVLPKSKMAIGGGYRGEGVAGVSSIDSGNMTIKGTAS 577
DB 754 -----TVGGQGGKNEFTVALDNGTTFVFLGNATFNGMTTAAAN-STIQIGGNTADEVAS 807
QY 578 GNSRG 582
DB 808 ADGTG 812

RESULT 14
WAPA_BACSU STANDARD; PRT; 2334 AA.
ID WAPA_BACSU
AC C078833
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Wall-associated protein precursor.
GN WAPA OR N17g.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93302506; PubMed=8316082;
RA Foster S.J.;
RT "Molecular analysis of three major wall-associated proteins of
RT Bacillus subtilis 168: evidence for processing of the product of a
RT gene encoding a 258 kDa precursor two-domain ligand-binding
RT 'protein'."
RL Mol. Microbiol. 8:299-310(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=95219088; PubMed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Yanai N.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RT genome containing the hut and wapa loci."
RL Microbiology 141:337-343(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97124196; PubMed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.;
RT "Molecular analysis of a 65 kb region of the Bacillus subtilis genome
RT containing the lic and cel loci, and creation of a 177 kb contig
RT covering the gnt-sacX region."
RL Microbiology 142:3113-3123(1996).
CC -1- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
CC INTO THE MEDIUM.
CC -1- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -1- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E. COLI RHS GROUP OF PROTEINS (RHS-A-D).
CC -----
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DR EMBL: L05634; AAA22883.1; -  
 DR EMBL: D31856; BAA06656.1; -  
 DR EMBL: D29985; BAA06260.1; -  
 DR EMBL: D83026; BAA11683.1; -  
 DR EMBL: Z99124; CAB15959.1; -  
 DR PIR: S32920; S32920.  
 DR Subtilist; BG10797; wapa.  
 DR Interpro: IPR003305; CBD\_6.  
 DR Pfam: PF02018; CBD\_6; 1.  
 KW Cell wall; Repeat; Signal; Complete proteome.  
 FT CHAIN 1 28 OR 32 (POTENTIAL).  
 FT DOMAIN 29 2334 WALL-ASSOCIATED PROTEIN.  
 FT REPEAT 504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 504 605 1-1.  
 FT REPEAT 769 869 1-2.  
 FT REPEAT 769 869 1-3.  
 FT DOMAIN 1021 2139 31 X 21 AA APPROXIMATE TANDEM REPEATS OF  
 FT REPEAT 1021 1040 X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).  
 FT REPEAT 1042 1061 2-2.  
 FT REPEAT 1063 1082 2-3.  
 FT REPEAT 1083 1102 2-4.  
 FT REPEAT 1109 1128 2-5.  
 FT REPEAT 1129 1148 2-6.  
 FT REPEAT 1150 1169 2-7.  
 FT REPEAT 1174 1193 2-8.  
 FT REPEAT 1199 1218 2-9.  
 FT REPEAT 1219 1238 2-10.  
 FT REPEAT 1646 1665 2-11.  
 FT REPEAT 1667 1686 2-12.  
 FT REPEAT 1690 1709 2-13.  
 FT REPEAT 1711 1730 2-14.  
 FT REPEAT 1732 1751 2-15.  
 FT REPEAT 1753 1772 2-16.  
 FT REPEAT 1795 1814 2-17.  
 FT REPEAT 1820 1839 2-18.  
 FT REPEAT 1840 1859 2-19.  
 FT REPEAT 1861 1880 2-20.  
 FT REPEAT 1887 1906 2-21.  
 FT REPEAT 1908 1927 2-22.  
 FT REPEAT 1929 1948 2-23.  
 FT REPEAT 1969 1982 2-24 (APPROXIMATE).  
 FT REPEAT 1983 2002 2-25.  
 FT REPEAT 2008 2027 2-26.  
 FT REPEAT 2028 2047 2-27.  
 FT REPEAT 2051 2070 2-28.  
 FT REPEAT 2071 2090 2-29.  
 FT REPEAT 2093 2112 2-30.  
 FT REPEAT 2120 2139 2-31.  
 SQ SEQUENCE 2334 AA; 258329 MW; B75138CD278BA3 CRC64;

Query Match 6.3%; Score 190; DB 1; Length 2334;  
 Best Local Similarity 23.6%; Pred. No. 0.054;  
 Matches 113; Conservative 65; Mismatches 156; Indels 144; Gaps 24;

OY 45 ATVOASTDDDDLYLEFPORTAVLVSRSDKEGTGEK-----EVTEDSN-----W 89  
 DB 950 AETSVISTDGCAMYID---BDATFHRTKRAKADGYOPTGVYLELTETADQFILTKTDQT 1006  
 OY 90 GYVEDKRGVLTAGITITAKADNLIKIKONTNENTMASSFTSLKDLTDLISVGEEKISFS 149  
 DB 1007 NAFENKRGKGG-----KLQKVVDGHNNAVTYTNDRKQMLAITDASGRKLFT 1052  
 OY 150 ANSKRVITSDTKGLNFAKKTAAETNGDTFVHLNGLIGSTLIDTLLNTGATTNVTNDVNTDD 209

DB 1053 YDENG-HVTSITGPKN--KKV-----TYSYENDLLAKVDT---DQTVSYDYDSGRL 1100  
 OY 210 EKKRAASVKVVLNAGMIKVKPGETA-----SDNDEVRTDYVEFLSADT 256  
 DB 1101 VKQISA-----NSTEAKPVFTFYQYSGHLEAIKANKKETTYSYSD-----ADK 1144  
 OY 257 KTTTVNESKDNKGRTEV---KIGAKTSVIREKDKLVTKDGENDS-----STDGKE 307  
 DB 1145 KTLIM---TQNGRKQYGVNENAGNPFOYIDDAEGKLITNTKREGNNVEDVDPNVGT 1201  
 OY 308 GLVTAKEVDAVNKAKRMKTTTANGOTGAADKEFYTS-----GIVVTASGKGTATV 362  
 DB 1202 GKAT-----ESYQYDKXGNTSVKADAGTE-TYEYNNKNDVTK 1238  
 OY 363 SKDDGNIT-VMDYVNGDALNVQNLNDSGMNLDKRAVSSSGVTSIGNVSPSG-KMDE 420  
 DB 1239 MKDTGAVTDIAYD-----GDAVSETDQSGKSSAAVYDKXGNQIS 1281  
 OY 421 TVNINAGNIEITPENGKNIDATSMTPQFSSVIGAGADAPTLSV--DDEGALNVGSK 476  
 DB 1282 SKDISASTN--ILKDG-----SFEAKSGMNLASKDRKRKISVADKSGVLS-GSK 1329

RESULT 15  
 YPJA\_ECOLI STANDARD; PRT; 1569 AA.  
 ID YPJA\_ECOLI  
 AC P52143; P76610; P77017; P77019;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical outer membrane protein yjyA.  
 GN YPJA OR B2647.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_Taxid=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yamagata S., Horiiuchi T.;  
 RT Construction of a contiguous 874-kb sequence of the Escherichia coli  
 RT - K12 genome corresponding to 50,000-68,8 min on the linkage map and  
 RT analysis of its sequence features";  
 RL DNA Res. 4:91-113(1997).  
 CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).  
 CC -1- SIMILARITY: STRONG TO BORDETELLA PERTACTIN.  
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DR EMBL: U36840; AAA79815.1; ALT\_SEQ.  
 DR EMBL: AE000350; AAC75695.1; -.

